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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:06:22 ; Search time 7.91209 Seconds
(without alignments)
141.522 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VFPSVAKSVKSLVIG 15

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	678	1	US-08-282-141-2
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3	72	100.0	678	1	US-08-435-436-2
4	72	100.0	678	2	US-08-438-863-2
5	72	100.0	678	2	US-08-438-864-2
6	72	100.0	678	3	US-08-438-862-2
7	72	100.0	678	3	US-08-438-863-2
8	72	100.0	678	3	US-08-402-253-2
9	72	100.0	678	3	US-08-443-866B-2
10	69	95.8	673	1	US-08-282-141-3
11	69	95.8	673	1	US-08-435-434-1
12	69	95.8	673	1	US-08-435-436-1
13	69	95.8	673	2	US-08-438-863-1
14	69	95.8	673	2	US-08-438-864-1
15	69	95.8	673	3	US-08-438-862-1
16	69	95.8	673	3	US-08-402-253-1
17	69	95.8	673	3	US-08-443-866B-1
18	69	95.8	673	3	US-09-107-532A-4410
19	44	61.1	77	4	US-09-721-870-24
20	44	61.1	374	4	US-09-270-767-60047
21	42	58.3	186	4	US-08-843-530B-36
22	42	58.3	1220	2	US-09-636-728-32
23	42	58.3	1220	4	US-09-248-796A-15046
24	41	56.9	292	4	US-08-416-603-4
25	41	56.9	3457	2	US-08-416-603-4
26	39	54.2	99	4	US-09-248-796A-18222
27	39	54.2	369	4	US-09-519-232-74

28	37	51.4	169	4	US-09-270-767-60047	Sequence 60047, A
29	37	51.4	224	4	US-09-270-767-44600	Sequence 44600, A
30	37	51.4	266	4	US-09-489-039A-8199	Sequence 8199, A
31	37	51.4	316	4	US-09-107-532A-5019	Sequence 5019, A
32	37	51.4	334	1	US-08-118-270-22	Sequence 22, Appl
33	37	51.4	334	5	PCT-US93-08528-22	Sequence 22, Appl
34	37	51.4	729	4	US-09-248-796A-17702	Sequence 17702, A
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36	36	50.0	12	3	US-09-185-501B-6	Sequence 6, Appl
37	36	50.0	74	4	US-09-489-039A-8829	Sequence 8829, A
38	36	50.0	207	3	US-09-185-501B-14	Sequence 14, Appl
39	36	50.0	297	3	US-09-632-947B-4	Sequence 4, Appl
40	36	50.0	551	3	US-09-503-391-2	Sequence 2, Appl
41	36	50.0	551	3	US-09-503-391-2	Sequence 2, Appl
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43	35	48.6	148	4	US-09-902-540-13147	Sequence 13147, A
44	35	48.6	279	4	US-09-252-991A-32921	Sequence 32921, A
45	35	48.6	303	4	US-09-328-352-4879	Sequence 4879, A
46	35	48.6	332	4	US-09-489-039A-7261	Sequence 7261, A
47	35	48.6	379	1	US-08-121-714-4	Sequence 4, Appl
48	35	48.6	379	1	US-08-477-108A-4	Sequence 4, Appl
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51	35	48.6	386	4	US-09-328-352-7556	Sequence 7556, A
52	35	48.6	391	5	PCT-US91-08177-3	Sequence 3, Appl
53	35	48.6	396	4	US-09-567-458A-5	Sequence 5, Appl
54	35	48.6	413	4	US-09-543-681A-6252	Sequence 6252, A
55	35	48.6	445	4	US-09-252-991A-24335	Sequence 24335, A
56	35	48.6	452	4	US-09-530-836-6	Sequence 6, Appl
57	35	48.6	452	4	US-09-530-838-2	Sequence 2, Appl
58	35	48.6	460	4	US-09-252-991A-19007	Sequence 19007, A
59	35	48.6	465	4	US-09-328-352-6141	Sequence 6141, A
60	35	48.6	469	4	US-09-538-092-416	Sequence 416, App
61	35	48.6	606	4	US-09-134-000C-4093	Sequence 4093, A
62	35	48.6	922	4	US-09-248-796A-18806	Sequence 18806, A
63	34.5	47.9	335	3	US-09-247-155-176	Sequence 176, App
64	34.5	47.9	346	4	US-09-540-236-2411	Sequence 2411, A
65	34.5	47.9	348	3	US-09-286-803-2	Sequence 2, Appl
66	34.5	47.9	350	4	US-09-800-729-91	Sequence 91, Appl
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68	34	47.2	72	4	US-09-134-000C-6242	Sequence 6242, A
69	34	47.2	72	4	US-09-248-796A-27413	Sequence 27413, A
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76	34	47.2	267	3	US-09-290-602-4	Sequence 4, Appl
77	34	47.2	291	4	US-09-248-796A-20693	Sequence 20693, A
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83	34	47.2	335	3	US-08-961-083-110	Sequence 110, App
84	34	47.2	335	4	US-09-536-784-110	Sequence 110, App
85	34	47.2	358	4	US-09-270-767-44738	Sequence 44738, A
86	34	47.2	371	4	US-09-583-110-3815	Sequence 3815, A
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106	34	47.2	547	4	US-09-583-110-3718	Sequence 3718, Ap	179	33	45.8	282	4	US-09-985-442-7	Sequence 7, Appli
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115	34	47.2	764	3	US-09-184-937-2	Sequence 2, Appli	188	33	45.8	321	4	US-09-252-991A-29420	Sequence 29420, A
116	34	47.2	790	4	US-09-949-016-11220	Sequence 11220, A	189	33	45.8	332	4	US-09-248-796A-18170	Sequence 18170, A
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122	33.5	46.5	343	2	US-08-788-539A-2	Sequence 2, Appli	195	33	45.8	354	4	US-09-949-016-7936	Sequence 7936, Ap
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124	124	33	45.8	27	US-08-218-369-4	Sequence 4, Appli	197	33	45.8	357	4	US-09-710-279-410	Sequence 410, App
125	33	45.8	27	4	US-09-304-599A-4	Sequence 4, Appli	198	33	45.8	357	4	US-09-270-767-42662	Sequence 42662, A
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127	127	33	45.8	57	US-09-621-976-5488	Sequence 5488, Ap	200	33	45.8	362	4	US-09-875-114-1	Sequence 1, Appli
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144	33	45.8	125	2	US-08-665-202-57	Sequence 57, Appl	217	33	45.8	389	4	US-09-248-796A-17443	Sequence 17443, A
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256	33	45.8	2133	4	US-09-523-656-30	Sequence 30, Appl	329	32	44.4	394	1	US-07-603-133B-11	Sequence 11, Appl
257	32.5	45.1	314	3	US-08-927-219-6	Sequence 6, Appli	330	32	44.4	395	3	US-09-088-216-2	Sequence 2, Appli
258	32.5	45.1	314	4	US-09-710-099-4	Sequence 4, Appli	331	32	44.4	395	3	US-09-088-216-2	Sequence 4, Appli
259	32.5	45.1	314	4	US-09-710-099-12	Sequence 12, Appl	332	32	44.4	400	4	US-09-889-746-2	Sequence 2, Appli
260	32.5	45.1	314	4	US-10-200-910-4	Sequence 4, Appli	333	32	44.4	405	1	US-08-121-714-7	Sequence 7, Appli
261	32.5	45.1	314	4	US-10-200-910-12	Sequence 12, Appl	334	32	44.4	405	1	US-08-477-108A-7	Sequence 7, Appli
262	32.5	45.1	351	4	US-09-710-099-2	Sequence 2, Appli	335	32	44.4	405	1	US-08-477-112-7	Sequence 7, Appli
263	32.5	45.1	351	4	US-09-710-099-10	Sequence 10, Appl	336	32	44.4	405	5	PCT-US93-08322-7	Sequence 7, Appli
264	32.5	45.1	351	4	US-10-200-910-2	Sequence 2, Appli	337	32	44.4	415	1	US-07-911-531-19	Sequence 19, Appl
265	32.5	45.1	351	4	US-10-200-910-10	Sequence 10, Appl	338	32	44.4	415	1	US-07-693-636A-19	Sequence 19, Appl
266	32.5	45.1	399	4	US-09-710-099-8	Sequence 8, Appli	339	32	44.4	415	1	US-07-768-286B-2	Sequence 2, Appli
267	32.5	45.1	399	4	US-10-200-910-8	Sequence 8, Appli	340	32	44.4	415	3	US-09-026-408-4	Sequence 4, Appli
268	32.5	45.1	415	3	US-08-927-219-8	Sequence 8, Appli	341	32	44.4	415	4	US-09-902-684-4	Sequence 4, Appli
269	32.5	45.1	436	4	US-09-710-099-6	Sequence 6, Appli	342	32	44.4	417	4	US-09-252-991A-25870	Sequence 25870, A
270	32.5	45.1	436	4	US-10-200-910-6	Sequence 6, Appli	343	32	44.4	434	1	US-07-679-052A-15	Sequence 15, Appl
271	32.5	45.1	630	3	US-08-927-219-2	Sequence 2, Appli	344	32	44.4	436	3	US-09-150-213-4	Sequence 4, Appli
272	32.5	45.1	630	3	US-08-927-219-4	Sequence 4, Appli	345	32	44.4	436	4	US-09-328-352-6067	Sequence 6067, Ap
273	32.5	45.1	631	3	US-08-927-219-127	Sequence 127, App	346	32	44.4	438	1	US-07-679-052A-17	Sequence 17, Appl
274	32.5	45.1	670	2	US-08-473-750-11	Sequence 11, Appl	347	32	44.4	444	4	US-09-107-532A-4848	Sequence 4848, Ap
275	32.5	45.1	670	2	US-08-477-326-11	Sequence 11, Appl	348	32	44.4	447	4	US-09-270-767-45673	Sequence 45673, A
276	32.5	45.1	949	4	US-10-164-595-65	Sequence 65, Appl	349	32	44.4	457	4	US-09-270-767-44881	Sequence 44881, A
277	32.5	45.1	1214	4	US-10-164-595-24	Sequence 24, Appl	350	32	44.4	462	4	US-09-252-991A-31372	Sequence 31372, A
278	32	44.4	20	4	US-09-157-689-31	Sequence 31, Appl	351	32	44.4	471	4	US-09-325-256-26	Sequence 26, Appl
279	32	44.4	20	4	US-08-447-398-31	Sequence 31, Appl	352	32	44.4	471	4	US-09-704-917-20	Sequence 20, Appl
280	32	44.4	20	4	US-09-953-510-31	Sequence 31, Appl	353	32	44.4	471	4	US-09-151-999-20	Sequence 20, Appl
281	32	44.4	28	4	US-09-270-767-58413	Sequence 58413, A	354	32	44.4	471	4	US-09-418-212-18	Sequence 18, Appl
282	32	44.4	85	4	US-09-732-210-1119	Sequence 1119, Ap	355	32	44.4	485	3	US-09-384-212-2	Sequence 2, Appli
283	32	44.4	85	4	US-09-621-976-6425	Sequence 6425, Ap	356	32	44.4	500	1	US-07-755-573C-8	Sequence 8, Appli
284	32	44.4	86	4	US-09-543-681A-8300	Sequence 8300, Ap	357	32	44.4	500	4	US-09-519-878-2	Sequence 2, Appli
285	32	44.4	91	4	US-09-513-999C-4169	Sequence 4169, Ap	358	32	44.4	504	4	US-09-519-878-4	Sequence 4, Appli
286	32	44.4	115	4	US-09-543-681A-7586	Sequence 7586, Ap	359	32	44.4	520	4	US-09-949-016-10586	Sequence 10586, A
287	32	44.4	133	4	US-09-270-767-34410	Sequence 34410, A	360	32	44.4	524	4	US-09-248-796A-20256	Sequence 20256, A
288	32	44.4	133	4	US-09-270-767-49627	Sequence 49627, A	361	32	44.4	540	4	US-09-513-057C-33	Sequence 33, Appl
289	32	44.4	134	4	US-09-270-767-60852	Sequence 60852, A	362	32	44.4	540	4	US-09-746-801A-33	Sequence 33, Appl
290	32	44.4	140	4	US-09-270-767-38333	Sequence 38333, A	363	32	44.4	563	4	US-08-311-731A-142	Sequence 142, App
291	32	44.4	140	4	US-09-270-767-53750	Sequence 53750, A	364	32	44.4	567	3	US-09-347-878-42	Sequence 42, Appl
292	32	44.4	142	4	US-09-248-796A-15418	Sequence 15418, A	365	32	44.4	591	4	US-09-519-232-66	Sequence 66, Appl
293	32	44.4	146	3	US-09-373-750-3	Sequence 3, Appli	366	32	44.4	597	4	US-09-252-991A-32073	Sequence 32073, A
294	32	44.4	146	3	US-09-373-750-4	Sequence 4, Appli	367	32	44.4	615	4	US-09-898-165B-7	Sequence 7, Appli
295	32	44.4	158	4	US-09-270-767-31923	Sequence 31923, A	368	32	44.4	619	4	US-09-786-240-6	Sequence 6, Appli
296	32	44.4	158	4	US-09-270-767-47140	Sequence 47140, A	369	32	44.4	628	4	US-09-602-787A-550	Sequence 550, App
297	32	44.4	172	4	US-09-270-767-43079	Sequence 43079, A	370	32	44.4	628	4	US-09-602-787A-666	Sequence 666, App
298	32	44.4	189	4	US-09-270-767-61188	Sequence 61188, A	371	32	44.4	641	4	US-09-949-016-7796	Sequence 7796, Ap
299	32	44.4	201	4	US-09-902-540-12974	Sequence 12974, A	372	32	44.4	649	4	US-09-270-767-61886	Sequence 61886, A
300	32	44.4	202	4	US-09-248-796A-25290	Sequence 25290, A	373	32	44.4	664	4	US-09-328-352-6193	Sequence 6193, Ap
301	32	44.4	218	4	US-09-107-433-3813	Sequence 3813, Ap	374	32	44.4	682	1	US-07-998-003A-107	Sequence 107, App
302	32	44.4	233	4	US-09-270-767-45122	Sequence 45122, A	375	32	44.4	682	1	US-08-453-274B-107	Sequence 107, App
303	32	44.4	245	4	US-09-248-796A-17097	Sequence 17097, A	376	32	44.4	682	1	US-08-453-695A-107	Sequence 107, App
304	32	44.4	256	4	US-09-270-767-42933	Sequence 42933, A	377	32	44.4	682	1	US-08-268-161A-107	Sequence 107, App
305	32	44.4	257	4	US-09-543-681A-4193	Sequence 4193, Ap	378	32	44.4	682	2	US-08-453-702A-107	Sequence 107, App
306	32	44.4	259	2	US-08-808-550-39	Sequence 39, Appl	379	32	44.4	682	3	US-09-099-639-107	Sequence 107, App
307	32	44.4	265	4	US-09-134-000C-5847	Sequence 5847, Ap	380	32	44.4	682	5	PCT-US93-12588-107	Sequence 107, App
308	32	44.4	294	4	US-09-248-796A-20697	Sequence 20697, A	381	32	44.4	682	5	PCT-US95-08071-107	Sequence 107, App
309	32	44.4	296	4	US-09-540-236-2650	Sequence 2650, Ap	382	32	44.4	725	4	US-09-540-236-2026	Sequence 2026, Ap
310	32	44.4	298	4	US-09-252-991A-20712	Sequence 20712, A	383	32	44.4	789	1	US-08-431-080-20	Sequence 20, Appl
311	32	44.4	308	4	US-09-328-352-8155	Sequence 8155, Ap	384	32	44.4	789	2	US-08-938-534-20	Sequence 20, Appl
312	32	44.4	309	1	US-08-729-202-1	Sequence 1, Appli	385	32	44.4	789	3	US-09-345-294-20	Sequence 20, Appl
313	32	44.4	309	1	US-08-896-371-1	Sequence 1, Appli	386	32	44.4	828	4	US-09-540-236-3107	Sequence 3107, Ap
314	32	44.4	327	4	US-09-134-000C-4685	Sequence 4685, Ap	387	32	44.4	836	1	US-07-998-003A-105	Sequence 105, App
315	32	44.4	354	1	US-08-753-233-2	Sequence 2, Appli	388	32	44.4	836	1	US-08-453-274B-105	Sequence 105, App
316	32	44.4	354	1	US-08-984-246-2	Sequence 2, Appli	389	32	44.4	836	1	US-08-453-695A-105	Sequence 105, App
317	32	44.4	354	2	US-09-149-674-2	Sequence 2, Appli	390	32	44.4	836	1	US-08-268-161A-105	Sequence 105, App
318	32	44.4	364	4	US-09-270-767-46731	Sequence 46731, A	391	32	44.4	836	2	US-08-453-702A-105	Sequence 105, App
319	32	44.4	372	1	US-08-753-233-3	Sequence 3, Appli	392	32	44.4	836	3	US-09-099-639-105	Sequence 105, App

393	32	44.4	836	5	PCT-US93-12588-105	Sequence 105, App	466	31	43.1	265	4	US-09-543-681A-5083	Sequence 5083, Ap
394	32	44.4	836	5	PCT-US95-08071-105	Sequence 105, App	467	31	43.1	266	4	US-09-489-039A-7484	Sequence 7484, Ap
395	32	44.4	904	1	US-07-998-003A-97	Sequence 97, Appl	468	31	43.1	268	4	US-09-248-796A-19955	Sequence 19955, A
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397	32	44.4	904	1	US-08-453-695A-97	Sequence 97, Appl	471	31	43.1	281	4	US-09-543-681A-6233	Sequence 6233, Ap
398	32	44.4	904	1	US-08-268-163A-97	Sequence 97, Appl	471	31	43.1	281	4	US-09-543-681A-6233	Sequence 10, Appl
399	32	44.4	904	2	US-08-453-702A-97	Sequence 97, Appl	471	31	43.1	309	4	US-09-252-991A-25953	Sequence 25953, A
400	32	44.4	904	2	US-09-099-639-97	Sequence 97, Appl	473	31	43.1	317	4	US-09-540-236-3830	Sequence 3830, Ap
401	32	44.4	904	5	PCT-US93-12588-97	Sequence 97, Appl	474	31	43.1	320	4	US-09-489-039A-13989	Sequence 13989, A
402	32	44.4	904	5	PCT-US95-08071-97	Sequence 97, Appl	475	31	43.1	330	4	US-09-489-039A-12859	Sequence 12859, A
403	32	44.4	910	3	US-09-228-986-72	Sequence 72, Appl	476	31	43.1	332	4	US-09-949-016-10159	Sequence 10159, A
404	32	44.4	910	4	US-10-101-464A-72	Sequence 72, Appl	477	31	43.1	338	4	US-09-252-991A-28498	Sequence 28498, A
405	32	44.4	932	4	US-09-949-016-8989	Sequence 8989, Ap	478	31	43.1	342	4	US-09-107-532A-4845	Sequence 4845, Ap
406	32	44.4	934	4	US-09-949-016-6242	Sequence 6242, Ap	479	31	43.1	361	4	US-09-902-540-12257	Sequence 12257, A
407	32	44.4	941	4	US-09-949-016-10983	Sequence 10983, A	480	31	43.1	362	2	US-08-290-731C-15	Sequence 15, Appl
408	32	44.4	941	4	US-09-949-016-10984	Sequence 10984, A	481	31	43.1	365	4	US-09-248-796A-20907	Sequence 20907, A
409	32	44.4	941	4	US-09-949-016-10985	Sequence 10985, A	482	31	43.1	371	3	US-09-382-155-22	Sequence 22, Appl
410	32	44.4	982	4	US-09-023-905A-7	Sequence 7, Appl1	483	31	43.1	371	3	US-09-074-044A-22	Sequence 22, Appl
411	32	44.4	1005	4	US-09-134-000C-6322	Sequence 6322, Ap	484	31	43.1	376	4	US-09-564-954-2	Sequence 2, Appl1
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413	32	44.4	1205	4	US-09-949-016-9041	Sequence 9041, Ap	485	31	43.1	385	4	US-09-380-287A-2	Sequence 2, Appl1
414	32	44.4	1505	4	US-09-538-092-1102	Sequence 1102, Ap	487	31	43.1	395	4	US-09-459-133-2	Sequence 2, Appl1
415	32	44.4	1693	4	US-09-560-385A-4	Sequence 4, Appl1	488	31	43.1	405	4	US-09-603-208A-262	Sequence 262, App
416	32	44.4	1693	4	US-09-560-385A-8	Sequence 8, Appl1	489	31	43.1	412	3	US-09-134-001C-4885	Sequence 4885, Ap
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418	32	44.4	1713	4	US-09-560-385A-6	Sequence 6, Appl1	491	31	43.1	424	2	US-09-165-234-9	Sequence 9, Appl1
419	32	44.4	1713	4	US-09-538-092-1359	Sequence 1359, Ap	492	31	43.1	424	3	US-09-274-570-9	Sequence 1317, Ap
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421	32	44.4	1724	4	US-09-560-385A-2	Sequence 2, Appl1	494	31	43.1	433	4	US-09-380-287A-6	Sequence 4, Appl1
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427	31.5	43.8	510	4	US-09-121-211-16	Sequence 16, Appl	500	31	43.1	465	4	US-09-270-767-37268	Sequence 37268, A
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429	31	43.1	36	1	US-08-139-862-6	Sequence 6, Appl1	502	31	43.1	484	4	US-09-902-540-11231	Sequence 11231, A
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432	31	43.1	72	4	US-09-270-767-41152	Sequence 41152, A	505	31	43.1	518	4	US-09-198-452A-172	Sequence 172, App
433	31	43.1	72	4	US-09-270-767-56368	Sequence 56368, A	506	31	43.1	518	4	US-09-438-185A-153	Sequence 153, App
434	31	43.1	88	4	US-09-726-219A-172	Sequence 172, App	507	31	43.1	529	4	US-09-902-540-15802	Sequence 15802, A
435	31	43.1	95	4	US-09-153-447-31	Sequence 31, Appl	508	31	43.1	555	4	US-09-134-000C-3906	Sequence 3906, Ap
436	31	43.1	106	4	US-09-270-767-58711	Sequence 58711, A	509	31	43.1	556	4	US-09-134-000C-5850	Sequence 5850, Ap
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438	31	43.1	110	4	US-09-248-796A-22555	Sequence 22555, A	511	31	43.1	568	4	US-09-248-796A-20839	Sequence 20839, A
439	31	43.1	124	3	US-08-905-223-343	Sequence 343, App	512	31	43.1	590	4	US-09-248-796A-20379	Sequence 20379, A
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441	31	43.1	125	4	US-09-543-681A-7941	Sequence 7941, Ap	514	31	43.1	616	1	US-08-453-695A-115	Sequence 115, App
442	31	43.1	127	4	US-09-252-991A-28758	Sequence 28758, A	515	31	43.1	616	2	US-08-268-161A-115	Sequence 115, App
443	31	43.1	141	4	US-09-732-210-789	Sequence 789, App	516	31	43.1	616	3	US-08-453-702A-115	Sequence 115, App
444	31	43.1	142	4	US-09-732-210-786	Sequence 786, App	517	31	43.1	616	5	PCT-US95-08071-115	Sequence 115, App
445	31	43.1	144	4	US-09-328-352-7108	Sequence 7108, Ap	518	31	43.1	653	4	US-09-438-185A-730	Sequence 730, App
446	31	43.1	155	4	US-09-134-000C-3920	Sequence 3920, Ap	519	31	43.1	660	4	US-09-902-540-10693	Sequence 10693, A
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448	31	43.1	157	4	US-09-270-767-52975	Sequence 52975, A	521	31	43.1	676	4	US-09-252-991A-24713	Sequence 24713, A
449	31	43.1	157	4	US-10-101-464A-788	Sequence 788, App	522	31	43.1	676	4	US-09-107-532A-6028	Sequence 6028, Ap
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453	31	43.1	195	4	US-09-248-796A-14170	Sequence 14170, A	526	31	43.1	724	1	US-08-835-268-62	Sequence 62, Appl
454	31	43.1	207	2	US-08-793-229-30	Sequence 30, Appl	527	31	43.1	724	2	US-09-060-692-62	Sequence 62, Appl
455	31	43.1	207	3	US-09-285-957-30	Sequence 30, Appl	528	31	43.1	724	2	US-08-833-391-62	Sequence 62, Appl
456	31	43.1	208	3	US-09-134-001C-4007	Sequence 4007, Ap	529	31	43.1	724	3	US-09-060-610-62	Sequence 62, Appl
457	31	43.1	215	4	US-09-270-767-43363	Sequence 43363, A	530	31	43.1	724	5	PCT-US94-10151A-62	Sequence 62, Appl
458	31	43.1	216	4	US-09-540-236-2124	Sequence 2124, Ap	531	31	43.1	727	3	US-09-134-001C-4067	Sequence 4067, Ap
459	31	43.1	219	4	US-09-270-767-46282	Sequence 46282, A	532	31	43.1	792	4	US-09-645-835A-4	Sequence 4, Appl1
460	31	43.1	223	4	US-10-112-802-4	Sequence 4, Appl1	533	31	43.1	792	2	US-08-223-617A-8	Sequence 8, Appl1
461	31	43.1	228	4	US-09-710-279-2936	Sequence 2936, Ap	534	31	43.1	823	4	US-09-252-991A-21027	Sequence 21027, A
462	31	43.1	228	4	US-09-710-279-3196	Sequence 3196, Ap	535	31	43.1	857	4	US-09-107-532A-4201	Sequence 4201, Ap
463	31	43.1	228	4	US-09-538-092-360	Sequence 360, App	536	31	43.1	884	4	US-09-741-150-4	Sequence 4, Appl1
464	31	43.1	233	3	US-09-134-001C-3643	Sequence 3643, Ap	537	31	43.1	884	4	US-10-160-187-4	Sequence 4, Appl1
465	31	43.1	246	4	US-09-248-796A-15053	Sequence 15053, A	538	31	43.1	884	4		

539	31	43.1	932	4	US-09-949-016-8990	Sequence 8990, Ap	612	30	41.7	179	6	5463025-4	Patent No. 5463025
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547	31	43.1	1180	4	US-09-543-681A-6436	Sequence 6436, Ap	620	30	41.7	218	3	US-09-650-855-105	Sequence 105, App
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549	31	43.1	1734	4	US-09-724-126A-19	Sequence 19, Appl	622	30	41.7	220	1	US-08-107-755A-11	Sequence 11, Appl
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555	31	43.1	2595	3	US-09-603-207-2	Sequence 2, Appli	628	30	41.7	240	4	US-09-270-767-42421	Sequence 42421, A
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573	30.5	42.4	617	4	US-09-198-452A-155	Sequence 155, App	646	30	41.7	304	4	US-09-248-796A-19355	Sequence 19355, A
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576	30.5	42.4	1897	4	US-09-792-024-98	Sequence 98, Appl	649	30	41.7	312	3	US-09-171-517B-11	Sequence 11, Appl
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578	30.5	42.4	3712	2	US-08-222-617A-4	Sequence 4, Appli	651	30	41.7	313	2	US-08-671-320-15	Sequence 15, Appl
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582	30	41.7	36	4	US-09-721-456-143	Sequence 143, App	655	30	41.7	314	3	US-09-171-517B-9	Sequence 9, Appli
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588	30	41.7	66	3	US-09-328-352-7355	Sequence 7355, Ap	661	30	41.7	333	1	US-08-309-985-2	Sequence 2, Appli
589	30	41.7	72	4	US-09-270-767-40827	Sequence 40827, A	662	30	41.7	338	4	US-09-252-991A-31928	Sequence 31928, A
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594	30	41.7	103	4	US-08-899-330-11	Sequence 11, Appl	667	30	41.7	354	1	US-07-868-353A-13	Sequence 13, Appl
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606	30	41.7	152	4	US-09-270-767-37006	Sequence 37006, A	679	30	41.7	364	4	US-09-949-016-9994	Sequence 9994, Ap
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608	30	41.7	164	4	US-09-302-540-15953	Sequence 15953, A	681	30	41.7	366	4	US-09-755-630B-251	Sequence 251, App
609	30	41.7	168	4	US-09-198-452A-431	Sequence 431, App	682	30	41.7	366	4	US-09-755-630B-255	Sequence 255, App
610	30	41.7	176	4	US-09-248-796A-20480	Sequence 20480, A	683	30	41.7	366	4	US-09-755-630B-259	Sequence 259, App
611	30	41.7	179	4	US-09-248-796A-22488	Sequence 22488, A	684	30	41.7	366	4	US-09-755-630B-263	Sequence 263, App

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686	30	41.7	366	4	US-09-755-274-23	Sequence 23, Appl	759	30	41.7	461	4	US-09-866-570B-70	Sequence 70, Appl
687	30	41.7	366	4	US-09-755-274-25	Sequence 25, Appl	760	30	41.7	464	6	5463025-1	Patent No. 5463025
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711	30	41.7	384	4	US-09-248-796A-18614	Sequence 18614, A	783	30	41.7	498	2	US-08-357-598-9	Sequence 9, Appli
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714	30	41.7	386	4	US-09-755-630B-285	Sequence 285, App	786	30	41.7	509	4	US-09-252-991A-28680	Sequence 28680, A
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716	30	41.7	386	4	US-09-755-630B-279	Sequence 279, App	788	30	41.7	517	4	US-09-540-236-2403	Sequence 2403, Ap
717	30	41.7	386	4	US-09-755-630B-282	Sequence 282, App	789	30	41.7	523	4	US-09-328-352-4880	Sequence 4880, Ap
718	30	41.7	386	4	US-09-755-630B-286	Sequence 286, App	790	30	41.7	524	4	US-09-265-585C-35	Sequence 35, Appl
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721	30	41.7	386	4	US-09-755-274-5	Sequence 5, Appli	793	30	41.7	552	4	US-09-356-643B-11	Sequence 11, Appl
722	30	41.7	386	4	US-09-755-274-6	Sequence 6, Appli	794	30	41.7	552	4	US-10-053-510-11	Sequence 11, Appl
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725	30	41.7	389	4	US-09-755-630B-275	Sequence 271, App	797	30	41.7	562	3	US-08-854-050-5	Sequence 5, Appli
726	30	41.7	389	4	US-09-755-630B-233	Sequence 33, Appl	798	30	41.7	562	3	US-09-430-323-5	Sequence 5, Appli
727	30	41.7	389	4	US-09-755-274-33	Sequence 35, Appl	799	30	41.7	562	4	US-09-766-253-5	Sequence 5, Appli
728	30	41.7	392	4	US-09-755-274-33	Sequence 35, Appl	800	30	41.7	574	4	US-09-902-540-10370	Sequence 10370, A
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731	30	41.7	393	4	US-09-248-796A-16393	Sequence 16393, A	803	30	41.7	588	4	US-09-538-092-1040	Sequence 1040, Ap
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735	30	41.7	413	4	US-09-491-577-72	Sequence 72, Appli	807	30	41.7	602	4	US-09-410-416-3	Sequence 3, Appli
736	30	41.7	420	4	US-09-252-991A-30038	Sequence 30038, A	808	30	41.7	602	4	US-09-949-016-7417	Sequence 7417, Ap
737	30	41.7	431	4	US-09-103-331-39	Sequence 39, Appl	809	30	41.7	602	4	US-09-949-016-7418	Sequence 7418, Ap
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743	30	41.7	444	4	US-08-374-009-15	Sequence 15, Appl	815	30	41.7	624	4	US-09-949-016-7339	Sequence 7339, Ap
744	30	41.7	444	4	US-09-191-724-15	Sequence 15, Appl	816	30	41.7	625	4	US-09-538-092-1064	Sequence 1064, Ap
745	30	41.7	444	4	US-09-631-603-11	Sequence 11, Appl	817	30	41.7	625	4	US-09-949-016-6671	Sequence 6671, Ap
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747	30	41.7	447	4	US-09-107-532A-6751	Sequence 6751, Ap	819	30	41.7	638	4	US-09-902-540-11575	Sequence 11575, A
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750	30	41.7	451	4	US-09-583-110-3695	Sequence 3695, Ap	822	30	41.7	655	3	US-09-228-986-70	Sequence 70, Appl
751	30	41.7	451	4	US-09-248-796A-19526	Sequence 19526, A	823	30	41.7	655	4	US-09-242-435-2	Sequence 2, Appli
752	30	41.7	452	4	US-09-755-630B-6	Sequence 6, Appli	824	30	41.7	655	4	US-10-101-464A-70	Sequence 70, Appl
753	30	41.7	452	4	US-09-755-274-40	Sequence 40, Appl	825	30	41.7	660	4	US-09-462-606-51	Sequence 51, Appl
754	30	41.7	453	4	US-09-489-039A-8916	Sequence 8916, Ap	826	30	41.7	660	4	US-09-907-794A-28	Sequence 28, Appl
755	30	41.7	456	4	US-09-543-681A-6828	Sequence 6828, Ap	827	30	41.7	660	4	US-09-905-125A-28	Sequence 28, Appl
756	30	41.7	461	3	US-09-457-046B-70	Sequence 70, Appl	828	30	41.7	660	4	US-09-902-775A-28	Sequence 28, Appl
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833	30	41.7	660	4	US-09-909-064-28	Sequence 28, Appl	906	30	41.7	4302	3	US-09-052-469-8	Sequence 8, Appli
834	30	41.7	660	4	US-09-905-381A-28	Sequence 28, Appl	907	30	41.7	4302	4	US-08-422-583-8	Sequence 8, Appli
835	30	41.7	660	4	US-09-906-618-28	Sequence 28, Appl	908	30	41.7	4302	4	US-09-052-263-8	Sequence 8, Appli
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837	30	41.7	683	4	US-09-949-016-7267	Sequence 7267, Ap	910	30	41.7	4303	4	US-09-479-467A-2	Sequence 2, Appli
838	30	41.7	687	4	US-09-248-796A-18468	Sequence 18468, A	911	30	41.7	4339	3	US-09-052-469-6	Sequence 6, Appli
839	30	41.7	691	4	US-09-949-016-8255	Sequence 8255, Ap	912	30	41.7	4339	4	US-08-422-582-6	Sequence 6, Appli
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841	30	41.7	713	4	US-09-538-092-1022	Sequence 1022, Ap	914	30	41.7	4654	3	US-08-476-515A-84	Sequence 84, Appl
842	30	41.7	713	4	US-09-949-016-6214	Sequence 6214, Ap	915	30	41.7	4655	3	US-08-652-877-84	Sequence 84, Appl
843	30	41.7	714	4	US-09-792-024-117	Sequence 117, App	916	30	41.7	4655	3	US-08-652-877-86	Sequence 86, Appl
844	30	41.7	722	4	US-09-984-890-4	Sequence 4, Appli	917	30	41.7	4655	3	US-08-652-877-88	Sequence 88, Appl
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846	30	41.7	722	4	US-10-274-194-4	Sequence 4, Appli	919	29.5	41.0	70	4	US-09-621-976-4825	Sequence 7284, Ap
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852	30	41.7	726	3	US-09-517-605-6	Sequence 6, Appli	925	29.5	41.0	403	3	US-09-222-851-4	Sequence 4, Appli
853	30	41.7	729	2	US-08-677-298-2	Sequence 2, Appli	926	29.5	41.0	450	1	US-08-194-338-5	Sequence 5, Appli
854	30	41.7	729	4	US-09-523-849-33	Sequence 33, Appl	927	29.5	41.0	450	1	US-08-196-989B-11	Sequence 11, Appl
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857	30	41.7	743	4	US-09-489-847-168	Sequence 168, App	930	29.5	41.0	450	2	US-09-225-024-11	Sequence 11, Appl
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864	30	41.7	793	4	US-09-523-849-32	Sequence 32, Appl	937	29	40.3	44	1	US-08-118-270-287	Sequence 287, App
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866	30	41.7	815	3	US-09-134-001C-3614	Sequence 3614, Ap	939	29	40.3	44	5	PCT-US93-08528-287	Sequence 287, App
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869	30	41.7	921	4	US-09-889-572-4	Sequence 4, Appli	942	29	40.3	48	5	PCT-US93-08528-288	Sequence 288, App
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873	30	41.7	1074	4	US-09-134-000C-6090	Sequence 6090, Ap	946	29	40.3	58	3	US-08-322-137-85	Sequence 85, Appl
874	30	41.7	1076	4	US-09-171-991-7	Sequence 7, Appli	947	29	40.3	58	3	US-08-322-137-85	Sequence 85, Appl
875	30	41.7	1078	4	US-09-583-110-4036	Sequence 4036, Ap	948	29	40.3	59	4	US-09-621-976-6937	Sequence 6937, Ap
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879	30	41.7	1143	4	US-09-949-016-6137	Sequence 6137, Ap	952	29	40.3	63	4	US-09-205-258-732	Sequence 732, App
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900	30	41.7	1296	4	US-09-614-912-140	Sequence 140, App	973	29	40.3	116	3	US-07-808-453-6	Sequence 6, Appli
901	30	41.7	1487	3	US-08-840-062-7	Sequence 7, Appli	974	29	40.3	116	3	US-09-099-333-2	Sequence 2, Appli
902	30	41.7	1670	4	US-09-902-540-15506	Sequence 15506, A	975	29	40.3	116	3	US-09-124-900-7	Sequence 7, Appli
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981 29 40.3 120 4 US-09-732-210-1364 Sequence 1364, Ap
982 29 40.3 120 4 US-09-107-433-5193 Sequence 5193, Ap
983 29 40.3 121 3 US-08-974-899-5 Sequence 5, Appli
984 29 40.3 121 3 US-08-974-899-24 Sequence 24, Appl
985 29 40.3 121 4 US-09-795-798-5 Sequence 5, Appli
986 29 40.3 121 4 US-09-795-798-24 Sequence 24, Appl
987 29 40.3 121 4 US-09-270-767-61829 Sequence 61829, A
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990 29 40.3 131 4 US-09-270-767-37442 Sequence 37442, A
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992 29 40.3 131 4 US-09-270-767-52659 Sequence 52659, A
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994 29 40.3 134 4 US-09-270-767-54832 Sequence 54832, A
995 29 40.3 136 4 US-08-826-134-15 Sequence 15, Appl
996 29 40.3 136 4 US-08-826-134-26 Sequence 26, Appl
997 29 40.3 137 4 US-09-248-796A-26932 Sequence 26932, A
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999 29 40.3 139 4 US-09-270-767-49142 Sequence 49142, A
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ALIGNMENTS

RESULT 1
US-08-282-141-2
; Sequence 2, Application US/08282141
; Patent No. 5538861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Guidoalberto
; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-2

Query Match 100.0%; Score 72; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298

RESULT 2
US-08-435-434-2
; Sequence 2, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-2

Query Match 100.0%; Score 72; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298

RESULT 3
US-08-435-436-2
; Sequence 2, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
US-08-435-436-2

Qy 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; TYPE: amino acid
; TOPOLOGY: linear
; US-08-435-436-2

Query Match 100.0%; Score 72; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 4

US-08-438-863-2
; Sequence 2, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,863
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-863-2

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 5

US-08-438-864-2
; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929p1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-864-2

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 6

US-08-438-862-2

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/ Sequence 2, Application US/08438862
/ Patent No. 6033660
/ GENERAL INFORMATION:
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ APPLICANT: Chen, Jian
/ TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/438,862
/ FILING DATE: 10-MAY-1995
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 946-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 678 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 946-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 678 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-438-862-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298

RESULT 7
US-08-628-747-2
/ Sequence 2, Application US/08628747
/ Patent No. 6169070
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Jian
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Hammonds, R. Glenn
/ APPLICANT: Mark, Melanie
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: One DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/628,747
/ FILING DATE: 17-APR-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/402,253
/ FILING DATE: 10-MAR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/438,861
/ FILING DATE: 10-MAY-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: P929P2PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-225-1994
/ TELEFAX: 650-952-9881
/ TELEX: 910-371-7168
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 678 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-628-747-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298

RESULT 8
US-08-402-253-2
/ Sequence 2, Application US/08402253
/ Patent No. 6211142
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Jian
/ APPLICANT: Hammonds, R. Glenn
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Mark, Melanie R.
/ TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/402,253
/ FILING DATE: 10-MAR-1995
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wendy M. Lee
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 929
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-402-253-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 284 VPFSVAKSVKSLYLIG 298

RESULT 9
US-08-443-866B-2
Sequence 2, Application US/08443866B
Patent No. 6255068
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Hammonds, R. Glenn
APPLICANT: Mark, Melanie R.
TITLE OF INVENTION: RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,866B
FILING DATE: 31-May-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P0929D1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-443-866B-2

Query Match 100.0%; Score 72; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 284 VPFSVAKSVKSLYLIG 298

RESULT 10
US-08-282-141-3
Sequence 3, Application US/08282141
Patent No. 5538861
GENERAL INFORMATION:
APPLICANT: Schneider, Claudio
APPLICANT: Varnum, Brian
APPLICANT: Avanzi, Giancarlo
APPLICANT: Brancolini, Claudio
APPLICANT: Manioletti, Guido
TITLE OF INVENTION: Stimulating factor for the AXL Receptor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: United States
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/282,141
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-282-141-3

Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSVAKSVKSLYLIG 295

RESULT 11
US-08-435-434-1
Sequence 1, Application US/08435434
Patent No. 5714385
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,434
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:


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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-435-434-1
;
Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 12
US-08-435-436-1
; Sequence 1, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; APPLICATION NUMBER:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-435-436-1
;
Query Match 95.8%; Score 69; DB 1; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 13
US-08-438-863-1
; Sequence 1, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; APPLICATION NUMBER:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-438-863-1
;
Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 14
US-08-438-864-1
; Sequence 1, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,864
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929P1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-864-1

Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 15
US-08-438-862-1
Sequence 1, Application US/08438862
Patent No. 6033660
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-1

Query Match 95.8%; Score 69; DB 3; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.00037;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
DB 281 VPFSMAKSVKSLYLIG 295

RESULT 16
US-08-628-747-1
Sequence 1, Application US/08628747
Patent No. 6169070
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Godowski, Paul J.
APPLICANT: Hammonds, R. Glenn
APPLICANT: Mark, Melanie
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: One DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: United States
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,747
FILING DATE: 17-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,253
FILING DATE: 10-MAR-1995
APPLICATION NUMBER: US 08/438,861
FILING DATE: 10-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: P929P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-225-1994
TELEFAX: 650-952-9881
TELEX: 910-371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-628-747-1

Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.00037;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSMAKSVKSLYL 295

RESULT 17
 US-08-402-253-1
 ; Sequence 1, Application US/08402253
 ; Patent No. 6211142
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Hammonds, R. Glenn
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Mark, Melanie R.
 ; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/402,253
 FILING DATE: 10-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wendy M. Lee
 REGISTRATION NUMBER: 00,000
 REFERENCE/DOCKET NUMBER: 929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

US-08-402-253-1
 Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.00037;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSMAKSVKSLYL 295

RESULT 18
 US-08-443-866B-1
 ; Sequence 1, Application US/08443866B
 ; Patent No. 6255068
 ; GENERAL INFORMATION:
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Hammonds, R. Glenn
 ; APPLICANT: Mark, Melanie R.
 ; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION

Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.00037;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSMAKSVKSLYL 295

US-08-443-866B-1
 Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.00037;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSMAKSVKSLYL 295

NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/443,866B
 FILING DATE: 31-May-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/402253
 FILING DATE: 10-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 00,000
 REFERENCE/DOCKET NUMBER: P0929D1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415/225-1994
 TELEFAX: 415/952-9881
 TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 673 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear

US-08-443-866B-1
 Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.00037;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSMAKSVKSLYL 295

RESULT 19
 US-09-107-532A-4410
 ; Sequence 4410, Application US/09107532A
 ; Patent No. 6583275
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn A Doucette-Stamm and David Bush
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 ; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
 STREET: 100 Beaver Street
 CITY: Waltham
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02354

COMPUTER READABLE FORM:
 MEDIUM TYPE: CD-ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4410:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...77
; SEQUENCE DESCRIPTION: SEQ ID NO: 4410:
US-09-107-532A-4410

Query Match 61.1%; Score 44; DB 4; Length 77;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 8; Conservative 3; Mismatches 0; Indels 3; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 44 IPISIAKKEIVLYL 57

RESULT 20
US-09-721-870-24
; Sequence 24, Application US/09721870
; Patent No. 6632621
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Geary, Timothy G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Marsha J.
; TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 28341/6223
; CURRENT APPLICATION NUMBER: US/09/721,870
; CURRENT FILING DATE: 2000-11-24
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-721-870-24

Query Match 61.1%; Score 44; DB 4; Length 374;
Best Local Similarity 61.5%; Pred. No. 6.7;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
Db 142 LPFAIAASVNSLY 154

RESULT 21
US-09-270-767-60337
; Sequence 60337, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 60337
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-60337

Query Match 58.3%; Score 42; DB 4; Length 186;
Best Local Similarity 53.3%; Pred. No. 7;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
Db 65 IAFSTTKGVRSQLG 79

RESULT 22
US-08-843-530B-36
; Sequence 36, Application US/08843530B
; Patent No. 5939306
; GENERAL INFORMATION:
; APPLICANT: Selitrennikoff, Claude
; APPLICANT: Agnan, Jacqueline
; APPLICANT: Alex, Lisa A.
; APPLICANT: Simon, Melvin I.
; TITLE OF INVENTION: Osmosensing Histidine Kinases
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/843,530B
; FILING DATE: 16-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-02717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1220 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-843-530B-36

Query Match 58.3%; Score 42; DB 2; Length 1220;
Best Local Similarity 81.8%; Pred. No. 59;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKS 11
Db 955 VKFSVAKSVKS 965

RESULT 23
US-09-636-728-32
; Sequence 32, Application US/09636728
; Patent No. 6716625
```

; GENERAL INFORMATION:
 ; APPLICANT: Selitrennikoff, Claude
 ; APPLICANT: Pott, Greg
 ; TITLE OF INVENTION: Histidine Kinases of Aspergillus and Other Fungal
 ; TITLE OF INVENTION: Species, Related Compositions, and Methods of Use
 ; FILE REFERENCE: UTC-03758
 ; CURRENT APPLICATION NUMBER: US/09/636,728
 ; CURRENT FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: 08/843,530
 ; PRIOR FILING DATE: 1997-04-16
 ; NUMBER OF SEQ ID NOS: 73
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 32
 ; LENGTH: 1220
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 ; US-09-636-728-32

Query Match 58.3%; Score 42; DB 4; Length 1220;
 Best Local Similarity 81.8%; Pred. No. 59;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11
 DB 955 VKFSVAKSIKS 965
 |||||:|

RESULT 24
 US-09-248-796A-15046
 ; Sequence 15046, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 15046
 ; LENGTH: 292
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; US-09-248-796A-15046

Query Match 56.9%; Score 41; DB 4; Length 292;
 Best Local Similarity 53.8%; Pred. No. 18;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
 DB 54 PFNVKSLQTIYL 66
 ||:||||:|

RESULT 25
 US-08-416-603-4
 ; Sequence 4, Application US/08416603
 ; Patent No. 5866780
 ; GENERAL INFORMATION:

; APPLICANT: Law, Marcus
 ; APPLICANT: Hebara, Ledare
 ; APPLICANT: Reddick, Bradford B.
 ; TITLE OF INVENTION: Maize Chlorotic Dwarf Virus Genome and
 ; TITLE OF INVENTION: Uses Therefor
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Saliwanchik & Saliwanchik
 ; STREET: 2421 N.W. 41st Street, Suite A-1
 ; CITY: Gainesville

; STATE: FL
 ; COUNTRY: USA
 ; ZIP: 32606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/416,603
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lloyd, Jeffrey
 ; REGISTRATION NUMBER: 35,589
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 904-375-8100
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 3457 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-416-603-4

Query Match 56.9%; Score 41; DB 2; Length 3457;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
 DB 1386 VPFSIAKTAKVL 1397
 ||||:|:|

RESULT 26

US-09-248-796A-18222
 ; Sequence 18222, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 18222
 ; LENGTH: 99
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (6), (46)
 ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow

Query Match 54.2%; Score 39; DB 4; Length 99;
 Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
 DB 47 PFGVAKSKSKELG 60
 |||||:|

RESULT 27

US-09-519-232-74
 ; Sequence 74, Application US/09519232
 ; Patent No. 6528702

```

; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
; US-09-519-232-74

Query Match      54.2%; Score 39; DB 4; Length 369;
Best Local Similarity 53.8%; Pred. No. 53;
Matches 7; Conservative 4; Mismatches 4; Indels 2; Gaps 0;

Qy      1 VPFSVAKSVKSLY 13
      ||| ||| |||
Db      237 VPPEVAENIKLLW 249

RESULT 28
US-09-270-767-60047
; Sequence 60047, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60047
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-60047

Query Match      51.4%; Score 37; DB 4; Length 169;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 8; Conservative 0; Mismatches 0; Indels 4; Gaps 0;

Qy      3 FSVAKSVKSLYL 14
      ||| ||| |||
Db      154 FSVKSKXKGAYL 165

RESULT 29
US-09-270-767-44600
; Sequence 44600, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44600
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-44600

Query Match      51.4%; Score 37; DB 4; Length 224;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 FSVAKSVKSLYL 14
      ||| ||| |||
Db      154 FSVKSKXKGAYL 165

RESULT 30
US-09-489-039A-8199
; Sequence 8199, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8199
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-8199

Query Match      51.4%; Score 37; DB 4; Length 266;
Best Local Similarity 58.3%; Pred. No. 85;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      1 VPFSVAKSVKSL 12
      :||| ||| :|||
Db      83 IPFCVAGGIKSL 94

RESULT 31
US-09-107-532A-5019
; Sequence 5019, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Atinello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5019:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...316
SEQUENCE DESCRIPTION: SEQ ID NO: 5019:
US-09-107-532A-5019

Query Match 51.4%; Score 37; DB 4; Length 316;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 FSVSVKSKSLYL 14
|:|:|:|:|
DB 119 FAVSKNVEPLYL 130

RESULT 32
US-08-118-270-22
; Sequence 22, Application US/08118270
; Patent No. 5508384
; GENERAL INFORMATION:
; APPLICANT: Murphy, Randall B.
; APPLICANT: Schuster, David I.
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/118,270
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-118-270-22

Query Match 51.4%; Score 37; DB 1; Length 334;
Best Local Similarity 58.3%; Pred. No. 1e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
:|:|:|:|:|
DB 55 IPFSLANEVMYWF 69

RESULT 33
PCT-US93-08528-22
; Sequence 22, Application PC/TUS9308528
; GENERAL INFORMATION:
; APPLICANT: New York University
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
; NUMBER OF SEQUENCES: 348
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08528
; FILING DATE: 09-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,236
; FILING DATE: 10-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, Kevin G.
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 334 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-08528-22

Query Match 51.4%; Score 37; DB 5; Length 334;
Best Local Similarity 46.7%; Pred. No. 1.1e+02;
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
:|:|:|:|:|
DB 55 IPFSLANEVMYWF 69

RESULT 34
US-09-248-796A-17702
; Sequence 17702, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

RESULT 39
US-09-632-947B-4
; Sequence 4, Application US/09632947B
; Patent No. 6356845
; GENERAL INFORMATION:
; APPLICANT: Pharmacia & Upjohn
; TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS
; TITLE OF INVENTION: UDP-N-ACETYLENOUPURVYLGLUCOSAMINE REDUCTASE (S. aureus
; TITLE OF INVENTION: MuB)
; FILE REFERENCE: 268.6241 0101
; CURRENT APPLICATION NUMBER: US/09/632,947B
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/147,164
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Aquifex aeolicus
US-09-632-947B-4

Query Match 50.0%; Score 36; DB 3; Length 297;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
: ||| : ||| |
Db 97 IRFSVKENKVSFY 109

RESULT 40
US-09-503-391-2
; Sequence 2, Application US/09503391
; Patent No. 6300091
; GENERAL INFORMATION:
; APPLICANT: Patton, David A.
; APPLICANT: Ashby, Carl S.
; APPLICANT: Thomas, Carla R.
; APPLICANT: McElver, John A.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Levin, Joshua Z.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30852A
; CURRENT APPLICATION NUMBER: US/09/503,391
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-503-391-2

Query Match 50.0%; Score 36; DB 3; Length 551;
Best Local Similarity 63.8%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11
: ||| : ||| |
Db 322 VPFSVIRAKS 332

RESULT 41
US-09-503-391-4
; Sequence 4, Application US/09503391
; Patent No. 6300091
; GENERAL INFORMATION:
; APPLICANT: Patton, David A.
; APPLICANT: Ashby, Carl S.
; APPLICANT: Thomas, Carla R.

; APPLICANT: McElver, John A.
; APPLICANT: Budziszewski, Gregory J.
; APPLICANT: Levin, Joshua Z.
; TITLE OF INVENTION: Herbicide Target Genes and Methods
; FILE REFERENCE: PB/5-30852A
; CURRENT APPLICATION NUMBER: US/09/503,391
; CURRENT FILING DATE: 2000-02-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-503-391-4

Query Match 50.0%; Score 36; DB 3; Length 551;
Best Local Similarity 63.6%; Pred. No. 3e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11
: ||| : ||| |
Db 322 VPFSVIRAKS 332

RESULT 42
US-08-471-119A-2
; Sequence 2, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Leitner, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoergendorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoff, Melvyn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tolypocladium niveum
; STRAIN: ATCC 34921
US-08-471-119A-2

Query Match 50.0%; Score 36; DB 2; Length 15281;

Best Local Similarity 58.3%; Pred. No. 1.2e+04;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLYLIG 15
Db 12922 SVLSSLESYLIG 12933

RESULT 43

US-09-902-540-13147
; Sequence 13147, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13147
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13147

Query Match 48.6%; Score 35; DB 4; Length 148;
Best Local Similarity 46.7%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
Db 6 LPMLVALGLELYIG 20

RESULT 44

US-09-252-991A-32921
; Sequence 32921, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32921
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (7)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-32921

Query Match 48.6%; Score 35; DB 4; Length 279;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKS 11
Db 142 IPFSEIKSIKN 152

RESULT 45

US-09-328-352-4879
; Sequence 4879, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4879
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4879

Query Match 48.6%; Score 35; DB 4; Length 303;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 AKSVKSLYLIG 15
Db 74 AKHVKEVILG 83

RESULT 46

US-09-489-039A-7261
; Sequence 7261, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7261
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7261

Query Match 48.6%; Score 35; DB 4; Length 332;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLYL 14
Db 187 PFSVAKGGQPFYV 199

RESULT 47

US-08-121-714-4
; Sequence 4, Application US/08121714
; Patent No. 5470970
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
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; APPLICATION NUMBER: US/08/121,714
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-121-714-4

Query Match 48.6%; Score 35; DB 1; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLG 15
|||::: :||
Db 32 PFSISSAMAMVFLG 45

RESULT 48
US-08-477-108A-4
; Sequence 4, Application US/08477108A
; Patent No. 5801001
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; APPLICANT: Zou, Zhiqiang
; APPLICANT: Anisowicz, Anthony
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; FILING DATE: 09/01/92
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; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-477-108A-4

Query Match 48.6%; Score 35; DB 1; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLG 15
|||::: :||
Db 32 PFSISSAMAMVFLG 45

RESULT 49
US-08-477-112-4
; Sequence 4, Application US/08477112
; Patent No. 5905023
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; FILING DATE: 09/01/92
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; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-477-112-4

Query Match          48.6%; Score 35; DB 2; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      2 PFSVAKSVKSLYLIG 15
Db      32 PFSISSAMAMVFLG 45

RESULT 50
PCT-US93-08322-4
; Sequence 4. Application PC/TUS9308322
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08322
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-08322-4

Query Match          48.6%; Score 35; DB 5; Length 379;
Best Local Similarity 35.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      2 PFSVAKSVKSLYLIG 15
Db      32 PFSISSAMAMVFLG 45
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:49:00 ; Search time 390.39 Seconds
(without alignments)
224.889 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRLDCINKYSGPYTNSGF.....LGRMFGTPIRLRFRKLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

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1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1297	100.0	678	2	AAR99414 Human gas
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4	1297	100.0	678	3	AAY29794 Human gro
5	1297	100.0	678	3	AAY57383 Amino aci
6	1297	100.0	678	8	ADL83231 Human PRO
7	1297	100.0	678	8	ADM40825 Human Gas
8	1297	100.0	678	8	ADM60275 Human Gas
9	1297	100.0	679	7	ADD48757 Human PRO
10	1269	97.8	624	8	ADM40823 Human PRO
11	1113	85.8	673	2	AAR99414 Human gas
12	1113	85.8	673	2	AAR99414 Human gas
13	1113	85.8	673	3	AAY29794 Human gro
14	1113	85.8	673	3	AAY57383 Amino aci
15	1113	85.8	673	5	ABB84840 Human PRO
16	1113	85.8	673	5	ABB95446 Human ang
17	1113	85.8	673	7	ADD10337 Human sec
18	1113	85.8	673	7	ADD11237 Human sec
19	1113	85.8	673	7	ADD37090 Human sec
20	1113	85.8	673	8	ADL41298 Human sec
21	1113	85.8	673	8	ADH43481 Human PRO
22	1113	85.8	673	8	ADK82826 Human PRO
23	1113	85.8	703	8	ABO84420 Mouse can
24	602.5	46.5	635	2	AAR72350 Mature hu
25	601.5	46.4	635	2	AAR31875 Vitamin K

99	344.5	26.6	798	8	ADN23442	Adn23442 Bacterial	172	330.5	25.5	845	2	AAR53089	Aar53089 Human mas
100	344.5	26.6	957	5	AD128028	ECMCAD pr	173	330.5	25.5	961	4	ABR41625	Abr41625 Human DIT
101	344.5	26.6	2695	5	ABG294032	Abg294032 Human NOV	174	330.5	25.5	1118	6	AAW50209	Aaw50209 Human fib
102	344.5	26.6	2695	7	AD135969	Ad135969 Human NOV	175	330.5	25.5	1342	6	AAO16655	Aao16655 Human ext
103	342.5	26.4	2809	5	AAAG66169	Aag66169 Human fib	176	330.5	25.5	1590	8	ABM82596	Abm82596 Human dia
104	341	26.3	653	7	ADD26679	Add26679 Human adi	177	330.5	25.5	1631	8	ABM82598	Abm82598 Human dia
105	339.5	26.2	1018	7	AD078255	Ad078255 Human CGD	178	330.5	25.5	1642	8	ABM82597	Abm82597 Human dia
106	339	26.1	524	8	ABO84713	Ab084713 Human can	179	330.5	25.5	1668	6	AAO16647	Aao16647 Human ext
107	339	26.1	556	2	AAW27598	Aaw27598 Human fib	180	330.5	25.5	1668	6	ABU52394	Abu52394 Human GPC
108	339	26.1	559	8	ABO84709	Ab084709 Human can	181	330.5	25.5	1668	6	ADL24123	Adl24123 Human NOV
109	339	26.1	566	2	AAK11148	Aak11148 Fibulin A	182	330.5	25.5	1720	6	ABU52393	Abu52393 Human GPC
110	339	26.1	566	5	AAE15574	Aae15574 Human fib	183	330.5	25.5	1721	6	AAO16650	Aao16650 Human ext
111	339	26.1	566	8	ADN03779	Adn03779 Antipsori	184	330.5	25.5	1721	6	ADL24121	Adl24121 Human NOV
112	339	26.1	566	8	ABO84714	Ab084714 Human can	185	330.5	25.5	1722	8	ADS10847	Ads10847 Human the
113	339	26.1	581	8	ABO84710	Ab084710 Human can	186	330.5	25.5	2844	5	ABG94629	Abg94629 Human NOV
114	339	26.1	601	2	AAK11149	Aak11149 Fibulin B	187	330.5	25.5	2844	7	ADL35963	Adl35963 Human NOV
115	339	26.1	601	2	AAW27599	Aaw27599 Human fib	188	330.5	25.5	2845	5	ABG94631	Abg94631 Human NOV
116	339	26.1	601	5	AAE15575	Aae15575 Human fib	189	330.5	25.5	2877	5	ABG94630	Abg94630 Human NOV
117	339	26.1	601	8	ABO84717	Ab084717 Human can	190	330.5	25.5	2877	7	ADL35965	Adl35965 Human NOV
118	339	26.1	641	8	ABO84712	Ab084712 Human can	191	330.5	25.5	2995	7	ADL35961	Adl35961 Human NOV
119	339	26.1	661	8	ABO84708	Ab084708 Human can	192	330.5	25.5	2910	8	ADQ97206	Adq97206 Mouse can
120	339	26.1	683	2	AAK11150	Aak11150 Fibulin C	193	329.5	25.4	2910	8	ADQ59382	Adq59382 Human can
121	339	26.1	683	2	AAW27600	Aaw27600 Human fib	194	328.5	25.3	1253	3	AAK12271	Aak12271 Mouse lat
122	339	26.1	683	5	AAE15576	Aae15576 Human fib	195	328.5	25.3	1253	4	AAK61420	Aak61420 Murine TA
123	339	26.1	683	8	ABO84716	Ab084716 Human can	196	328.5	25.3	1253	4	ADR31649	Adr31649 Murine la
124	339	26.1	686	4	ABG19385	Abg19385 Novel hum	197	327.5	25.3	333	3	AAAY84709	Aay84709 Amino aci
125	339	26.1	698	8	ABO84711	Ab084711 Human can	198	327	25.2	448	6	ABR59720	Abr59720 Human fib
126	339	26.1	703	2	AAW27601	Aaw27601 Human fib	199	327	25.2	448	7	ADD14954	Add14954 Human UP
127	339	26.1	703	5	AAE15577	Aae15577 Human fib	200	327	25.2	448	7	ADF90891	Adf90891 Human hep
128	339	26.1	703	8	ADN03922	Adn03922 Antipsori	201	327	25.2	448	8	ADL13450	Adl13450 Human UP5
129	339	26.1	703	8	ABO84715	Ab084715 Human can	202	327	25.2	448	8	ADQ67955	Adq67955 Human hep
130	339	26.1	703	8	ADT49905	Adt49905 Human FBL	203	327	25.2	897	4	AAAG65887	Aag65887 Amino aci
131	339	26.1	706	4	ABG19386	Abg19386 Novel hum	204	327	25.2	897	4	ABG06309	Abg06309 Novel hum
132	339	26.1	1221	8	ADT49892	Adt49892 Murine FB	205	327	25.2	897	5	ABG91402	Abg91402 Primate L
133	338	26.1	576	4	AAW80175	Aaw80175 Human pro	206	327	25.2	897	5	ADE07852	Ade07852 Novel pro
134	338	26.1	576	4	AAW80174	Aaw80174 Human pro	207	327	25.2	897	7	ADE08940	Ade08940 Novel pro
135	338	26.1	576	4	AAW41932	Aaw41932 Human pol	208	327	25.2	914	8	ADI27628	Adi27628 Human SCU
136	338	26.1	609	3	AAW79191	Aaw79191 Human pro	209	327	25.2	939	6	AAE29932	Aae29932 Human LP2
137	338	26.1	636	4	AAW40146	Aaw40146 Human pol	210	327	25.2	991	6	AAO16645	Aao16645 Human ext
138	338	26.1	650	4	AAW79190	Aaw79190 Human pro	211	327	25.2	993	4	AAAG65888	Aag65888 Amino aci
139	337	26.0	1184	7	ADE95474	Ade95474 Human NOV	212	327	25.2	993	6	AAE29931	Aae29931 Human LP2
140	337	26.0	1231	5	ABP63045	Abp63045 Human pol	213	327	25.2	993	8	ADI27637	Adi27637 Human SCU
141	336	25.9	974	6	ABU12093	Abu12093 Novel hum	214	327	25.2	993	7	AAE38806	Aae38806 Human POL
142	335.5	25.9	505	8	ADT49801	Adt49801 Murine BC	215	326.5	25.2	737	7	AAE38806	Aae38806 Human POL
143	334.5	25.8	733	8	ADQ65159	Adq65159 Novel hum	216	326.5	25.2	1288	8	ADQ59379	Adq59379 Human can
144	334.5	25.8	1121	4	AAW78887	Aaw78887 Human fib	217	326.5	25.2	1300	6	AAO16653	Aao16653 Human ext
145	334.5	25.8	1208	3	AAW70551	Aaw70551 Human lat	218	326.5	25.2	1353	6	AAO16654	Aao16654 Human ext
146	334.5	25.8	1256	8	ADR14553	Adr14553 Human NF-	219	326.5	25.2	1626	6	AAO16652	Aao16652 Human ext
147	334.5	25.8	1257	3	AAW70554	Aaw70554 Human lat	220	326.5	25.2	1679	6	AAO16651	Aao16651 Human ext
148	334.5	25.8	1260	4	AAW61460	Aaw61460 Human TAN	221	326.5	25.2	2676	7	ADL35971	Adl35971 Human NOV
149	334.5	25.8	1289	4	AAW61419	Aaw61419 Human TAN	222	325	25.1	735	5	AAAG68258	Aag68258 Human POL
150	333	25.7	596	7	AAO30833	Aao30833 Human cel	223	325	25.1	735	6	ABU12091	Abu12091 Novel hum
151	333	25.7	845	5	AAW68259	Aaw68259 Human POL	224	324	25.0	349	7	ADB65110	Adb65110 Human pro
152	333	25.7	845	6	ABU12092	Abu12092 Novel hum	225	324	25.0	974	7	AAE38808	Aae38808 Human POL
153	333	25.7	845	7	AAE38807	Aae38807 Human POL	226	323.5	24.9	682	8	ADR10465	Adr10465 Human pro
154	333	25.7	880	7	ADB64680	Adb64680 Human pro	227	323.5	24.9	1355	2	AAAR14584	Aar14584 TGF beta
155	333	25.7	973	5	AAAG68260	Aag68260 Human POL	228	323	24.9	335	3	AAAY76008	Aay76008 Rat EGF e
156	333	25.7	989	6	AAE30306	Aae30306 Human LP2	229	323	24.9	335	4	AAAB55947	Aab55947 Skin cell
157	333	25.7	1006	5	AAU79172	Aau79172 Human MEG	230	323	24.9	335	5	ABB72147	Abb72147 Rat prote
158	333	25.7	1009	6	AAE29930	Aae29930 Human LP2	231	323	24.9	392	2	AAAW31705	Aaw31705 Human ext
159	332.5	25.6	1218	6	ABJ19368	Abj19368 NOX rela	232	323	24.9	448	2	AAW79739	Aaw79739 Human EEG
160	332.5	25.6	1218	8	ADO41736	Ado41736 Novel hum	233	323	24.9	448	2	AAW95709	Aaw95709 Homo sapi
161	331.5	25.6	2000	8	ADP23488	Adp23488 PRO poly	234	323	24.9	448	2	AAW94281	Aaw94281 Human ext
162	331.5	25.6	2911	6	ABU56630	Abu56630 Lung canc	235	323	24.9	448	3	AAAY54989	Aay54989 Full leng
163	331.5	25.6	2911	6	ABO07259	Ab007259 Human p53	236	323	24.9	448	3	AAAY57058	Aay57058 Amino aci
164	331.5	25.6	2911	7	ADJ68615	Adj68615 Human hea	237	323	24.9	448	3	AAAM93573	Aam93573 Human pol
165	331.5	25.6	2911	7	ADN38844	Adn38844 Cancer/an	238	323	24.9	448	5	AAAU75494	Aau75494 Human ext
166	331.5	25.6	2911	8	ADQ18204	Adq18204 Human sof	239	323	24.9	448	6	AAAR59721	Aar59721 Human fib
167	331.5	25.6	2912	4	ABG06402	Abg06402 Novel hum	240	323	24.9	448	7	AADE59310	Ade59310 Human pro
168	330.5	25.5	315	6	ABR41616	Ab41616 Human DIT	241	323	24.9	448	7	AADE59304	Ade59304 Rat Prote
169	330.5	25.5	751	2	AAAR53088	Aar53088 Human mas	242	323	24.9	448	7	AADE59308	Ade59308 Rat Prote
170	330.5	25.5	752	2	AAAR53087	Aar53087 Human mas	243	323	24.9	448	7	AADE59308	Ade59308 Rat Prote
171	330.5	25.5	756	2	AAAR53086	Aar53086 Human mas	244	323	24.9	448	8	ADL31324	Adl31324 Human pro

245	323	24.9	448	8	ADQ95796	Adq95796	Human Fib	318	319.5	24.6	1251	2	AAR79475	Aar79475	Mouse LTB
246	323	24.9	448	8	ABO84629	AbO84629	Human can	319	319.5	24.6	1251	4	AAB61481	Aab61481	Murine LT
247	323	24.9	448	8	ABO84630	AbO84630	Human can	320	319.5	24.6	1251	4	AAB61483	Aab61483	Human TAN
248	322	24.8	565	5	ADR41503	AdR41503	Human CD-	321	319.5	24.6	1676	8	ABM84035	Abm84035	Human dia
249	322	24.8	782	8	ADH17486	AdH17486	Human NOV	322	319.5	24.6	1694	8	ABM84034	Abm84034	Human dia
250	322	24.8	794	4	AAR03820	AaR03820	Human gen	323	319.5	24.6	1695	8	ABM84033	Abm84033	Human dia
251	322	24.8	794	4	ABG64543	AbG64543	Human alb	324	319.5	24.6	1712	2	AAR22461	Aar22461	Masking p
252	322	24.8	794	4	ADL77810	AdL77810	Albumin f	325	319.5	24.6	1712	7	ADAE1336	AdaE1336	Rat Prote
253	322	24.8	920	8	ADH17488	AdH17488	Human NOV	326	319.5	24.6	1820	7	ADN95528	AdN95528	Human BCC
254	322	24.8	934	4	AAR03843	AaR03843	Human gen	327	319.5	24.6	1821	7	ADN95528	AdN95528	Human BCC
255	322	24.8	934	4	ABG64542	AbG64542	Human alb	328	319.5	24.6	1821	7	ADN95528	AdN95528	Human BCC
256	322	24.8	934	4	ADL77809	AdL77809	Albumin f	329	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
257	322	24.8	934	4	ADH17484	AdH17484	Human NOV	330	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
258	322	24.8	945	8	ADH17464	AdH17464	Human NOV	331	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
259	322	24.8	956	8	ADM12924	AdM12924	PROB3470	332	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
260	322	24.8	956	8	ADN03855	AdN03855	Antipsori	333	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
261	322	24.8	964	8	ADH17462	AdH17462	Human NOV	334	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
262	322	24.8	964	8	ADH17460	AdH17460	Human NOV	335	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
263	322	24.8	983	4	AAR03877	AaR03877	Human gen	336	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
264	321	24.7	348	2	AYT08490	AyT08490	Human EGF	337	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
265	321	24.7	350	2	AYT08066	AyT08066	Human EGF	338	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
266	321	24.7	387	4	AAG68188	AaG68188	Human EGF	339	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
267	321	24.7	387	4	ABR41112	AbR41112	Human ext	340	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
268	321	24.7	387	7	ADN98732	AdN98732	Human ext	341	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
269	321	24.7	387	7	ADN98732	AdN98732	Human ext	342	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
270	321	24.7	387	8	ADH13448	AdH13448	Human pro	343	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
271	321	24.7	387	8	ADH13448	AdH13448	Human pro	344	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
272	321	24.7	423	3	AYY56753	AyY56753	Human hep	345	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
273	321	24.7	423	3	AYY56751	AyY56751	Smooth mu	346	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
274	321	24.7	423	3	AYY56750	AyY56750	Smooth mu	347	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
275	321	24.7	448	3	AYY54990	AyY54990	Full leng	348	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
276	321	24.7	448	8	ADQ95798	AdQ95798	Murine FI	349	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
277	321	24.7	448	8	ADT49822	AdT49822	Murine FB	350	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
278	321	24.7	461	3	AYY56752	AyY56752	Smooth mu	351	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
279	321	24.7	461	3	AYY54991	AyY54991	Full leng	352	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
280	321	24.7	470	6	ABU03464	AbU03464	Angiogene	353	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
281	321	24.7	470	7	ADG10746	AdG10746	Human STA	354	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
282	321	24.7	493	4	AAE72892	AaE72892	Human ERE	355	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
283	321	24.7	493	4	AAE72892	AaE72892	Human ERE	356	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
284	321	24.7	493	6	ABU03463	AbU03463	Angiogene	357	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
285	321	24.7	493	6	ABU03463	AbU03463	Angiogene	358	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
286	321	24.7	493	6	ABU03463	AbU03463	Angiogene	359	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
287	321	24.7	493	7	ADL14952	AdL14952	Human UP	360	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
288	321	24.7	493	7	ADL14952	AdL14952	Human UP	361	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
289	321	24.7	493	7	ADL14952	AdL14952	Human UP	362	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
290	321	24.7	493	7	ADL14952	AdL14952	Human UP	363	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
291	321	24.7	493	7	ADL14952	AdL14952	Human UP	364	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
292	321	24.7	493	7	ADL14952	AdL14952	Human UP	365	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
293	321	24.7	493	7	ADL14952	AdL14952	Human UP	366	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
294	321	24.7	493	7	ADL14952	AdL14952	Human UP	367	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
295	321	24.7	493	7	ADL14952	AdL14952	Human UP	368	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
296	321	24.7	493	7	ADL14952	AdL14952	Human UP	369	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
297	321	24.7	493	7	ADL14952	AdL14952	Human UP	370	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
298	321	24.7	493	7	ADL14952	AdL14952	Human UP	371	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
299	321	24.7	493	7	ADL14952	AdL14952	Human UP	372	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
300	321	24.7	493	7	ADL14952	AdL14952	Human UP	373	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
301	321	24.7	493	7	ADL14952	AdL14952	Human UP	374	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
302	321	24.7	493	7	ADL14952	AdL14952	Human UP	375	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
303	321	24.7	493	7	ADL14952	AdL14952	Human UP	376	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
304	321	24.7	493	7	ADL14952	AdL14952	Human UP	377	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
305	321	24.7	493	7	ADL14952	AdL14952	Human UP	378	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
306	321	24.7	493	7	ADL14952	AdL14952	Human UP	379	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
307	321	24.7	493	7	ADL14952	AdL14952	Human UP	380	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
308	320.5	24.7	1786	8	ADJ82955	AdJ82955	Human lat	381	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
309	320.5	24.7	1821	8	ADJ82954	AdJ82954	Human lat	382	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
310	320.5	24.7	1821	8	ADJ82954	AdJ82954	Human lat	383	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
311	320.5	24.7	1821	8	ADJ82954	AdJ82954	Human lat	384	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
312	320.5	24.7	1821	8	ADJ82954	AdJ82954	Human lat	385	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
313	320.5	24.7	1821	8	ADJ82954	AdJ82954	Human lat	386	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
314	320	24.7	493	7	ADJ82954	AdJ82954	Human lat	387	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
315	320	24.7	493	7	ADJ82954	AdJ82954	Human lat	388	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
316	320	24.7	493	7	ADJ82954	AdJ82954	Human lat	389	319	24.6	1821	4	ADN95528	AdN95528	Human BCC
317	320	24.7	493	7	ADJ82954	AdJ82954	Human lat	390	319	24.6	1821	4	ADN95528	AdN95528	Human BCC

391	319	24.6	448	6	ABR60239	Human sec	464	319	24.6	448	6	ABO31673	Human sec
392	319	24.6	448	6	ABR67974	Human sec	465	319	24.6	448	6	ABM08090	Human sec
393	319	24.6	448	6	ABR65362	Human sec	466	319	24.6	448	6	ABO40570	Human sec
394	319	24.6	448	6	ABR68584	Human sec	467	319	24.6	448	6	ABO35995	Human PRO
395	319	24.6	448	6	ABR71996	Human sec	468	319	24.6	448	6	ABO44134	Human PRO
396	319	24.6	448	6	ABU85476	Human PRO	469	319	24.6	448	6	ADA78160	Human sec
397	319	24.6	448	6	ABU89166	Human sec	470	319	24.6	448	6	ABM24929	Human sec
398	319	24.6	448	6	ABU83246	Human sec	471	319	24.6	448	6	ABO03197	Human sec
399	319	24.6	448	6	ABU95102	Novel hum	472	319	24.6	448	6	ABR90453	Human sec
400	319	24.6	448	6	ABU90850	Novel hum	473	319	24.6	448	6	ABM17367	Human sec
401	319	24.6	448	6	ABU84161	Human sec	474	319	24.6	448	6	ABR95113	Human sec
402	319	24.6	448	6	ABU93812	Novel hum	475	319	24.6	448	6	ABR95418	Human sec
403	319	24.6	448	6	ABR65057	Human sec	476	319	24.6	448	6	ABO21656	Human sec
404	319	24.6	448	6	ABR68889	Human sec	477	319	24.6	448	6	ABR97920	Human sec
405	319	24.6	448	6	ABO06705	Human sec	478	319	24.6	448	6	ABR87708	Human sec
406	319	24.6	448	6	ABR99250	Human sec	479	319	24.6	448	6	ABM77749	Human sec
407	319	24.6	448	6	ABU57134	Human PRO	480	319	24.6	448	6	ABM27979	Human sec
408	319	24.6	448	6	ABU72040	Novel hum	481	319	24.6	448	6	ABM06260	Human sec
409	319	24.6	448	6	ABU86086	Novel hum	482	319	24.6	448	6	ABM03766	Human sec
410	319	24.6	448	6	ABU82373	Novel hum	483	319	24.6	448	6	ABM35217	Human sec
411	319	24.6	448	6	ABU87384	Human PRO	484	319	24.6	448	6	ABM26454	Human sec
412	319	24.6	448	6	ABU67141	Novel hum	485	319	24.6	448	6	ABO48236	Human sec
413	319	24.6	448	6	ABU83856	Human sec	486	319	24.6	448	6	ABR92978	Human sec
414	319	24.6	448	6	ABO08230	Human PRO	487	319	24.6	448	6	ABO24739	Human sec
415	319	24.6	448	6	ABU81941	Novel hum	488	319	24.6	448	6	ABM11750	Human sec
416	319	24.6	448	6	ABU66105	Novel hum	489	319	24.6	448	6	ABM02851	Human sec
417	319	24.6	448	6	ABR59934	Human sec	490	319	24.6	448	6	ABM16147	Human sec
418	319	24.6	448	6	ABU94122	Novel hum	491	319	24.6	448	6	ABO27708	Human sec
419	319	24.6	448	6	ABU99975	Novel hum	492	319	24.6	448	6	ABM29199	Human sec
420	319	24.6	448	6	ABR66645	Human sec	493	319	24.6	448	6	ABM07175	Human sec
421	319	24.6	448	6	ABR91063	Human sec	494	319	24.6	448	6	ABM21269	Human sec
422	319	24.6	448	6	ABU94490	Human PRO	495	319	24.6	448	6	ABM09615	Human sec
423	319	24.6	448	6	ABU79372	Human PRO	496	319	24.6	448	6	ABO41485	Human sec
424	319	24.6	448	6	ABU86701	Human sec	497	319	24.6	448	6	ABO36300	Human PRO
425	319	24.6	448	6	ABU87006	Novel hum	498	319	24.6	448	6	ABO43829	Human PRO
426	319	24.6	448	6	ABU94795	Human PRO	499	319	24.6	448	6	ABM76529	Human sec
427	319	24.6	448	6	ABO04722	Human PRO	500	319	24.6	448	6	ABM76225	Human sec
428	319	24.6	448	6	ABR70471	Human sec	501	319	24.6	448	6	ABM25844	Human sec
429	319	24.6	448	6	ABU98636	Human sec	502	319	24.6	448	6	ABM26149	Human sec
430	319	24.6	448	6	ABR66035	Human sec	503	319	24.6	448	6	ABO03502	Human sec
431	319	24.6	448	6	ABR64752	Human sec	504	319	24.6	448	6	ABO02587	Human sec
432	319	24.6	448	6	ABU79677	Human PRO	505	319	24.6	448	6	ABR90758	Human sec
433	319	24.6	448	6	ABU93068	Human sec	506	319	24.6	448	6	ABR73826	Human sec
434	319	24.6	448	6	ABU96027	Human PRO	507	319	24.6	448	6	ABO17078	Human sec
435	319	24.6	448	6	ABU91247	Novel hum	508	319	24.6	448	6	ABR94503	Human sec
436	319	24.6	448	6	ABU90340	Novel hum	509	319	24.6	448	6	ABR76010	Human sec
437	319	24.6	448	6	ABO09755	Human sec	510	319	24.6	448	6	ABR71386	Human sec
438	319	24.6	448	6	ABO11027	Human sec	511	319	24.6	448	6	ABR93283	Human sec
439	319	24.6	448	6	ABR71081	Human sec	512	319	24.6	448	6	ABR93588	Human sec
440	319	24.6	448	6	ABU87689	Human PRO	513	319	24.6	448	6	ABR88013	Human sec
441	319	24.6	448	6	ABU91557	Human PRO	514	319	24.6	448	6	ABO28013	Human sec
442	319	24.6	448	6	ABU84771	Human sec	515	319	24.6	448	6	ABO30148	Human sec
443	319	24.6	448	6	ABR69861	Human sec	516	319	24.6	448	6	ABO33357	Human PRO
444	319	24.6	448	6	ABU80238	Human PRO	517	319	24.6	448	6	ABM05045	Human sec
445	319	24.6	448	6	ABU93507	Human PRO	518	319	24.6	448	6	ABM09005	Human sec
446	319	24.6	448	6	ABO110060	Human sec	519	319	24.6	448	6	ABO36605	Human sec
447	319	24.6	448	6	ABO09145	Human sec	520	319	24.6	448	6	ABO35690	Human PRO
448	319	24.6	448	6	ABU10713	Human sec	521	319	24.6	448	6	ABO39655	Human sec
449	319	24.6	448	6	ABU95722	Human PRO	522	319	24.6	448	6	ABM10530	Human sec
450	319	24.6	448	6	ABU79783	Human sec	523	319	24.6	448	6	ABM12055	Human PRO
451	319	24.6	448	6	ABU96931	Novel hum	524	319	24.6	448	6	ABO52201	Human PRO
452	319	24.6	448	6	ABR70776	Human sec	525	319	24.6	448	6	ABO52506	Human PRO
453	319	24.6	448	6	ABO05127	Novel hum	526	319	24.6	448	6	ABO23824	Human sec
454	319	24.6	448	6	ABO08535	Human sec	527	319	24.6	448	6	ABR97310	Human sec
455	319	24.6	448	6	ABO05742	Human sec	528	319	24.6	448	6	ABR87098	Human sec
456	319	24.6	448	6	ABR74131	Human sec	529	319	24.6	448	6	ABM11140	Human sec
457	319	24.6	448	6	ABR95723	Human sec	530	319	24.6	448	6	ABM28284	Human sec
458	319	24.6	448	6	ABR81020	Human sec	531	319	24.6	448	6	ABO32283	Human sec
459	319	24.6	448	6	ABR81325	Human sec	532	319	24.6	448	6	ABM15410	Human sec
460	319	24.6	448	6	ABM01021	Human sec	533	319	24.6	448	6	ABM06565	Human sec
461	319	24.6	448	6	ABR88623	Human sec	534	319	24.6	448	6	ABM04376	Human sec
462	319	24.6	448	6	ABM77444	Human sec	535	319	24.6	448	6	ABM22489	Human sec
463	319	24.6	448	6	ABO28928	Human sec	536	319	24.6	448	6	ABM07785	Human sec

537	319	24.6	448	6	ABO40875	Human sec	610	319	24.6	448	6	ABM25234	Human sec
538	319	24.6	448	6	ABM35522	Human sec	611	319	24.6	448	6	ABO47626	Human sec
539	319	24.6	448	6	ABM33285	Human sec	612	319	24.6	448	6	ABO47931	Human sec
540	319	24.6	448	6	ABO52811	Human PRO	613	319	24.6	448	6	ABO48541	Human sec
541	319	24.6	448	6	ABO50371	Human sec	614	319	24.6	448	6	ABO51591	Human PRO
542	319	24.6	448	6	ABU99365	Human sec	615	319	24.6	448	6	ABO51896	Human PRO
543	319	24.6	448	6	ABO04417	Human sec	616	319	24.6	448	6	ABO50676	Human sec
544	319	24.6	448	6	ABO06047	Human sec	617	319	24.6	448	6	ABR79800	Human sec
545	319	24.6	448	6	ABM18587	Human sec	618	319	24.6	448	6	ABM17062	Human sec
546	319	24.6	448	6	ABR97615	Human sec	619	319	24.6	448	6	ABM18094	Human sec
547	319	24.6	448	6	ABM01326	Human sec	620	319	24.6	448	6	ABO21046	Human sec
548	319	24.6	448	6	ABR80715	Human sec	621	319	24.6	448	6	ABR97005	Human sec
549	319	24.6	448	6	ABR88928	Human sec	622	319	24.6	448	6	ABM12360	Human sec
550	319	24.6	448	6	ABM13580	Human sec	623	319	24.6	448	6	ABM16452	Human sec
551	319	24.6	448	6	ABM20964	Human sec	624	319	24.6	448	6	ABM24319	Human sec
552	319	24.6	448	6	ABO42095	Human sec	625	319	24.6	448	6	ABM14800	Human sec
553	319	24.6	448	6	ABO42705	Human sec	626	319	24.6	448	6	ABM04681	Human sec
554	319	24.6	448	6	ABM10225	Human sec	627	319	24.6	448	6	ABM06870	Human sec
555	319	24.6	448	6	ABO38740	Human sec	628	319	24.6	448	6	ABM09310	Human sec
556	319	24.6	448	6	ABM32980	Human sec	629	319	24.6	448	6	ABO39350	Human sec
557	319	24.6	448	6	ABM22794	Human sec	630	319	24.6	448	6	ABM75615	Human sec
558	319	24.6	448	6	ABM75005	Human sec	631	319	24.6	448	6	ABM25539	Human sec
559	319	24.6	448	6	ADA79952	Human sec	632	319	24.6	448	6	ABM20049	Human sec
560	319	24.6	448	6	ABR96395	Human sec	633	319	24.6	448	6	ABO46955	Human PRO
561	319	24.6	448	6	ABM02546	Human sec	634	319	24.6	448	6	ABO47260	Human PRO
562	319	24.6	448	6	ABR86488	Human sec	635	319	24.6	448	6	ADA83477	Human sec
563	319	24.6	448	6	ABR86793	Human sec	636	319	24.6	448	6	ABR71691	Human sec
564	319	24.6	448	6	ABM16757	Human sec	637	319	24.6	448	6	ABR72301	Human sec
565	319	24.6	448	6	ABM29809	Human sec	638	319	24.6	448	6	ABR98640	Human sec
566	319	24.6	448	6	ABO29233	Human sec	639	319	24.6	448	6	ABO07010	Human sec
567	319	24.6	448	6	ABM24014	Human sec	640	319	24.6	448	6	ABR84963	Human sec
568	319	24.6	448	6	ABM23404	Human sec	641	319	24.6	448	6	ABR73521	Human sec
569	319	24.6	448	6	ADA47187	Human sec	642	319	24.6	448	6	ABR76615	Human sec
570	319	24.6	448	6	ABM22184	Human sec	643	319	24.6	448	6	ABR73216	Human sec
571	319	24.6	448	6	ABO37825	Human sec	644	319	24.6	448	6	ABM18282	Human sec
572	319	24.6	448	6	ABM28589	Human sec	645	319	24.6	448	6	ABO20741	Human sec
573	319	24.6	448	6	ABM28894	Human sec	646	319	24.6	448	6	ABO25484	Human PRO
574	319	24.6	448	6	ABM66538	Human sec	647	319	24.6	448	6	ABO25789	Human PRO
575	319	24.6	448	6	ABM75920	Human sec	648	319	24.6	448	6	ABR94198	Human sec
576	319	24.6	448	6	ABM34200	Human sec	649	319	24.6	448	6	ABR80105	Human sec
577	319	24.6	448	6	ABM34505	Human sec	650	319	24.6	448	6	ABM11445	Human sec
578	319	24.6	448	6	ABO20436	Human sec	651	319	24.6	448	6	ABO33052	Human PRO
579	319	24.6	448	6	ABO221351	Human sec	652	319	24.6	448	6	ABO30758	Human sec
580	319	24.6	448	6	ABO22266	Human sec	653	319	24.6	448	6	ABO31063	Human sec
581	319	24.6	448	6	ABR96700	Human sec	654	319	24.6	448	6	ABM27369	Human sec
582	319	24.6	448	6	ABR85878	Human sec	655	319	24.6	448	6	ABM30114	Human sec
583	319	24.6	448	6	ABR99860	Human sec	656	319	24.6	448	6	ABM05650	Human sec
584	319	24.6	448	6	ABM00411	Human sec	657	319	24.6	448	6	ABM15715	Human sec
585	319	24.6	448	6	ABM00716	Human sec	658	319	24.6	448	6	ABM08700	Human sec
586	319	24.6	448	6	ABO29843	Human sec	659	319	24.6	448	6	ABO42400	Human sec
587	319	24.6	448	6	ABM23709	Human sec	660	319	24.6	448	6	ABO38130	Human sec
588	319	24.6	448	6	ABM29504	Human sec	661	319	24.6	448	6	ABO46040	Human PRO
589	319	24.6	448	6	ABO38435	Human sec	662	319	24.6	448	6	ABM66843	Human sec
590	319	24.6	448	6	ABO45735	Human PRO	663	319	24.6	448	6	ADB20520	Human sec
591	319	24.6	448	6	ABM20659	Human sec	664	319	24.6	448	6	ABM19744	Human sec
592	319	24.6	448	6	ADA81679	Human sec	665	319	24.6	448	6	ABO49456	Human sec
593	319	24.6	448	6	ABO16773	Human sec	666	319	24.6	448	6	ABO49761	Human sec
594	319	24.6	448	6	ABO18399	Human sec	667	319	24.6	448	6	ADA78772	Human sec
595	319	24.6	448	6	ABO22826	Human PRO	668	319	24.6	448	6	ABR88318	Human sec
596	319	24.6	448	6	ABO23131	Human sec	669	319	24.6	448	6	ABM27064	Human sec
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598	319	24.6	448	6	ABR81630	Human sec	671	319	24.6	448	7	ABO39960	Human sec
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600	319	24.6	448	6	ABR89843	Human sec	673	319	24.6	448	7	ABO50981	Human sec
601	319	24.6	448	6	ABM26759	Human sec	674	319	24.6	448	7	ABO5437	Human sec
602	319	24.6	448	6	ABM13885	Human sec	675	319	24.6	448	7	ABR74741	Human sec
603	319	24.6	448	6	ABO28623	Human sec	676	319	24.6	448	7	ABR77220	Human sec
604	319	24.6	448	6	ABO30453	Human sec	677	319	24.6	448	7	ABM17977	Human sec
605	319	24.6	448	6	ABM07480	Human sec	678	319	24.6	448	7	ABR96028	Human sec
606	319	24.6	448	6	ABM04071	Human sec	679	319	24.6	448	7	ABO21961	Human sec
607	319	24.6	448	6	ABO37215	Human sec	680	319	24.6	448	7	ABO20131	Human sec
608	319	24.6	448	6	ABO41790	Human sec	681	319	24.6	448	7	ABO24434	Human sec
609	319	24.6	448	6	ABO35385	Human PRO	682	319	24.6	448	7	ABR86183	Human sec

683	319	24.6	448	7	ABM10835	Abm10835	Human	sec	756	319	24.6	448	7	ADB86151	Adb86151	Human	sec
684	319	24.6	448	7	ABM76834	Abm76834	Human	sec	757	319	24.6	448	7	ABM32249	Abm32249	Human	sec
685	319	24.6	448	7	ABR89538	Abm76834	Human	sec	758	319	24.6	448	7	ABM32554	Abm32554	Human	sec
686	319	24.6	448	7	ABM12865	Abm12865	Human	sec	759	319	24.6	448	7	ABM31639	Abm31639	Human	sec
687	319	24.6	448	7	ABM05955	Abm05955	Human	sec	760	319	24.6	448	7	ABM31029	Abm31029	Human	sec
688	319	24.6	448	7	ABO35080	Abm05955	Human	sec	761	319	24.6	448	7	ADDO5881	Adc78773	Human	PRO
689	319	24.6	448	7	ABM03156	Abm03156	Human	sec	762	319	24.6	448	7	ADDC78773	Adc78773	Human	PRO
690	319	24.6	448	7	ABM19134	Abm19134	Human	sec	763	319	24.6	448	7	ADG02876	Adg02876	Novel	hum
691	319	24.6	448	7	ABM19439	Abm19439	Human	sec	764	319	24.6	448	7	ADG01583	Adg01583	Novel	hum
692	319	24.6	448	7	ABO46650	Abm19439	Human	PRO	765	319	24.6	448	7	ADP95758	Adp95758	Novel	hum
693	319	24.6	448	7	ABO49151	Abm19439	Human	PRO	766	319	24.6	448	7	ADG12573	Adg12573	Novel	hum
694	319	24.6	448	7	ABR69194	Abm19439	Human	sec	767	319	24.6	448	7	ADH09233	Adh09233	Human	PRO
695	319	24.6	448	7	ABR89233	Abm19439	Human	sec	768	319	24.6	448	7	ADG63696	Adg63696	Human	sec
696	319	24.6	448	7	ABR72606	Abm19439	Human	sec	769	319	24.6	448	7	ADL33014	Adl33014	Novel	hum
697	319	24.6	448	7	ABR74436	Abm19439	Human	sec	770	319	24.6	448	7	ADM30548	Adm30548	Novel	hum
698	319	24.6	448	7	ABO18704	Abm19439	Human	sec	771	319	24.6	448	8	ADG74545	Adg74545	Human	sec
699	319	24.6	448	7	ABR80410	Abm19439	Human	sec	772	319	24.6	448	8	ADG74545	Adg74545	Human	sec
700	319	24.6	448	7	ABM01631	Abm19439	Human	sec	773	319	24.6	448	8	ADG74545	Adg74545	Human	sec
701	319	24.6	448	7	ABM02241	Abm19439	Human	sec	774	319	24.6	448	8	ADG74545	Adg74545	Human	sec
702	319	24.6	448	7	ABR87403	Abm19439	Human	sec	775	319	24.6	448	8	ADG74545	Adg74545	Human	sec
703	319	24.6	448	7	ABM12970	Abm12970	Human	sec	776	319	24.6	448	8	ADG00801	Adg00801	Novel	hum
704	319	24.6	448	7	ABM30724	Abm12970	Human	sec	777	319	24.6	448	8	ADG83057	Adg83057	Human	PRO
705	319	24.6	448	7	ABM24624	Abm12970	Human	sec	778	319	24.6	448	8	ADH26338	Adh26338	Novel	hum
706	319	24.6	448	7	ABO29538	Abm12970	Human	sec	779	319	24.6	448	8	ADG63545	Adg63545	Human	sec
707	319	24.6	448	7	ABO31368	Abm12970	Human	sec	780	319	24.6	448	8	ADH33307	Adh33307	Human	PRO
708	319	24.6	448	7	ABM14495	Abm14495	Human	sec	781	319	24.6	448	8	ADJ55046	Adj55046	Human	PRO
709	319	24.6	448	7	ABM09920	Abm14495	Human	sec	782	319	24.6	448	8	ADJ64817	Adj64817	Human	PRO
710	319	24.6	448	7	ABO39045	Abm14495	Human	sec	783	319	24.6	448	8	ADM31713	Adm31713	Novel	hum
711	319	24.6	448	7	ABM34810	Abm14495	Human	sec	784	319	24.6	448	8	ADM36760	Adm36760	Novel	hum
712	319	24.6	448	7	ABO51286	Abm14495	Human	sec	785	319	24.6	448	8	ADM40565	Adm40565	Novel	hum
713	319	24.6	448	7	ABO04112	Abm14495	Human	sec	786	319	24.6	448	8	ADN38173	Adn38173	Novel	hum
714	319	24.6	448	7	ABO10582	Abm14495	Human	PRO	787	319	24.6	493	8	ADT49897	Adt49897	Murine	AK
715	319	24.6	448	7	ABR77825	Abm14495	Human	sec	788	318.5	24.6	1145	4	ADG95480	Adg95480	Human	NOV
716	319	24.6	448	7	ABR79035	Abm14495	Human	sec	789	318	24.5	451	4	ABE88420	AbE88420	Human	mem
717	319	24.6	448	7	ABO24129	Abm14495	Human	sec	790	318	24.5	811	5	ABP62957	Abp62957	Human	pol
718	319	24.6	448	7	ABR93893	Abm14495	Human	sec	791	318	24.5	830	5	ABP62956	Abp62956	Human	pol
719	319	24.6	448	7	ABM01936	Abm14495	Human	sec	792	318	24.5	848	8	ABM83038	Abm83038	Human	dia
720	319	24.6	448	7	ABM78359	Abm14495	Human	sec	793	318	24.5	889	8	ABM83037	Abm83037	Human	dia
721	319	24.6	448	7	ABR90148	Abm14495	Human	sec	794	318	24.5	915	2	AAV13350	Aay13350	Amino	aci
722	319	24.6	448	7	ABM27674	Abm14495	Human	sec	795	318	24.5	915	3	AAV95340	Aay95340	Human	PRO
723	319	24.6	448	7	ABM13275	Abm14495	Human	sec	796	318	24.5	915	3	ADC78354	Adc78354	Human	PRO
724	319	24.6	448	7	ABO31978	Abm14495	Human	sec	797	318	24.5	915	4	ABM80218	Abm80218	Human	PRO
725	319	24.6	448	7	ABM14190	Abm14190	Human	sec	798	318	24.5	915	4	AAU12318	Aau12318	Human	PRO
726	319	24.6	448	7	ABM08395	Abm14190	Human	sec	799	318	24.5	915	4	AAU53077	Aab53077	Human	ang
727	319	24.6	448	7	ABO40265	Abm14190	Human	sec	800	318	24.5	915	6	ABU71596	Abu71596	Human	PRO
728	319	24.6	448	7	ABM74700	Abm14190	Human	sec	801	318	24.5	915	6	ABO17762	Abu17762	Novel	hum
729	319	24.6	448	7	ABM33895	Abm14190	Human	sec	802	318	24.5	915	6	ABU71451	Abu71451	Human	PRO
730	319	24.6	448	7	ABM20354	Abm14190	Human	sec	803	318	24.5	915	6	ABU81016	Abu81016	Human	PRO
731	319	24.6	448	7	ABO48846	Abm14190	Human	sec	804	318	24.5	915	6	ABU71897	Abu71897	Human	sec
732	319	24.6	448	7	ABR72911	Abm14190	Human	sec	805	318	24.5	915	6	ABO01780	Abu66716	Novel	hum
733	319	24.6	448	7	ABO15553	Abm14190	Human	sec	806	318	24.5	915	6	ABU54353	Abu54353	Human	sec
734	319	24.6	448	7	ABR85268	Abm14190	Human	sec	807	318	24.5	915	6	ABO47368	Abu47368	Human	sec
735	319	24.6	448	7	ABO15248	Abm14190	Human	sec	808	318	24.5	915	6	ABU59797	Abu59797	Novel	sec
736	319	24.6	448	7	ABO17383	Abm14190	Human	sec	809	318	24.5	915	6	ABO24987	Abu24987	Human	sec
737	319	24.6	448	7	ABO19841	Abm14190	Human	sec	810	318	24.5	915	6	ABU64505	Abu64505	Human	sec
738	319	24.6	448	7	ABM17672	Abm17672	Human	sec	811	318	24.5	915	6	ABU67351	Abu67351	Human	sec
739	319	24.6	448	7	ABR85573	Abm17672	Human	sec	812	318	24.5	915	6	ABO14871	Abu14871	Human	sec
740	319	24.6	448	7	ABM77139	Abm17672	Human	sec	813	318	24.5	915	6	ABU66992	Abu66992	Human	sec
741	319	24.6	448	7	ABM028318	Abm17672	Human	sec	814	318	24.5	915	6	ABU69628	Abu69628	Novel	hum
742	319	24.6	448	7	ABM23099	Abm17672	Human	sec	815	318	24.5	915	6	ABO14810	Abu14810	Human	sec
743	319	24.6	448	7	ABM30419	Abm17672	Human	sec	816	318	24.5	915	6	ADA45813	Ada45813	Novel	hum
744	319	24.6	448	7	ABM21879	Abm21879	Human	sec	817	318	24.5	915	6	ADA76244	Ada76244	Human	PRO
745	319	24.6	448	7	ABM21574	Abm21574	Human	sec	818	318	24.5	915	6	ADb29239	Adb29239	Human	sec
746	319	24.6	448	7	ABM15105	Abm21574	Human	sec	819	318	24.5	915	6	ADA18894	Ada18894	Human	PRO
747	319	24.6	448	7	ABO41180	Abm21574	Human	sec	820	318	24.5	915	6	ADA61517	Ada61517	Homio	espi
748	319	24.6	448	7	ABO36910	Abm21574	Human	sec	821	318	24.5	915	6	ADB19302	Adb19302	Novel	hum
749	319	24.6	448	7	ABO37520	Abm21574	Human	sec	822	318	24.5	915	6	ADB27843	Adb27843	Human	PRO
750	319	24.6	448	7	ABM75310	Abm21574	Human	sec	823	318	24.5	915	6	ADA86322	Ada86322	Novel	hum
751	319	24.6	448	7	ABM33590	Abm21574	Human	sec	824	318	24.5	915	6	ADB15886	Adb15886	Human	PRO
752	319	24.6	448	7	ABO46345	Abm21574	Human	sec	825	318	24.5	915	6	ADA47672	Ada47672	Human	PRO
753	319	24.6	448	7	ADA82843	Abm21574	Human	sec	826	318	24.5	915	6	ADA18095	Ada18095	Human	sec
754	319	24.6	448	7	ABM31944	Abm21574	Human	sec	827	318	24.5	915	6	ABO32762	AbO32762	Human	sec
755	319	24.6	448	7	ABM31334	Abm31334	Human	sec	828	318	24.5	915	6				

829	318	24.5	915	6	ADA67467	Ada67467 Human PRO	902	318	24.5	915	7	ADB34411	ADB34411 Human PRO
830	318	24.5	915	6	ADB30474	ADB30474 Human PRO	903	318	24.5	915	7	ADB35515	ADB35515 Human PRO
831	318	24.5	915	6	ADA85770	Ada85770 Novel hum	904	318	24.5	915	7	ADB33859	ADB33859 Human PRO
832	318	24.5	915	6	ADA96982	Ada96982 Human PRO	905	318	24.5	915	7	ADB34963	ADB34963 Human PRO
833	318	24.5	915	6	ADA79286	Ada79286 Human PRO	906	318	24.5	915	7	ADB36067	ADB36067 Human PRO
834	318	24.5	915	6	ADA87425	Ada87425 Novel hum	907	318	24.5	915	7	ADB46462	ADB46462 Novel hum
835	318	24.5	915	6	ADA87425	Ada87425 Novel hum	908	318	24.5	915	7	ADC28342	ADC28342 Human sec
836	318	24.5	915	6	ABO34822	AbO34822 Human PRO	909	318	24.5	915	7	ADC39542	ADC39542 Human sec
837	318	24.5	915	6	ADA16070	Ada16070 Human sec	910	318	24.5	915	7	ADC40056	ADC40056 Human sec
838	318	24.5	915	6	ADA91719	Ada91719 Novel hum	911	318	24.5	915	7	ADC18884	ADC18884 Human sec
839	318	24.5	915	6	ADB14782	AdB14782 Human PRO	912	318	24.5	915	7	ADC34180	ADC34180 Human sec
840	318	24.5	915	6	ADB18743	AdB18743 Novel hum	913	318	24.5	915	7	ADC29235	ADC29235 Human sec
841	318	24.5	915	6	ADA93958	Ada93958 Human PRO	914	318	24.5	915	7	ADC28766	ADC28766 Human sec
842	318	24.5	915	6	ADB19854	AdB19854 Novel hum	915	318	24.5	915	7	ADC40651	ADC40651 Human sec
843	318	24.5	915	6	ADB13166	AdB13166 Human PRO	916	318	24.5	915	7	ADC19308	ADC19308 Human sec
844	318	24.5	915	6	ABO433295	AbO433295 Novel hum	917	318	24.5	915	7	ADC33756	ADC33756 Human sec
845	318	24.5	915	6	ADA74420	Ada74420 Human PRO	918	318	24.5	915	7	ADC12826	ADC12826 Human sec
846	318	24.5	915	6	ADA42215	Ada42215 Human sec	919	318	24.5	915	7	ADC50335	ADC50335 Novel hum
847	318	24.5	915	6	ADB24653	AdB24653 Human PRO	920	318	24.5	915	7	ADC71882	ADC71882 Novel hum
848	318	24.5	915	6	ADA82177	Ada82177 Human PRO	921	318	24.5	915	7	ADC59861	ADC59861 Novel hum
849	318	24.5	915	6	ADA75140	Ada75140 Human PRO	922	318	24.5	915	7	ADC52868	ADC52868 Novel hum
850	318	24.5	915	6	ADA85218	Ada85218 Human PRO	923	318	24.5	915	7	ADC57222	ADC57222 Novel hum
851	318	24.5	915	6	ADA84666	Ada84666 Novel hum	924	318	24.5	915	7	ADC60413	ADC60413 Novel hum
852	318	24.5	915	6	ABO17500	AbO17500 Human PRO	925	318	24.5	915	7	ADC50888	ADC50888 Novel hum
853	318	24.5	915	6	ADB29922	AdB29922 Human PRO	926	318	24.5	915	7	ADC65415	ADC65415 Human PRO
854	318	24.5	915	6	ADA80450	Ada80450 Human PRO	927	318	24.5	915	7	ADC54513	ADC54513 Novel hum
855	318	24.5	915	6	ADA75692	Ada75692 Human PRO	928	318	24.5	915	7	ADC53474	ADC53474 Novel hum
856	318	24.5	915	6	ADA46917	Ada46917 Human PRO	929	318	24.5	915	7	ADC58997	ADC58997 Novel hum
857	318	24.5	915	6	ADB25213	AdB25213 Human PRO	930	318	24.5	915	7	ADC55875	ADC55875 Novel hum
858	318	24.5	915	6	ADA93389	Ada93389 Human PRO	931	318	24.5	915	7	ADC58445	ADC58445 Novel hum
859	318	24.5	915	6	ADB26739	AdB26739 Human PRO	932	318	24.5	915	7	ADC12278	ADC12278 Human sec
860	318	24.5	915	6	ADB31026	AdB31026 Human PRO	933	318	24.5	915	7	ADC03119	ADC03119 Novel hum
861	318	24.5	915	6	ADA60954	Ada60954 Homo sapi	934	318	24.5	915	7	ADC90111	ADC90111 Novel hum
862	318	24.5	915	6	ADB24101	AdB24101 Human PRO	935	318	24.5	915	7	ADC69530	ADC69530 Human PRO
863	318	24.5	915	6	ADA96430	Ada96430 Human PRO	936	318	24.5	915	7	ADC48419	ADC48419 Human PRO
864	318	24.5	915	6	ADA81002	Ada81002 Human PRO	937	318	24.5	915	7	ADC09948	ADC09948 Human PRO
865	318	24.5	915	6	ADA95878	Ada95878 Human PRO	938	318	24.5	915	7	ADC04523	ADC04523 Novel hum
866	318	24.5	915	6	ADB26187	AdB26187 Human PRO	939	318	24.5	915	7	ADC80479	ADC80479 Novel hum
867	318	24.5	915	6	ADB21672	AdB21672 Novel hum	940	318	24.5	915	7	ADD10986	ADD10986 Human PRO
868	318	24.5	915	7	ADA77451	Ada77451 Human PRO	941	318	24.5	915	7	ADC47867	ADC47867 Human PRO
869	318	24.5	915	7	ADB18191	AdB18191 Human PRO	942	318	24.5	915	7	ADD04833	ADD04833 Human sec
870	318	24.5	915	7	ADA86874	Ada86874 Novel hum	943	318	24.5	915	7	ADC79927	ADC79927 Novel hum
871	318	24.5	915	7	ADA16494	Ada16494 Human sec	944	318	24.5	915	7	ADD09396	ADD09396 Human PRO
872	318	24.5	915	7	ADA12923	Ada12923 Human sec	945	318	24.5	915	7	ADD03839	ADD03839 Human sec
873	318	24.5	915	7	ADA41791	Ada41791 Human sec	946	318	24.5	915	7	ADD03415	ADD03415 Human sec
874	318	24.5	915	7	ADA87977	Ada87977 Novel hum	947	318	24.5	915	7	ADD41109	ADD41109 Novel hum
875	318	24.5	915	7	ADA46365	Ada46365 Novel hum	948	318	24.5	915	7	ADD52248	ADD52248 Human PRO
876	318	24.5	915	7	ADA17138	Ada17138 Human sec	949	318	24.5	915	7	ADD52988	ADD52988 Human PRO
877	318	24.5	915	7	ADA42641	Ada42641 Human sec	950	318	24.5	915	7	ADD53540	ADD53540 Novel hum
878	318	24.5	915	7	ADB28395	AdB28395 Human PRO	951	318	24.5	915	7	ADD51696	ADD51696 Human PRO
879	318	24.5	915	7	ADB28947	AdB28947 Human PRO	952	318	24.5	915	7	ADD02495	ADD02495 Human PRO
880	318	24.5	915	7	ADA76899	Ada76899 Human PRO	953	318	24.5	915	7	ADD01929	ADD01929 Human PRO
881	318	24.5	915	7	ADA88529	Ada88529 Novel hum	954	318	24.5	915	7	ADD54111	ADD54111 Novel hum
882	318	24.5	915	7	ADA97534	Ada97534 Human PRO	955	318	24.5	915	7	ADD92428	ADD92428 Human PRO
883	318	24.5	915	7	ADB27291	AdB27291 Human PRO	956	318	24.5	915	7	ADD91324	ADD91324 Human PRO
884	318	24.5	915	7	ADB22224	AdB22224 Novel hum	957	318	24.5	915	7	ADD90398	ADD90398 Human PRO
885	318	24.5	915	7	ABO17561	AbO17561 Human PRO	958	318	24.5	915	7	ADE32235	ADE32235 Novel hum
886	318	24.5	915	7	ADA66915	Ada66915 Human PRO	959	318	24.5	915	7	ADE22167	ADE22167 Human PRO
887	318	24.5	915	7	ADB22776	AdB22776 Human PRO	960	318	24.5	915	7	ADD79391	ADD79391 Human PRO
888	318	24.5	915	7	ADB23549	AdB23549 Human PRO	961	318	24.5	915	7	ADE41927	ADE41927 Human PRO
889	318	24.5	915	7	ADA92271	Ada92271 Novel hum	962	318	24.5	915	7	ADE17744	ADE17744 Human PRO
890	318	24.5	915	7	ADB15334	AdB15334 Human PRO	963	318	24.5	915	7	ADD91876	ADD91876 Human PRO
891	318	24.5	915	7	ADB38586	AdB38586 Novel hum	964	318	24.5	915	7	ADE33339	ADE33339 Novel hum
892	318	24.5	915	7	ADB38034	AdB38034 Novel hum	965	318	24.5	915	7	ADE33891	ADE33891 Novel hum
893	318	24.5	915	7	ADB66506	AdB66506 Novel hum	966	318	24.5	915	7	ADD79943	ADD79943 Human PRO
894	318	24.5	915	7	ADB89586	AdB89586 Human PRO	967	318	24.5	915	7	ADD92980	ADD92980 Human PRO
895	318	24.5	915	7	ADB90318	AdB90318 Human PRO	968	318	24.5	915	7	ADE19400	ADE19400 Human PRO
896	318	24.5	915	7	ADB77560	AdB77560 Human sec	969	318	24.5	915	7	ADE34667	ADE34667 Human sec
897	318	24.5	915	7	ADB7569	AdB7569 Novel hum	970	318	24.5	915	7	ADE18848	ADE18848 Human PRO
898	318	24.5	915	7	ADB39419	AdB39419 Novel hum	971	318	24.5	915	7	ADE43044	ADE43044 Human PRO
899	318	24.5	915	7	ADB74696	AdB74696 Human sec	972	318	24.5	915	7	ADD95833	ADD95833 Human PRO
900	318	24.5	915	7	ADB47042	AdB47042 Novel hum	973	318	24.5	915	7	ADD22719	ADD22719 Human PRO
901	318	24.5	915	7	ADB86649	AdB86649 Human PRO	974	318	24.5	915	7	ADD78837	ADD78837 Human PRO

975 318 24.5 915 7 ADE32787
 976 318 24.5 915 7 ADE42479
 977 318 24.5 915 7 AD80495
 978 318 24.5 915 7 AD80495
 979 318 24.5 915 7 AD89523
 980 318 24.5 915 7 ADE40807
 981 318 24.5 915 7 ADE04606
 982 318 24.5 915 7 ADE92735
 983 318 24.5 915 7 ADG21444
 984 318 24.5 915 7 ADG23085
 985 318 24.5 915 7 ADG97420
 986 318 24.5 915 7 ADG80484
 987 318 24.5 915 7 ADG79932
 988 318 24.5 915 7 ADH59150
 989 318 24.5 915 7 ADH55224
 990 318 24.5 915 7 ADH55776
 991 318 24.5 915 7 ADI37929
 992 318 24.5 915 7 ADI63995
 993 318 24.5 915 7 ADI64944
 994 318 24.5 915 7 ADI63443
 995 318 24.5 915 7 ADH81857
 996 318 24.5 915 7 ADH81305
 997 318 24.5 915 7 ADJ26197
 998 318 24.5 915 7 ADM82474
 999 318 24.5 915 7 ADN15873
 1000 318 24.5 915 7 ADN16502
 1000 318 24.5 915 7 ADN15321

ALIGNMENTS

RESULT 1
 AAR99414
 ID AAR99414 standard; protein; 678 AA.

AC AAR99414;
 XX
 XX
 DT 04-DEC-1996 (first entry)
 XX
 DE Human gas6 protein, an S protein homologue and axl receptor ligand.
 XX
 KW Axl receptor ligand; human protein S homologue; growth factor;
 KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;
 KW recombinant production.
 XX
 OS Homo sapiens.
 XX
 PN US5538861-A.
 XX
 PD 23-JUL-1996.
 XX
 PF 29-JUL-1994; 94US-00282141.
 XX
 PR 29-JUL-1994; 94US-00282141.
 XX
 PA (AMGE-) AMGEN INC.
 PA (SCHN/) SCHNEIDER C.
 XX
 PI Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;
 XX
 DR WPI; 1996-353825/35.
 DR N-PSDB; AAT41544.
 XX
 XX DNA encoding gas6, the axl receptor ligand - useful to regulate growth of
 PT myeloid cells and malignancies.
 XX
 PS Claim 1; Col 19-22; 36pp; English.
 XX
 CC AAR99414 is the gas6 protein [from the growth arrest specific gene number
 CC 6]. The gas6 protein has homology to human protein S which functions as a
 CC cofactor in a protease cascade that regulates coagulation. Gas6
 CC expression, as with gas1 and gas2, is associated with cell growth arrest
 CC which suggests a possible role of gas6 in the regulation of cell growth.

CC In fact the gas6 protein is an axl receptor (axlr) ligand and a growth
 CC factor for any cells expressing axlr e.g. bone marrow, spleen, thymus,
 CC ovary, heart, intestine and lung cells. The axl receptor is involved in
 CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate
 CC growth of such cells
 XX
 SQ Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.6e-83; Indels 0; Gaps 0;
 Matches 227; Conservative 0; Mismatches 0;
 QY 1 PRYLDCKNKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
 DB 90 PRYLDCKNKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
 QY 61 GRLCDKDVNECSQNGGCLQICHNKPGSFHCSHSGFELSDGRTCDQIDECADSEACGE 120
 DB 150 GRLCDKDVNECSQNGGCLQICHNKPGSFHCSHSGFELSDGRTCDQIDECADSEACGE 209
 QY 121 ARCKNLPGSYSCLDCEGFAYSSQEKACRDVDECIQGRCEQVCVNSPGSYTCHCDGRGLK 180
 DB 210 ARCKNLPGSYSCLDCEGFAYSSQEKACRDVDECIQGRCEQVCVNSPGSYTCHCDGRGLK 269
 QY 181 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKELQP 227
 DB 270 LSQDMTDCEDILPCVPFSAKSVKSLYLGRMFSGTPVIRLRFKELQP 316

RESULT 2
 AAW46463
 ID AAW46463 standard; protein; 678 AA.
 XX
 AC AAW46463;
 XX
 DT 15-MAY-1998 (first entry)
 XX
 DE Human growth arrest specific-gene 6 (gas6) protein.
 XX
 KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
 KW receptor tyrosine kinase; regulation; protease cascade; insulin;
 KW growth regulation; serum-free culture medium; human; Schwann cell;
 KW receptor activator; erbB receptor; heregulin; CAMP level; proliferation;
 KW treatment; nervous system injury.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 49..89
 FT /note= "A domain of gas6"
 FT Domain 90..117
 FT /note= "B domain of gas6 comprising a thrombin sensitive
 FT loop"
 FT Domain 118..278
 FT /note= "C domain of gas6, contains 4 epidermal growth
 FT factor-like repeats"
 FT Domain 279..678
 FT /note= "D domain of gas6, homologous to steroid binding
 FT hormone"
 FT Domain 314..471
 FT /note= "G domain 1"
 FT Domain 503..671
 FT /note= "G domain 2"
 XX
 XX US5714385-A.
 XX
 XX 03-FEB-1998.
 XX
 XX 10-MAY-1995; 95US-00435434.
 XX
 XX 10-MAY-1995; 95US-00435434.
 XX
 XX (GETH) GENENTECH INC.

XX Chen J, Mather JP, Li R;
 XX WPI; 1998-129864/12.
 XX Medium for culturing human Schwann cells - is serum-free and contains Rse
 XX receptor activator and other mitogens.
 XX Disclosure; Fig 2; Sipp; English.
 XX The present sequence represents a human growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Rse and Axl receptor. Rse is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 1297; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.6e-83;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRLDCINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 60
 DB 90 PRLDCINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 149
 QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFSHCSHGFELSSDGRTCQDIDECADSEACGE 120
 DB 150 GRLCDKDVNECSQENGCGCLQICHNKPFSHCSHGFELSSDGRTCQDIDECADSEACGE 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 269
 QY 181 LSQMDTCTEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 227
 DB 270 LSQMDTCTEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 316
 RESULT 3
 AAY29794
 ID AAY29794 standard; protein; 678 AA.
 XX AC AAY29794;
 XX DT 15-NOV-1999 (first entry)
 XX DE Human growth arrest-specific gene 6 protein.
 XX Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW Gli3 cell; Schwann cell; fusion protein.
 XX OS Homo sapiens.
 XX PN US5955420-A.
 XX PD 21-SEP-1999.
 XX PF 10-MAY-1995; 95US-00438864.
 XX PR 10-MAR-1995; 95US-00402253.
 XX PA (GETH) GENENTECH INC.

XX Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
 XX WPI; 1999-539585/45.
 XX Activation of the Rse receptor on a cell, useful for promoting cell
 XX proliferation and differentiation.
 XX Disclosure; Fig 2; 48pp; English.
 XX A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents human gas6 given in the present invention
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 1297; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.6e-83;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PRLDCINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 60
 DB 90 PRLDCINKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 149
 QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFSHCSHGFELSSDGRTCQDIDECADSEACGE 120
 DB 150 GRLCDKDVNECSQENGCGCLQICHNKPFSHCSHGFELSSDGRTCQDIDECADSEACGE 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 269
 QY 181 LSQMDTCTEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 227
 DB 270 LSQMDTCTEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 316
 RESULT 4
 AAY57383
 ID AAY57383 standard; protein; 678 AA.
 XX AC AAY57383;
 XX DT 19-JUN-2000 (first entry)
 XX DE Amino acid sequence of human gas6 (h gas6) protein.
 XX Nervous system; Schwann cell; mitogen; Rse/Axl receptor activator;
 KW central nervous system; peripheral nervous system; injury; trauma;
 KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 KW protein S.
 XX OS Homo sapiens.
 XX PN US6033660-A.
 XX PD 07-MAR-2000.
 XX PF 10-MAY-1995; 95US-00438862.
 XX PR 10-MAY-1995; 95US-00438862.
 XX PA (GETH) GENENTECH INC.
 XX Mather JP, Chen J, Li R;
 XX WPI; 2000-246046/21.
 XX Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.

PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;

XX WPI; 2004-316097/29.

XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
PT manufacturing medicines or for identifying inhibitors of Gas6 and its
PT receptors.

XX Disclosure; SEQ ID NO 3; 28pp; English.

XX The present invention describes an isolated growth arrest specific gene 6
CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
CC ID NO:2, ADW40824), or a polyhistidine sequence. The variant Gas6
CC polypeptide has 75% identity to native human Gas6 protein. Also
CC described: (1) a recombinant DNA molecule encoding the amino acid
CC sequence of the polypeptide described above; (2) a vector comprising the
CC above nucleic acid; (3) a host cell comprising the vector, where the host
CC cell is of mammalian origin; and (4) a composition comprising the
CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
CC activity. The composition is useful for manufacturing medicines or for
CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
CC may also be used for Gas6-dependent receptor phosphorylation, receptor
CC internalisation, cell proliferation, prevention of cell apoptosis, or
CC induction of signaling molecules or cell markers. The present sequence
CC represents the human Gas6 protein from the present invention.

XX Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 8; Length 678;

Best Local Similarity 100.0%; Pred. No. 2.6e-83;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYLDICINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 60

DB 90 PRYLDICINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 149

OY 61 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGSELSGDRTCQDIDECADSEACGE 120

DB 150 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGSELSGDRTCQDIDECADSEACGE 209

OY 121 ARCKNLPGSYCLDCEGFAYSSQKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180

DB 210 ARCKNLPGSYCLDCEGFAYSSQKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269

OY 181 LSQDMTDCEDILPCVPFFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227

DB 270 LSQDMTDCEDILPCVPFFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316

RESULT 7

ID ADN60275 standard; protein; 678 AA.

XX AC ADN60275;

XX 18-NOV-2004 (first entry)

XX Human growth arrest-specific 6 (GAS6) protein.

XX angiogenesis modulator; tumorigenesis modulator; angiogenesis; Axl;
KW tubulin cofactor D; transglutaminase 2; cytosine deaminase;
KW peptidase M41; paralogin; CD13 aminopeptidase; PPK-1; zip kinase; Gas6;
KW SRM160; non-muscle myosin heavy chain; calmodulin 2; symporter;
KW semaphorin; zinc finger helicase; plexin-A2; deoxycytidylate deaminase;
KW sugar transporter; tumorigenesis; antiangiogenic; cytosolic;
KW cerebroprotective; vasotrophic; antiinfertility; cardiac;
KW antibody therapy; antisense therapy; RNA interference therapy;
KW RNAi therapy; cancer; stroke; infertility; heart disease; human.

OS Homo sapiens.

XX WO2004039955-A2.

XX 13-MAY-2004.

XX 29-OCT-2003; 2003WO-US034281.

XX 29-OCT-2002; 2002US-0421989P.

XX 17-OCT-2003; 2003US-0512251P.

XX (RIGE-) RIGEL PHARM INC.

XX Lorens JB, Atchison RE, Frieria A, Holland S;

XX WPI; 2004-376181/35.

XX N-PSDB; ADN60274.

XX Identifying a compound that modulates angiogenesis or tumorigenesis,
PT useful in diagnosing and treating angiogenesis, cancer, stroke,
PT infertility and heart disease, comprises contacting the compound with
PT angiogenesis polypeptide.

XX Disclosure; Page 65; 105pp; English.

XX The present invention describes a method for identifying a compound that
CC modulates angiogenesis or tumorigenesis. The method comprises: (a)
CC contacting the compound with angiogenesis polypeptide, e.g. Axl, tubulin
CC cofactor D, transglutaminase 2, cytosine deaminase, peptidase M41
CC (paralogin), CD13 aminopeptidase, PPK-1, zip kinase, Gas6, SRM160, non-
CC muscle myosin heavy chain, calmodulin 2, novel symporter, novel
CC semaphorin, novel zinc finger helicase (FLJ22611), plexin-A2,
CC deoxycytidylate deaminase or novel sugar transporter; (b) determining the
CC functional effector of the compound upon the angiogenesis polypeptide or
CC the physical effect of the compound upon the target polypeptide or its
CC fragment or inactive variant; and (c) determining the chemical or
CC phenotypic effect of the compound upon a cell comprising the target
CC polypeptide or its fragment or inactive variant, thus identifying a
CC compound that modulates cell cycle arrest. Also described is a method of
CC modulating angiogenesis in a subject. The angiogenesis or tumorigenesis
CC modulating compound has antiangiogenic, cytostatic, cerebroprotective,
CC vasotrophic, antiinfertility and cardiac activities, and can be used in
CC antibody, antisense and RNA interference (RNAi) therapies. The method is
CC useful in identifying a compound that modulates angiogenesis. The methods
CC and compounds or compositions are useful in diagnosing and treating
CC angiogenesis, cancer, stroke, infertility and heart disease. The present
CC sequence represents a human growth arrest-specific 6 (GAS6) protein,
CC which is used in the exemplification of the present invention.

XX Sequence 678 AA;

Query Match 100.0%; Score 1297; DB 8; Length 678;

Best Local Similarity 100.0%; Pred. No. 2.6e-83;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PRYLDICINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 60

DB 90 PRYLDICINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 149

OY 61 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGSELSGDRTCQDIDECADSEACGE 120

DB 150 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGSELSGDRTCQDIDECADSEACGE 209

OY 121 ARCKNLPGSYCLDCEGFAYSSQKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180

DB 210 ARCKNLPGSYCLDCEGFAYSSQKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269

OY 181 LSQDMTDCEDILPCVPFFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227

DB 270 LSQDMTDCEDILPCVPFFSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316

RESULT 8

ADD48757

ID ADD48757 standard; protein; 679 AA.

XX

AC ADD48757;
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Human Protein L13720, SEQ ID NO 14467.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI
XX
XX WPI; 2003-268312/26.
DR GENBANK; L13720.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 1297; DB 7; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.6e-83;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLFDQCTPNPCDRKGTQACQDLMGNFCCCKAGWG 60
|||||

Db 90 PRYLDCKNGSPYTKNSGFATCVQNLFDQCTPNPCDRKGTQACQDLMGNFCCCKAGWG 149
QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFHCSCHSGFELSSDGRTCODIDECADSEACGE 120
|||||
Db 150 GRLCDKDVNECSQENGGLQICHNKPGSFHCSCHSGFELSSDGRTCODIDECADSEACGE 209
|||||
QY 121 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
|||||
Db 210 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 269
|||||
QY 181 LSQDMTCEBILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
|||||
Db 270 LSQDMTCEBILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 316
|||||

RESULT 9
ADM40823
ID ADM40823 standard; protein; 686 AA.
XX
AC ADM40823;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human Gas6 protein with a C-terminal epitope tag SEQ ID NO:1.
XX
XX growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
KW receptor internalisation; cell proliferation; cell apoptosis prevention;
KW signaling molecule; cell marker; human.
XX
OS Homo sapiens.
XX
XX WO2004029209-A2.
XX
PD 08-APR-2004.
XX
XX 24-SEP-2003; 2003WO-US030330.
XX
XX 24-SEP-2002; 2002US-0413157P.
XX
XX (CENZ) CENTOCOR INC.
XX
XX Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
WPI; 2004-316097/29.
XX
XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
PT manufacturing medicines or for identifying inhibitors of Gas6 and its
PT receptors.
XX
XX Claim 2; SEQ ID NO 1; 28pp; English.
XX
XX The present invention describes an isolated growth arrest specific gene 6
CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
CC ID NO:2, ADM40824), or a polyhistidine sequence. The variant Gas6
CC polypeptide has 75% identity to native human Gas6 protein. Also
CC described: (1) a recombinant DNA molecule encoding the amino acid
CC sequence of the polypeptide described above; (2) a vector comprising the
CC above nucleic acid; (3) a host cell comprising the vector, where the host
CC cell is of mammalian origin; and (4) a composition comprising the
CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
CC activity. The composition is useful for manufacturing medicines or for
CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
CC may also be used for Gas6-dependent receptor phosphorylation, receptor
CC internalisation, cell proliferation, prevention of cell apoptosis, or
CC induction of signaling molecules or cell markers. The present sequence
CC represents the human Gas6 protein with an epitope tag fused at the C-
CC terminus, from the present invention.
XX
XX Sequence 686 AA;

Query Match 100.0%; Score 1297; DB 8; Length 686;

Best Local Similarity 100.0%; Pred. No. 2.6e-83;		Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	PRYLDICINIKYSPYTKNSGFATCVQNL	PDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB	90	PRYLDICINIKYSPYTKNSGFATCVQNL	PDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY	61	GRLCDKDVNECSQENGCGCLOI	CHNKP
DB	150	GRLCDKDVNECSQENGCGCLOI	CHNKP
QY	121	ARCKNLPGSVSCLCDGFPAYSSOEKAC	RDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB	210	ARCKNLPGSVSCLCDGFPAYSSOEKAC	RDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 269
QY	181	LSQDMTCDILPCVPFVSVAKSILYLGR	MFSGTPIRLRFKRLQP 227
DB	270	LSQDMTCDILPCVPFVSVAKSILYLGR	MFSGTPIRLRFKRLQP 316
RESULT 10			
ADQ67207			
ID	ADQ67207 standard; protein; 624 AA.		
XX			
AC	ADQ67207;		
XX			
DT	07-OCT-2004 (first entry)		
XX			
DE	Novel human protein sequence #2180.		
XX			
KW	osteopathic; neuroprotective; neurotropic; antiparkinsonian; cytostatic;		
KW	gene therapy; diagnostic marker; morbid state; osteoporosis;		
KW	neurological disease; Alzheimer's disease; Parkinson's disease; dementia;		
KW	cancer.		
XX			
OS	Homo sapiens.		
XX			
PN	EP1440981-A2.		
XX			
PD	28-JUL-2004.		
XX			
PF	21-JAN-2004; 2004EP-00001196.		
XX			
PR	21-JAN-2003; 2003JP-00102206.		
PR	09-MAY-2003; 2003JP-00131392.		
XX			
PA	(REAS-) RES ASSOC BIOTECHNOLOGY.		
XX			
PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;		
PI	Yamamoto J, Isono Y, Nagai K, Irie R;		
XX			
DR	WPI: 2004-535376/52.		
DR	N-PSDB; ADQ65019.		
XX			
PT	Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,		
PT	Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.		
XX			
PS	Claim 1; SEQ ID NO 4368; 2449pp; English.		
XX			
CC	The invention relates to 2495 novel polynucleotides (I) and their encoded		
CC	polypeptides, sequences hybridizing to these nucleotides, sequences		
CC	encoding partial polypeptides and sequences having 70% or 90% identity to		
CC	the nucleotide and protein sequences. The nucleotides and polypeptides		
CC	are useful as diagnostic markers or therapeutic target for the diseases		
CC	or morbid states. They are also useful for treating osteoporosis,		
CC	neurological diseases, Alzheimer's diseases, Parkinson's diseases,		
CC	dementia and various cancers. This sequence corresponds to a protein		
CC	sequence of the invention.		
XX			
SQ	Sequence 624 AA;		
Query Match 97.8%; Score 1269; DB 8; Length 624;			
Best Local Similarity 99.6%; Pred. No. 2.3e-81;			

Matches 222; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
QY	5 DCINKYGSPTKNSGFATCVQNL
DB	40 NCINKYGSPTKNSGFATCVQNL
QY	65 KDVNECSQENGCGCLOICHNKP
DB	100 KDVNECSQENGCGCLOICHNKP
QY	125 NLPGSVSCLCDGFPAYSSOEKAC
DB	160 NLPGSVSCLCDGFPAYSSOEKAC
QY	185 MDTCEDILPCVPFVSVAKSILYLGR
DB	220 MDTCEDILPCVPFVSVAKSILYLGR
RESULT 11	
AAW46462	
ID	AAW46462 standard; protein; 673 AA.
XX	
AC	AAW46462;
XX	
DT	15-MAY-1998 (first entry)
XX	
DE	Murine growth arrest specific-gene 6 (gas6) protein.
XX	
KW	Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
KW	receptor tyrosine kinase; regulation; protease cascade; insulin;
KW	growth regulation; serum-free culture medium; human; Schwann cell;
KW	receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
KW	treatment; nervous system injury.
XX	
OS	Mus sp.
XX	
PN	US5714385-A.
XX	
PD	03-FEB-1998.
XX	
PF	10-MAY-1995; 95US-00435434.
XX	
PR	10-MAY-1995; 95US-00435434.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Chen J, Mather JP, Li R;
XX	
DR	WPI; 1998-129864/12.
XX	
PT	Medium for culturing human Schwann cells - is serum-free and contains Rse
PT	receptor activator and other mitogens.
XX	
PS	Disclosure; Fig 2; 51pp; English.
CC	The present sequence represents a murine growth arrest specific-gene 6
CC	(gas6) protein which is able to activate the Rsa and Axl receptor. Rse is
CC	a receptor tyrosine kinase that is preferentially expressed in the adult
CC	brain. Gas6 is a vitamin K dependent protein which may play a role in the
CC	regulation of a protease cascade relevant in growth regulation. The
CC	protein is used in a serum-free culture medium for culturing human
CC	Schwann cells, which does not support fibroblast growth. Gas6 functions
CC	as a mitogenic agent which is a Rse/Axl receptor activator. A second
CC	mitogenic agent e.g. insulin or an erbB receptor activator such as
CC	heregulin, is also required to raise cAMP levels and enhance survival or
CC	proliferation of human Schwann cells. The culture medium additionally
CC	comprises a molecule or composition that provides Fe ions to the Schwann
CC	cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
CC	cells can be used to treat patients with nervous system injuries
XX	
SQ	Sequence 673 AA;

Query Match		85.8%;	Score 1113;	DB 2;	Length 673;
Best Local Similarity		82.8%;	Pred. No. 2.3e-70;		
Matches 188;		Conservative 15;	Mismatches 24;	Indels 0;	Gaps 0;
QY	1	PRYLDCKVNECSQENSGGCLQICHNKP	GSFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	60	
DB	87	PRYQECMKYGRPEKKNPDKFACVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	146		
QY	61	GRLCDKDVNECSQENSGGCLQICHNKP	GSFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	120	
DB	147	GRLCDKDVNECSQENSGGCLQICHNKP	GSFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	206	
QY	121	ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGGLK	180		
DB	207	ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGGLK	266		
QY	181	LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFS	GTPVIRLRFKRLQ	227	
DB	267	LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFS	GTPVIRLRFKRLQ	313	
RESULT 12					
AAV29793					
ID	AAV29793	standard; protein; 673 AA.			
XX					
AC	AAV29793;				
DT	15-NOV-1999	(first entry)			
XX					
DE	Murine growth arrest-specific gene 6 protein.				
XX					
KW	Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;				
KW	growth arrest-specific gene 6; proliferation; differentiation;				
KW	glial cell; Schwann cell; fusion protein.				
XX					
OS	Mus sp.				
XX					
PN	US955420-A.				
XX					
PD	21-SEP-1999.				
XX					
PF	10-MAY-1995; 95US-00438864.				
XX					
PR	10-MAR-1995; 95US-00402253.				
XX					
PA	(GETH) GENENTECH INC.				
XX					
PI	Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;				
XX					
DR	WPI; 1999-539585/45.				
XX					
PT	Activation of the Rse receptor on a cell, useful for promoting cell				
PT	proliferation and differentiation.				
XX					
PS	Disclosure; Fig 2; 48pp; English.				
XX					
CC	A method has been developed for activating the Rse receptor on a cell.				
CC	The method comprises exposing the receptor to the exogenous growth arrest				
CC	-specific gene 6 (gas6) polypeptide. The method is useful for enhancing				
CC	cell proliferation and cell differentiation. The present sequence				
CC	represents murine gas6 given in the present invention				
XX					
SQ	Sequence 673 AA;				
Query Match					
Best Local Similarity		85.8%;	Score 1113;	DB 2;	Length 673;
Matches 188;		Conservative 15;	Mismatches 24;	Indels 0;	Gaps 0;
QY	1	PRYLDCKVNECSQENSGGCLQICHNKP	GSFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	60	
DB	87	PRYQECMKYGRPEKKNPDKFACVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	146		
QY	61	GRLCDKDVNECSQENSGGCLQICHNKP	GSFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFPFLCKAGWG	120	

Db	147	GRLCDKDVNECVQKNGGCSQVCHNKP	GSFQACAHSGFSLASDGTQDIDECTDSTCGD	206	
Qy	121	ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGGLK	180		
Db	207	ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGGLK	266		
Qy	181	LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFS	GTPVIRLRFKRLQ	227	
Db	267	LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFS	GTPVIRLRFKRLQ	313	
RESULT 13					
AAB33459					
ID	AAB33459 standard; protein; 673 AA.				
XX					
AC	AAB33459;				
XX					
DT	29-JAN-2001 (first entry)				
XX					
DE	Human PRO21 protein UNQ21 SEQ ID NO:231.				
XX					
KW	Human; immune related disease; diagnosis; antinflammatory; cardiant;				
KW	dermatological; antiarthritic; antirheumatic; immunosuppressive;				
KW	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;				
KW	antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;				
KW	antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;				
KW	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;				
KW	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;				
KW	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;				
KW	autoimmune thrombocytopaenia; immune-mediated renal disease;				
KW	denervating disease; hepatobiliary disease; Whipple's disease;				
KW	inflammatory bowel disease; gluten-sensitive enteropathy;				
KW	autoimmune disease; immune-mediated skin disease; allergic disease;				
KW	immunological disease; transplantation associated disease;				
KW	graft rejection; Graft-versus-host-disease.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200053758-A2.				
XX					
PD	14-SEP-2000.				
XX					
PF	02-MAR-2000; 2000WO-US005841.				
XX					
PR	08-MAR-1999; 99WO-US005028.				
PR	10-MAR-1999; 99US-0123618P.				
PR	12-MAR-1999; 99US-0123957P.				
PR	23-MAR-1999; 99US-0125775P.				
PR	12-APR-1999; 99US-0128849P.				
PR	20-APR-1999; 99WO-US008615.				
PR	28-APR-1999; 99US-0131445P.				
PR	04-MAY-1999; 99US-0132371P.				
PR	14-MAY-1999; 99US-0134287P.				
PR	02-JUN-1999; 99WO-US012252.				
PR	23-JUN-1999; 99US-0141037P.				
PR	26-JUL-1999; 99US-0144758P.				
PR	28-JUL-1999; 99US-0145698P.				
PR	01-SEP-1999; 99US-0146222P.				
PR	08-SEP-1999; 99WO-US020111.				
PR	13-SEP-1999; 99WO-US020594.				
PR	15-SEP-1999; 99WO-US020940.				
PR	15-SEP-1999; 99WO-US021090.				
PR	05-OCT-1999; 99WO-US021547.				
PR	29-OCT-1999; 99WO-US023089.				
PR	30-NOV-1999; 99US-0162506P.				
PR	30-NOV-1999; 99WO-US028214.				
PR	30-NOV-1999; 99WO-US028313.				
PR	30-NOV-1999; 99WO-US028409.				
PR	01-DEC-1999; 99WO-US028301.				
PR	01-DEC-1999; 99WO-US028634.				
PR	02-DEC-1999; 99WO-US028551.				
PR	02-DEC-1999; 99WO-US028564.				

PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030995.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
XX (GETH) GENENTECH INC.

XX
XX

PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX

DR WPI: 2000-572271/53.
DR N-PSDB; AAC58624.

XX

PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX
XX Claim 33; Fig 92; 309pp; English.

CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention

XX
XX Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCINKYGSPTKNSGFATCVQNLPOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDKFACVQNLPOCTPNPCDRKGTQACODLMGNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGGLCIQIHNKPGSFHCSHGFSLSGRTCCODIDECADSEACGE 120
DB 147 GRLCDKDVNECVKNGGCSQVCHNPGSFQACHGFSLSASDGTCCODIDETSDTCDG 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNPGSYTCHCDGRGLK 180
DB 207 ARCKNLPGSYSLCDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266
QY 181 LSQMDTCEIDILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
DB 267 LSPDMDTCEIDILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 14

AY57382

ID AAY57382 standard; protein; 673 AA.

XX
AC

AAY57382;

XX
DT 19-JUN-2000 (first entry)

XX
DE Amino acid sequence of murine gas6 (m gas6) protein.

XX
KW Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
KW central nervous system; peripheral nervous system; injury; trauma;
KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
XX protein S.

XX
OS Mus sp.

XX
PN US6033660-A.

XX
PD 07-MAR-2000.

XX
PF 10-MAY-1995; 95US-00438862.

XX
PR 10-MAY-1995; 95US-00438862.

XX
PA (GETH) GENENTECH INC.

XX
PI Mather JP, Chen J, Li R;

XX
DR WPI: 2000-246046/21.

XX
PT Repairing nervous system injuries in mammals, by administering human
PT Schwann cells that have been propagated in medium supplemented with
PT mitogens.

XX
PS Disclosure; Fig 2; 52pp; English.

CC The invention relates to a method for treating nervous system injuries in
CC mammals by administering human Schwann cells (SC) that have been cultured
CC in serum-free medium. The serum-free medium is a nutrient solution
CC supplemented with two mitogens, one of which, is a Res/Axl receptor
CC activator, to increase survival and proliferation of SC. The method is
CC used to treat (or prevent) central or peripheral nervous system injury,
CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
CC or lesions associated with nutritional deficiencies, systemic disease,
CC toxins or demyelination. Culturing cells in the specified medium allows
CC proliferation of adult SC for use in autologous transplants. The present
CC sequence represents a murine gas6 (m gas6) protein, having 43% sequence
CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
CC survival factor for SCs in defined serum-free culture

XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCINKYGSPTKNSGFATCVQNLPOCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDKFACVQNLPOCTPNPCDRKGTQACODLMGNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGGLCIQIHNKPGSFHCSHGFSLSGRTCCODIDECADSEACGE 120
DB 147 GRLCDKDVNECVKNGGCSQVCHNPGSFQACHGFSLSASDGTCCODIDETSDTCDG 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVCHNPGSYTCHCDGRGLK 180
DB 207 ARCKNLPGSYSLCDEGYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266
QY 181 LSQMDTCEIDILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
DB 267 LSPDMDTCEIDILPCVPFSAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 15

ABB4840

ID	ABB84840 standard; protein; 673 AA.
XX	
AC	ABB84840;
XX	
DT	16-MAY-2002 (first entry)
XX	
DE	Human PRO21 protein sequence SEQ ID NO:48.
XX	
KW	Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW	vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW	age-related macular degeneration; arterial restenosis; angina;
KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW	wound healing; chromosome mapping; gene mapping.
XX	
OS	Homo sapiens.
XX	
PN	WO200200690-A2.
XX	
PD	03-JAN-2002.
XX	
PF	20-JUN-2001; 2001WO-US019692.
XX	
PR	23-JUN-2000; 2000US-0213637P.
PR	20-JUL-2000; 2000US-0219556P.
PR	25-JUL-2000; 2000US-0220624P.
PR	25-JUL-2000; 2000US-0220664P.
PR	28-JUL-2000; 2000WO-US020710.
PR	02-AUG-2000; 2000US-0222695P.
PR	17-AUG-2000; 2000US-00643657.
PR	23-AUG-2000; 2000WO-US023522.
PR	24-AUG-2000; 2000WO-US023328.
PR	07-SEP-2000; 2000US-0230378P.
PR	18-SEP-2000; 2000US-00664610.
PR	18-SEP-2000; 2000US-00665350.
PR	24-OCT-2000; 2000US-0242922P.
PR	08-NOV-2000; 2000US-00709238.
PR	08-NOV-2000; 2000WO-US030952.
PR	10-NOV-2000; 2000WO-US030873.
PR	01-DEC-2000; 2000WO-US032678.
PR	20-DEC-2000; 2000US-00747259.
PR	20-DEC-2000; 2000WO-US034956.
PR	22-JAN-2001; 2001US-00767609.
PR	28-FEB-2001; 2001US-00796498.
PR	28-FEB-2001; 2001WO-US008520.
PR	01-MAR-2001; 2001WO-US008666.
PR	09-MAR-2001; 2001US-00802706.
PR	14-MAR-2001; 2001US-00808689.
PR	22-MAR-2001; 2001US-00816744.
PR	05-APR-2001; 2001US-00828366.
PR	10-MAY-2001; 2001US-00854208.
PR	10-MAY-2001; 2001US-00854280.
PR	25-MAY-2001; 2001US-00866028.
PR	25-MAY-2001; 2001US-00866034.
PR	25-MAY-2001; 2001WO-US017092.
PR	30-MAY-2001; 2001US-00870574.
PR	30-MAY-2001; 2001WO-US017443.
PR	01-JUN-2001; 2001WO-US017800.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Baker KP, Ferrara N, Gerber H, Gerttsen ME, Goddard A;
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	
WI	WPI; 2002-090516/12.
DR	N-PSDB; ABL88095.
XX	
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal.

XX	Claim 11; Fig 48; 565pp; English.
XX	
XX	
CC	ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC	ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC	antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing
CC	a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC	cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC	healing. The PRO polynucleotides have applications in molecular biology,
CC	including use as hybridisation probes, and in chromosome and gene
CC	mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC	exemplification of the present invention
XX	
XX	Sequence 673 AA;
QY	Query Match 85.8%; Score 1113; DB 5; Length 673;
PS	Best Local Similarity 82.8%; Pred. No. 2.3e-70;
XX	Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY	1 PRLVLCINKYGSPTYNKSGFATCVONLPDQCTPNPCDRKGTQACQDLMGNFCLCKAGWG 60
DB	87 PRYQCEMKRYGRPEEKNPDFAKVQNLPDQCTPNPCDKKGTHTICQDLMGNFVCTDGMG 146
QY	61 GRLCDKDVNECSQENGGCLOICHNKPGEFCHSGFELSSDGRTCODIDECADSEACGE 120
DB	147 GRLCDKDVNECVQKNGGCSQVCHNKPGEFQACHSGFSLASDGTQODIDECTDSDTCGD 206
QY	121 ARCKNLPGSYSLCDEGPAYSOBKARDVDDECLQGRCEQVCVNSPGSYTCHDCDGRGGLK 180
DB	207 ARCKNLPGSYSLCDEGYTYSKEKTQDVDECCQDRCEQTCVNSPGSYTCHDCDGRGGLK 266
QY	181 LSPDMTDCEDILPCVPFVNAKSVKSLYLGRMFSGTTPVIRLRFKRLQ 227
DB	267 LSPDMTDCEDILPCVPFVNAKSVKSLYLGRMFSGTTPVIRLRFKRLQ 313
RESULT 16	
ABB95446	ID ABB95446 standard; protein; 673 AA.
XX	ABB95446;
XX	
XX	19-JUL-2002 (first entry)
DT	
DE	
DE	
KW	Human angiogenesis related protein PRO21 SEQ ID NO: 48.
KW	Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW	atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW	cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
XX	antiarteriosclerotic.
XX	
OS	Homo sapiens.
XX	
PN	WO200208284-A2.
XX	
PD	31-JAN-2002.
XX	
XX	09-JUL-2001; 2001WO-US021735.
XX	
PR	20-JUL-2000; 2000US-0219556P.
PR	25-JUL-2000; 2000US-0220624P.
PR	28-JUL-2000; 2000US-0220664P.
PR	28-JUL-2000; 2000WO-US020710.
PR	02-AUG-2000; 2000US-0222695P.
PR	17-AUG-2000; 2000US-00643657.
PR	23-AUG-2000; 2000WO-US023522.
PR	24-AUG-2000; 2000WO-US023328.
PR	07-SEP-2000; 2000US-0230978P.

PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 25-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 30-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95584.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 48; 567pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 673 AA;
Query Match 85.8%; Score 1113; DB 5; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKYKSGPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLMGNFFCLCKAGWG 60

DB 87 PRYQECMKYGRPEKNPDFAKCVQNLDPQCTPNPCDKKGTHICQDLMGNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGCLQICHNKPGSFHCSHSGFELSDGRTCDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPGSFQACSHGFSLSADGGTCQDIDECTSDTGD 206
QY 121 ARCKNLPGSYCLCDEGFPAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHDCRGGGLK 180
DB 207 ARCKNLPGSYCLCDEGTYSSKEKTCQDVDECCQDCRCEQTCVNSPGSYTCHDCRGGGLK 266
QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPIRLRFRKLOP 227
DB 267 LSPDMTDCEDILPCVPFSSMAKSVKSLYLGRMFSGTPIRLRFRKLOP 313
RESULT 17
ADD10337
ID ADD10337 standard; protein; 673 AA.
XX
AC ADD10337;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #24.
XX
KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003105011-A1.
XX
PD 05-JUN-2003.
XX
PF 16-AUG-2002; 2002US-00223084.
XX
PR 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2003-810831/76.
DR N-PSDB; ADD10336.
XX
PT New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 11; SEQ ID NO 48; 493pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of Pgf-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis. A PRO
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to

CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;
Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKYNGSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEEKNPDAKCVQNLPDQCTPNPCDKKGGTHICQDLGMNFFCVCTDGGW 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFHCSHGFPESLDGRTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSQACHSGLASDGTQCDIDECTSDTDCG 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDEGYTYSSEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGTTPVIRLRFKRLQ 227
Db 267 LSPDMTCEIDILPCVPFSAKSVKSLYLGRMFGTTPVIRLRFKRLQ 313

RESULT 18
ADD11297
ID ADD11297 standard; protein; 673 AA.
AC ADD11297;
XX
XX 01-JAN-2004 (first entry)
DE Human secreted/transmembrane PRO polypeptide #24.
XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX Homo sapiens.
XX
XX US2003105013-A1.
XX
XX 05-JUN-2003.
XX 16-AUG-2002; 2002US-00223090.
XX 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2003-801242/75.
DR N-PSDB; ADD11296.
XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, useful for treating a cardiovascular, endothelial, or
PT angiogenic disorder in a mammal, such as cancer or age-related macular
PT degeneration.
XX
XX Claim 11; SEQ ID NO 48; 493pp; English.
PS The invention relates to an isolated nucleic acid encoding a secreted and
XX transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded

CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal.
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKYNGSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEEKNPDAKCVQNLPDQCTPNPCDKKGGTHICQDLGMNFFCVCTDGGW 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFHCSHGFPESLDGRTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSQACHSGLASDGTQCDIDECTSDTDCG 206
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDEGYTYSSEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTCEIDILPCVPFSAKSVKSLYLGRMFGTTPVIRLRFKRLQ 227
Db 267 LSPDMTCEIDILPCVPFSAKSVKSLYLGRMFGTTPVIRLRFKRLQ 313

RESULT 19
ADD37090
ID ADD37090 standard; protein; 673 AA.
XX
XX ADD37090;
XX
XX 15-JAN-2004 (first entry)
DE Human secreted/transmembrane PRO polypeptide #24.
XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX Homo sapiens.
XX
XX US2003105012-A1.
XX
XX 05-JUN-2003.
XX
XX 16-AUG-2002; 2002US-00223088.
XX
XX 15-SEP-2000; 2000US-0232887P.
PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX

DR WPI; 2003-829354/77.
DR N-PSDB; ADD37089.
XX
PT New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX
PS Claim 11; SEQ ID NO 48; 492pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGR-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 7; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCKINIKYSGPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEEKNPDFAKCVQNLDPDQCTPNPCDKKGTGTHICQDLGMNFFCVCTDGMG 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPFSFCHSGFELSSDGRCTCODIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACCHSGFSLASDGTQCDIDECTSDTCGD 206

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSLCDEGYTYSKKTCDQVDECCQDRCEQTQVNSPGSYTCHCDGRGGLK 266

QY 181 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFGTPTVIRLRFKRLQP 227
DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFGTPTVIRLRFKRLQP 313

RESULT 20
ADE41298
ID ADE41298 standard; protein; 673 AA.
AC ADE41298;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted/transmembrane PRO polypeptide #24.
XX
KW human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
XX
OS Homo sapiens.
XX
PN US2003100497-A1.
XX
PD 29-MAY-2003.
XX
PF 16-AUG-2002; 2002US-00223085.
XX

PR 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Stephan JF;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Wood WI, Ye W;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2004-008957/01.
DR N-PSDB; ADE41297.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or
PT PRO214, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and for treating disorders involving
PT angiogenesis.
XX
PS Claim 11; SEQ ID NO 48; 492pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGR-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX
SQ Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 8; Length 673;
Best Local Similarity 82.8%; Pred. No. 2.3e-70;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCKINIKYSGPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEEKNPDFAKCVQNLDPDQCTPNPCDKKGTGTHICQDLGMNFFCVCTDGMG 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPFSFCHSGFELSSDGRCTCODIDECADSEACGE 120
DB 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACCHSGFSLASDGTQCDIDECTSDTCGD 206

QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSLCDEGYTYSKKTCDQVDECCQDRCEQTQVNSPGSYTCHCDGRGGLK 266

QY 181 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFGTPTVIRLRFKRLQP 227
DB 267 LSPDMTDCEDILPCVPFSSVAKSVKSLYLGRMFGTPTVIRLRFKRLQP 313

RESULT 21
ADH43481
ID ADH43481 standard; protein; 673 AA.
XX
AC ADH43481;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human PRO polypeptide #24.
XX
KW Human; PRO; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
KW cell apoptosis; cell tube formation; angiogenesis;
KW

PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 05-APR-2001; 2001US-00828366.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00872035.
PR 14-JUN-2001; 2001WO-US017800.
PR 19-JUN-2001; 2001US-00863442.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 13-AUG-2001; 2001US-00929404.
PR 16-AUG-2001; 2001US-00931836.
PR 28-AUG-2001; 2001US-00941992.
PR 04-SEP-2001; 2001US-00946374.
PR 07-SEP-2001; 2001US-00948901.
PR 15-NOV-2001; 2001US-00002796.
PR 30-NOV-2001; 2001US-00001054.
PR 06-DEC-2001; 2001US-00006867.
PR 19-DEC-2001; 2001US-00028072.
PR 15-JAN-2002; 2002US-00052586.
PR 17-JAN-2002; 2002US-00053107.
PR 18-JAN-2002; 2002US-00052594.
PR 08-FEB-2002; 2002US-00072068.
PR 09-APR-2002; 2002US-00119480.

(GETH) GENENTECH INC.

PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
XX WPI; 2004-225727/21.
DR N-PSDB; ADR82825.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
PT PRO21383, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 11; SEQ ID NO 48; 494pp; English.

XX The invention relates to human PRO polypeptides and the PRO
XX polynucleotides encoding them. The invention also relates to treating
CC cardiovascular, endothelial or angiogenic disorders in mammals,
CC inhibiting endothelial cell growth, stimulating endothelial cell growth,

CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
CC stimulating angiogenesis or smooth muscle cell growth by administering
CC polypeptides of the invention. The PRO polypeptides and polynucleotides
CC are useful for treating cardiovascular, endothelial or angiogenic
CC disorders, e.g. myocardial infarction, endocardial or angiotonic
CC cancer or age-related macular degeneration. The PRO polynucleotides are
CC useful as hybridisation probes in chromosome and gene mapping and in
CC generating antisense RNA and DNA, and for chromosome identification and
CC tissue typing. The PRO polypeptides and polynucleotides are also useful
CC in gene therapy and as molecular weight markers for protein
CC electrophoresis purposes. This sequence represents a human PRO
CC polypeptide of the invention. Note: The sequence data for this patent is
CC also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html.

XX Sequence 673 AA;

Query Match 85.8%; Score 1113; DB 8; Length 673;

Best Local Similarity 82.8%; Pred. No. 2.3e-70;

Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLNMFCLCKAGWG 60

Db PRYQECMEKYGRPEKNPDKVQNLDPDQCTPNPCDRKGTQACQDLNMFCLCKAGWG 146

QY 61 GRLCDKDVNECSQENGCGCLQICHNKPGRSFHCSHSGFELSSDGRTCQDIDECADSEACGE 120

Db GRLCDKDVNECSQENGCGCGVCHNKPGRSFHCSHSGFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYCLCDEGFAYSSOEKACRDVDECLQRCQVNSPGSVTCHDCGRGGLK 180

Db ARCKNLPGSYCLCDEGYTSSKERTCDQVDECCQDRCEQTCVNSPGSVTCHDCGRGGLK 266

QY 181 LSQMDTDCEDILPCVPFVSAKSVKSLYLGRMFSGTFVIRLRFKRLQP 227

Db LSPDMTDCEDILPCVPFVSAKSVKSLYLGRMFSGTFVIRLRFKRLQP 313

RESULT 23

ABO84420

ID ABO84420 standard; protein; 703 AA.

AC ABO84420;

XX 18-NOV-2004 (first entry)

DE Mouse cancer-associated protein MF7-153.1.

XX Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;

KW lymphoma; CAP.

OS Mus musculus.

XX WO2004074320-A2.

XX 02-SEP-2004.

XX 17-FEB-2004; 2004WO-US004730.

XX 14-FEB-2003; 2003US-00367094.

XX 14-MAR-2003; 2003US-00388838.

XX 15-APR-2003; 2003US-00417375.

XX 13-JUN-2003; 2003US-00461862.

XX 15-SEP-2003; 2003US-00663431.

XX 15-DEC-2003; 2003US-00737318.

XX (SAGR-) SAGRES DISCOVERY INC.

XX Morris DW, Morris DW, Malandro MS;

XX WPI; 2004-652914/53.

XX N-PSDB; ABD32565.

XX

PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.

XX disclosure; seqid 51; 310pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 703 AA;

Query Match 85.8%; Score 1113; DB 8; Length 703;
 Best Local Similarity 82.8%; Pred. No. 2.4e-70;
 Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFFCLCKAGWG 60
 DB 120 PRYQCMKRYGRPEEKPNDFAKCVQNLDPDQCTPNPCDKKGGTHICQDLMGNFFCVCTDGMG 179
 QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHCSCHGPFSLSDGRTCCQDIDECADSEACGE 120
 DB 180 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACHSFGSLADGGTCCQDIDECTSDTCDG 239
 QY 121 ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLOGRCEQCVNSPGSYTCHCDGRGLK 180
 DB 240 ARCKNLPGSYCLCDEGYTSSKERTCQDVDECQDRCCEQTCVNSPGSYTCHCDGRGLK 299
 QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKLP 227
 DB 300 LSPDMTDCEDILPCVPFVSMAKSVKSLYLGRMFSGTPTVIRLRFKLP 346

RESULT 24

AAR72350
 ID AAR72350 standard; protein; 635 AA.

XX AAR72350;

XX AC

XX 29-DEC-1995 (first entry)

XX DT

XX Mature human protein S.

XX DE

XX Protein S; PS; vitamin K-dependent protein.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 425..426
 /label= I425A/I426A

FT Misc-difference 429
 /label= K429E

FT Misc-difference 432
 /label= K432E

XX US5405946-A.

XX 11-APR-1995.

XX 02-DEC-1992; 92US-00985691.

XX 02-DEC-1992; 92US-00985691.

XX (SCRI) SCRIPPS RES INST.

XX Bertina R, Griffin JH, Bouma BN;

XX WPI; 1995-154630/20.

XX New recombinant protein S variants - having reduced C4b binding protein
 PT binding activity and anticoagulant activity for treating thrombosis.

XX Claim 1; Col 31-36; 24pp; English.

XX For preparing a protein S (PS) expression vector, partial cDNAs coding
 CC for human protein S were first isolated as described by Ploos van Amstel
 CC et al., FEBS Lett. 222:186-190 (1987) from a pUC9 human liver cDNA
 CC library. The cDNA sequence is given in Q86348. The PS nt sequence is also
 CC listed in GenBank having the accession number Y00692. The mRNA encodes a
 CC preprotein having 676 AAs. After post- translation processing the
 CC corresp. translated mature PS consists of 635 AAs as given in R72350. The
 CC AA sequence is also listed in GenBank having the accession no. A26157. PS
 CC can be modified without significant loss of anticoagulant activity by
 CC introducing one or more mutations in the region between residues 425 and
 CC 432 to reduce significantly or eliminate the ability of PS to bind C4BP.
 CC A variant protein S is claimed having AA residue substitutions selected
 CC from the group indicated in R72350 FT

XX Sequence 635 AA;

Query Match 46.5%; Score 602.5; DB 2; Length 635;
 Best Local Similarity 43.4%; Pred. No. 2e-34;
 Matches 102; Conservative 46; Mismatches 74; Indels 13; Gaps 5;

QY 1 PRYLDCKNKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLMGNFF 52
 DB 42 PRYLVCDURSFQTLGFTFAAROSTNAYPDLRSCVNAIPDQCSFLPCNEDGYNSCKDGKASFT 101
 QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSFHCSCHGPFSLSDGRTCCQDI 109
 DB 102 CTCKPGWQGEKCEFDINECKDPNSNINGGCSQICDNTPGSYHSCCKNGFVMLSNKDKCKDV 161
 QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLOGRCEQCVNSPGS 168
 DB 162 DECSLKPSICGTAVCKNIPGDPECECPGYRYNLKSKSCQDIDECSENMAQLCWNYPGG 221
 QY 169 YTHCDGRGGIKLSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFK 223
 DB 222 YTCYCDGKGGFKLAQDQKSCVSVCLPMLDITFKYELLYLAEPAGV-VLYLKF 275

RESULT 25

AAR31875

ID AAR31875 standard; protein; 635 AA.

XX

XX AAR31875;

XX

DT 25-MAR-2003 (revised)
XX 24-MAY-1993 (first entry)
DE Vitamin K-dependent protein S.
XX Diagnosis; immunoassay; PS.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 32..46
FT Peptide /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 187..200
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 188..199
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 347..631
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 347..361
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 408..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 413..418
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 417..422
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 418..432
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 420..434
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 421..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 423..427
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 427..434
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 427..433
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 603..616
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 621..635
FT /note="inhibits binding of protein S to C4b binding
FT protein"
FT Peptide 621..627
FT /note="inhibits binding of protein S to C4b binding
FT protein"
XX EP524737-A2.
XX

PD 27-JAN-1993.
XX
PF 02-JUL-1992; 92EP-00306116.
XX
PR 02-JUL-1991; 91US-00724746.
PR 01-JUL-1992; 92US-00907190.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Griffin JH, Fernandez JA;
XX WPI; 1993-028796/04.
XX
DR Protein S polypeptide(s) and anti-PS antibodies - capable of inhibiting
FT binding of proteins to C4BP.
XX
PS Disclosure; Page 39; 61pp; English.
XX
CC The sequence is that of vitamin K-dependent protein S (PS), peptides
CC (claimed) derived from the PS sequence (see features) may be used to
CC inhibit the binding of PS to C4b binding protein. These peptides can be
CC used in diagnostic systems and a variety of direct or competitive
CC immunoassay formats for detecting the presence of free protein S in a
CC vascular fluid. The assays are based on the specific binding interaction
CC between a PS peptide or an antibody with free PS. Antibodies
CC immunoreactive with the peptides may be used for purifying free PS from
CC fluid samples. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 635 AA;
Query Match 46.4%; Score 601.5; DB 2; Length 635;
Best Local Similarity 43.4%; Pred. No. 2.3e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCINKY-----GSPYTKNS--GPATCVQNLPDCTNPCKDRKCTQACODLWGNFF 52
DB 42 PKYLVLRSFOTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMCKDKASFT 101
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKGSGFHCSCHSFELSDGRTCDI 109
DB 102 CTCRPGWQGEKCFDINECKDPSNINGSQSOICDTPGSHYHSCCKNGFVMSLNKKDKDV 161
QY 110 DECA-DSACAEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCRQVCVNSPGS 168
DB 162 DECSLKPSICGTAVCKNIPGDFECECPGYRYNLKSKSCEDIDECSNMCALQCVNYPGG 221
QY 169 YTCDCRGGGLKLSQDMDCEDILPCVPFVSAKSVKSLYLGRMFSGTPIRLRFK 223
DB 222 YTCYDGGKGFKAQDQKSCBVSVCPLNLDITYELLYLAEQFAGV-VLYLKR 275
RESULT 26
ADQ17650
ID ADQ17650 standard; protein; 650 AA.
XX
AC ADQ17650;
XX
DT 26-AUG-2004 (first entry)
XX
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 467.
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX Homo sapiens.
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX

PA (PROT-) PROTEIN DESIGN LABS INC.
XX Aziz N, Gineburg WM, Zlotnik A;
XX WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
XX of a gene in a first soft tissue sample and a normal soft tissue sample
XX and comparing the gene expression, also useful in treating soft tissue
XX sarcoma.
XX
XX Example 2; SEQ ID NO 467; 210pp; English.
XX
XX The invention relates to a novel method for detecting soft tissue sarcoma
XX which comprises obtaining a first soft tissue sample from an individual
XX and a normal soft tissue sample from the same or different individual,
XX determining the expression of a gene in both samples and comparing the
XX expression of the gene in both soft tissue samples, where a higher level
XX of protein expression in the first soft tissue sample indicates the
XX presence of soft tissue sarcoma. The method of the invention has
XX cyrostatic applications and may be useful for detecting soft tissue
XX sarcoma, possibly via gene therapy or vaccine production. The nucleic
XX acid sequences may be useful in diagnostic and screening applications.
XX The current sequence is that of a human soft tissue sarcoma-upregulated
XX protein of the invention. The current sequence is not shown within the
XX specification per se but was submitted in CD format by the inventor.
XX
XX Sequence 650 AA;
SQ
Query Match 46.4%; Score 601.5; DB 8; Length 650;
Best Local Similarity 43.4%; Pred. No. 2.3e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
Qy 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDQCTNPDCRKGTOACDLMGNFF 52
Db 57 PKYLVLCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCPLPCNEDGYMSCKDGKASFT 116
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 117 CTCKPGWQGEKCEFDINECKDPSNINGSQICDNTFGSYHCSCKNGFVMSLNKKDCKDV 176
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCRCEQVCVNSPGS 168
Db 177 DECSLKPSICGTAVCKNIPGDPECEPGRYNLKSKSCEDIDECSENMCAQLCVNYPGG 236
Qy 169 YTCDCRGGGLKLSQDMDTCEILPCVPFVSVAKSVKSLYLGRMPSGTPIRLRFK 223
Db 237 YTCYCDGKKGKFLAQDQKSCVWSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 290
RESULT 27
AAW46464
ID AAW46464 standard; protein; 676 AA.
XX
XX AAW46464;
AC
XX 15-MAY-1998 (first entry)
DT
XX Human protein S.
DE
XX Protein S; mitogenic agent; insulin; growth regulation; treatment;
XX serum-free culture medium; human; Schwann cell; receptor activator;
KW erbB receptor; heregulin; cAMP level; proliferation;
XX nervous system injury.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH 1..52
FT Domain
FT /note= "A domain which is rich in gamma-carboxylglutamic
FT acid residues which mediate the Ca2+ dependent binding of
FT Protein S to negatively charged phospholipids"
FT 83..118
FT Domain

FT /note= "B domain of gas6 comprising a thrombin sensitive
loop"
PN US5714385-A.
XX
XX 03-FEB-1998.
PD
XX 10-MAY-1995; 95US-00435434.
PF
XX 10-MAY-1995; 95US-00435434.
PR
XX (GETH) GENENTECH INC.
PA
XX Chen J, Mather JP, Li R;
PI
XX WPI; 1998-129864/12.
DR
XX Medium for culturing human Schwann cells - is serum-free and contains Rse
FT receptor activator and other mitogens.
PT
XX Disclosure; Fig 2; 51pp; English.
PS
XX The present sequence represents a human protein S, which is a ligand for
CC tyrosine3. Protein S is a vitamin K dependent plasma protein that
CC functions as an anticoagulant by acting as a cofactor to stimulate the
CC proteolytic inactivation of factors Va and VIIIa by activated protein C.
CC Protein S may also be involved in the complement cascade. Protein S is
CC used in a serum-free culture medium for culturing human Schwann cells,
CC which does not support fibroblast growth. It functions as a mitogenic
CC agent which is a Rse/Axl receptor activator. A second mitogenic agent
CC e.g. insulin or an erbB receptor activator such as heregulin, is also
CC required to raise cAMP levels and enhance survival or proliferation of
CC human Schwann cells. The culture medium additionally comprises a molecule
CC or composition that provides Fe ions to the Schwann cells, vitamin E, a
CC protease inhibitor, and progesterone. The Schwann cells can be used to
CC treat patients with nervous system injuries
XX
XX Sequence 676 AA;
SQ
Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
Qy 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDQCTNPDCRKGTOACDLMGNFF 52
Db 83 PKYLVLCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCPLPCNEDGYMSCKDGKASFT 142
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 143 CTCKPGWQGEKCEFDINECKDPSNINGSQICDNTFGSYHCSCKNGFVMSLNKKDCKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDPECEPGRYNLKSKSCEDIDECSENMCAQLCVNYPGG 262
Qy 169 YTCDCRGGGLKLSQDMDTCEILPCVPFVSVAKSVKSLYLGRMPSGTPIRLRFK 223
Db 263 YTCYCDGKKGKFLAQDQKSCVWSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316
RESULT 28
AAW29795
ID AAW29795 standard; protein; 676 AA.
XX
XX AAW29795;
AC
XX 15-NOV-1999 (first entry)
DT
XX Human protein S.
DE
XX Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; Gas6;
KW growth arrest-specific gene 6; proliferation; differentiation;
XX glial cell; Schwann cell; fusion protein.


```
XX OS Homo sapiens.
XX PN US5955420-A.
XX PD 21-SEP-1999.
XX PF 10-MAY-1995; 95US-00438864.
XX PR 10-MAR-1995; 95US-00402253.
XX PA (GETH ) GENENTECH INC.
XX PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
XX DR WPI; 1999-539585/45.
XX PT Activation of the Rse receptor on a cell, useful for promoting cell
XX PT proliferation and differentiation.
XX PS Disclosure; Fig 2; 48pp; English.
XX CC A method has been developed for activating the Rse receptor on a cell.
XX CC The method comprises exposing the receptor to the exogenous growth arrest
XX CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
XX CC cell proliferation and cell differentiation. The present sequence
XX CC represents human protein S given in the present invention
XX SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKNKY-----GSPYTKNS--GFATCVONLPDQCTNPDCRKGFTQACODLMGNHFF 52
DB 83 PKYLVLRLSFTQGLFTAAQSTNAYPDLRSCVNAIPDQCPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGGRLCDXDVNEC---SQENGGLQICHNKGPSFHCSHGFELSDGRTCDI 109
DB 143 CTCFPGWQGEKCEFDINECKDPFNGGCSQICDNTPGSYHCSCKNGFVMLSNKKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGPSYCLDDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSCICGTAVCKNIPGDFECPECEGYRYNLKSKCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTCDCDGRGGLKLSQDMDTCEILPCVPFVSAKSVKSLYLGRMFSCTPVIRLRFK 223
DB 263 YTCYCDGKKGKFLAQDQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316
RESULT 29
AAV57384
ID AAV57384 standard; protein; 676 AA.
XX AC AAV57384;
XX DT 19-JUN-2000 (first entry)
XX DE Amino acid sequence of human protein S.
XX KW Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
XX KW central nervous system; peripheral nervous system; injury; trauma;
XX KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
XX KW protein S.
XX OS Homo sapiens.
XX PN US6033660-A.
XX PD 07-MAR-2000.
XX PF 10-MAY-1995; 95US-00438862.
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XX PR 10-MAY-1995; 95US-00438862.
XX PA (GETH ) GENENTECH INC.
XX PI Mather JP, Chen J, Li R;
XX DR WPI; 2000-246046/21.
XX PT Repairing nervous system injuries in mammals, by administering human
XX PT Schwann cells that have been propagated in medium supplemented with
XX PT mitogens.
XX PS Disclosure; Fig 2; 52pp; English.
XX CC The invention relates to a method for treating nervous system injuries in
XX CC mammals by administering human Schwann cells (SC) that have been cultured
XX CC in serum-free medium. The serum-free medium is a nutrient solution
XX CC supplemented with two mitogens, one of which, is a Res/Axl receptor
XX CC activator, to increase survival and proliferation of SC. The method is
XX CC used to treat (or prevent) central or peripheral nervous system injury,
XX CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
XX CC or lesions associated with nutritional deficiencies, systemic disease,
XX CC toxins or demyelination. Culturing cells in the specified medium allows
XX CC proliferation of adult SC for use in autologous transplants. The present
XX CC sequence represents a human protein S, having 43% and 44% sequence
XX CC identity to murine and human gas6. Gas6 is demonstrated to be a potent
XX CC growth/survival factor for SCs in defined serum-free culture
XX SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDCKNKY-----GSPYTKNS--GFATCVONLPDQCTNPDCRKGFTQACODLMGNHFF 52
DB 83 PKYLVLRLSFTQGLFTAAQSTNAYPDLRSCVNAIPDQCPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGGRLCDXDVNEC---SQENGGLQICHNKGPSFHCSHGFELSDGRTCDI 109
DB 143 CTCFPGWQGEKCEFDINECKDPFNGGCSQICDNTPGSYHCSCKNGFVMLSNKKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGPSYCLDDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSCICGTAVCKNIPGDFECPECEGYRYNLKSKCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTCDCDGRGGLKLSQDMDTCEILPCVPFVSAKSVKSLYLGRMFSCTPVIRLRFK 223
DB 263 YTCYCDGKKGKFLAQDQKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316
RESULT 30
ADD46140
ID ADD46140 standard; protein; 676 AA.
XX AC ADD46140;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein P07225, SEQ ID NO 11815.
XX KW Human; pain; neuronal tissue; gene therapy;
XX KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX KW spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
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XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEOH) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P07225.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 676 AA;
XX Query Match 46.4%; Score 601.5; DB 7; Length 676;
XX Best Local Similarity 43.4%; Pred. No. 2.4e-34;
XX Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
OY 1 PRYLDCKINX-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 KYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKGKASFT 142
OY 53 CLCAGWGRCLDKDNEC---SQNGGCLQICHNKPGSHCSHSGFELSSDGRCTODI 109
DB 143 CTCRPGWQGEKCFDINPKDPSNNGGCSQICDNTPGSYHCCKNGFVMLSNKDKCKDV 202
OY 110 DECA-DSBACGEARCNLPFGSVCLDCBGFAYSSQEKACRVDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCNIPGDFECHECPGGRYNLKSCKSCBIDECSENWCAQLCVNYPGG 262
OY 169 YTHCDGRGGKLSQDMOTCDIILPCVPFVSVAKSYSILGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKKGKFLAQDKSCSEVSVCLPLNLTDTKVELLYLAEQFAGV-VLYLKER 316
RESULT 31
ADE62065
ID ADE62065 standard; protein; 676 AA.
XX

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AC ADE62065;
XX 29-JAN-2004 (first entry)
XX Human Protein P07225, SEQ ID NO 7994.
DE Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS WO2003016475-A2.
XX 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-0333347P.
XX (GEOH) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX GENBANK; P07225.
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 676 AA;
XX Query Match 46.4%; Score 601.5; DB 7; Length 676;
XX Best Local Similarity 43.4%; Pred. No. 2.4e-34;
XX Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
OY 1 PRYLDCKINX-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 KYLVCLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKGKASFT 142

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QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLCLQICHNKPGSFHSCSGFELSDGRTCDI 109
DB 143 CTCKPGWQGEKECFDINECKDPNSNGGCSQICDNTPGSYHSCSKNGFVNLNKKDKCDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCNKIPGFECEPGEYRNLKSKSCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLQADQKSCVSVCLPLNLDTKVELLYLAQFAGV-VLYLKF 316

RESULT 32
ADP24054
ID ADP24054 standard; protein; 676 AA.
XX
AC ADP24054;
XX
DT 18-NOV-2004 (first entry)
XX
DE PRO polypeptide SEQ ID NO:1232.
XX
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX Unidentified.
XX WO2004041170-A2.
XX
XX
PD 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GETH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI: 2004-419628/39.
DR N-PSDB; ADP24053.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.
XX
XX Claim 7; SEQ ID NO 1232; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic

CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hyperesensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.
XX
SQ Sequence 676 AA;
Query Match 46.4%; Score 601.5; DB 8; Length 676;
Best Local Similarity 43.4%; Pred. No. 2.4e-34;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLIPDOCTNPDRKGTQACQDLMGNPF 52
DB 83 PKYLVCLRSFQTGLFTAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKGKASPT 142
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLCLQICHNKPGSFHSCSGFELSDGRTCDI 109
DB 143 CTCKPGWQGEKECFDINECKDPNSNGGCSQICDNTPGSYHSCSKNGFVNLNKKDKCDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCNKIPGFECEPGEYRNLKSKSCEDIDECSENWCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMTCEDILPCVPFSVAKSVKSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLQADQKSCVSVCLPLNLDTKVELLYLAQFAGV-VLYLKF 316

RESULT 33
AAP81136
ID AAP81136 standard; protein; 675 AA.
XX
AC AAP81136;
XX
DT 25-MAR-2003 (revised)
DT 17-OCT-1990 (first entry)
XX
DE Bovine Protein S.
XX
KW Protein S; anti-thrombolytic agent; antibodies.
XX
XX Bos taurus.
XX
XX EP255771-A.
XX
XX 10-FEB-1988.
XX
XX 24-JUL-1987; 87EP-00306564.
XX
XX 25-JUL-1986; 86US-00890401.
XX
XX (INUA) INTEGRATED GENETICS INC.
XX
XX Wydro R, Cohen E, Dackowski W, Stenflo J, Lundwall A, Dahlback B;
PI WPI: 1988-037719/06.
XX
XX N-PSDB; AAN81441.
XX
XX Recombinant DNA encoding mature human Protein S - used therapeutically as
XX anti-thrombolytic agent and for producing antibodies for diagnostic use.
XX Disclosure; Page ?; 22pp; English.
XX
XX See also AAN81442. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 675 AA;
Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 5.5e-34;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;


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FT Disulfide-bond 286. .509
FT Disulfide-bond 527. .555
XX PN WO9501433-Al.
XX PD 12-JAN-1995.
XX PF 28-JUN-1994; 94WO-NL000149.
XX PR 30-JUN-1993; 93EP-00201906.
XX PA (UYLE-) RIJKSUNIV LEIDEN.
XX PI Bouma BN, Bertina RM;
XX DR WPI; 1995-060997/08.
XX PT New deletion mutants of protein S retaining anticoagulant activity - are
XX PT not neutralised by C4b binding protein, useful in treating thrombosis,
XX PT sepsis etc.
XX PS Claim 2; Fig 5; 3lpp; English.
XX CC AAR70728 is the human protein S, from which the new deletion mutants
XX CC described in AAR70729-R70733 were derived. The mutants retain the
XX CC anticoagulant activity of the wild type protein, useful for the treatment
XX CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
XX CC lack the 2 putative C4b binding protein domains of the sex hormone
XX CC binding globulin domain of the wild type protein. As the mutants are
XX CC resistant to neutralisation by C4b binding protein they can provide
XX CC increased plasma levels of free protein S, and higher potency per unit
XX CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
XX CC to correct PN field.)
XX SQ Sequence 565 AA;

Query Match 45.3%; Score 587.5; DB 2; Length 565;
Best Local Similarity 43.0%; Pred. No. 28-33;
Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;

OY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLGMGNFF 52
DB 81 PKYLVCLRSFQTGLFTAAARQSTNAVPLDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 140
OY 53 CLCKAGWGRCLCDKDVNEC---SQBGGCLOICHNKGPSFHCSHGFSLSDDGRTCDI 109
DB 141 CTCKDGMQGEKCEFDINECKDFSNINGGCSQICDNTPGSYHCCKNGFVWLSNKKDKDV 200
OY 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 201 DECSLKPSICGTAVCKNIPGDFECPCEGRYNLSKSCEDIDECSENMAQLCVNYPGG 260
OY 169 YTCDCDGRGLKLSQDMDFCEILPCVPFSVAKSVKSLYLGRMFGSTPVIRLREK 223
DB 261 YTCYCDGKGKPKLAQDKSCVSVCLPLNLTOTKELYLAEPQAGV-VLYLKFR 314

RESULT 36
AAR70728
ID AAR70728 standard; protein; 675 AA.
XX
AC AAR70728;
XX
XX 25-MAR-2003 (revised)
DT 20-SEP-1995 (first entry)
XX
DE Human protein S.
XX
XX Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
FH Key

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FT Peptide
FT Disulfide-bond 1. .41
FT Disulfide-bond /note= "pre-pro leader sequence"
FT Domain 56. .61
FT Domain 59. .70
FT Domain /note= "GLA domain"
FT Domain 86. .280
FT Disulfide-bond /note= "growth factor domains"
FT Disulfide-bond 86. .111
FT Disulfide-bond 119. .132
FT Disulfide-bond 124. .141
FT Disulfide-bond 143. .152
FT Disulfide-bond 159. .173
FT Disulfide-bond 169. .182
FT Disulfide-bond 184. .197
FT Disulfide-bond 203. .215
FT Disulfide-bond 210. .224
FT Disulfide-bond 226. .239
FT Disulfide-bond 245. .254
FT Disulfide-bond 250. .263
FT Disulfide-bond 265. .280
FT Disulfide-bond 286. .566
FT Disulfide-bond 447. .473
FT Disulfide-bond 638. .666
XX WO9501433-Al.
XX PN 12-JAN-1995.
XX PD 28-JUN-1994; 94WO-NL000149.
XX PF 30-JUN-1993; 93EP-00201906.
XX PR (UYLE-) RIJKSUNIV LEIDEN.
XX PA Bouma BN, Bertina RM;
XX PI WPI; 1995-060997/08.
XX DR New deletion mutants of protein S retaining anticoagulant activity - are
XX DR not neutralised by C4b binding protein, useful in treating thrombosis,
XX DR sepsis etc.
XX PS Disclosure; Fig 5; 3lpp; English.
XX CC AAR70728 is the human protein S, from which the new deletion mutants
XX CC described in AAR70729-R70733 were derived. The mutants retain the
XX CC anticoagulant activity of the wild type protein, useful for the treatment
XX CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
XX CC lack the 2 putative C4b binding protein domains of the sex hormone
XX CC binding globulin domain of the wild type protein. As the mutants are
XX CC resistant to neutralisation by C4b binding protein they can provide
XX CC increased plasma levels of free protein S, and higher potency per unit
XX CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
XX CC to correct PN field.)
XX SQ Sequence 675 AA;

Query Match 45.3%; Score 587.5; DB 2; Length 675;
Best Local Similarity 43.0%; Pred. No. 2.3e-33;
Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;

OY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLGMGNFF 52
DB 81 PKYLVCLRSFQTGLFTAAARQSTNAVPLDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 140
OY 53 CLCKAGWGRCLCDKDVNEC---SQBGGCLOICHNKGPSFHCSHGFSLSDDGRTCDI 109
DB 141 CTCKDGMQGEKCEFDINECKDFSNINGGCSQICDNTPGSYHCCKNGFVWLSNKKDKDV 200
OY 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 201 DECSLKPSICGTAVCKNIPGDFECPCEGRYNLSKSCEDIDECSENMAQLCVNYPGG 260
XX
XX Query Match 45.3%; Score 587.5; DB 2; Length 675;
XX Best Local Similarity 43.0%; Pred. No. 2.3e-33;
XX Matches 101; Conservative 45; Mismatches 76; Indels 13; Gaps 5;

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QY 169 YTHCDGRGGLKLSQDMTCEDILPCVFPFSAKSVKSLYLGRMFSGTPVIRLRFK 223
AAP81137
DB 261 YTCYCDGKKGPKLAQDKSCEVWSVCLPLNLDTKYELLYLAEQAGV-VLYLKER 314

RESULT 37
ID AAP81137 standard; protein; 650 AA.
XX AAP81137;
AC AAP81137;
XX
XX
XX 25-MAR-2003 (revised)
DT 17-OCT-1990 (first entry)
XX
XX Human protein S.
XX
XX Protein S; anti-thrombolytic agent; antibodies.
XX
XX Homo sapiens.
XX
XX EP255771-A.
XX
XX 10-FEB-1988.
XX
XX 24-JUL-1987; 87EP-00306564.
XX
XX 25-JUL-1986; 86US-00890401.
XX (INUA) INTEGRATED GENETICS INC.
XX
XX Wydro R, Cohen E, Dackowski W, Stenflo J, Lundwall A, Dahlback B;
XX WPI: 1988-037719/06.
XX N-PSDB; AAN81442.
XX
XX Recombinant DNA encoding mature human Protein S - used therapeutically as
XX anti-thrombolytic agent and for producing antibodies for diagnostic use.
XX
XX Disclosure; Page ?; 22pp; English.
XX
XX The mature human Protein S is used therapeutically as an antithrombolytic
XX agent and for producing antibodies for diagnostic use. See also AAN81441.
XX (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 650 AA;

Query Match 45.2%; Score 586.5; DB 1; Length 650;
Best Local Similarity 42.6%; Pred. No. 2.7e-33;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDOCTPNPCDRKGTQACQDLMGNF 52
DB 57 KYLVCLRSFQTGLFTAAARSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116

QY 53 CLCKAGWGRCLDKDQVNEC---SQBNGGCLOICHNKGPSFHCSCHSFGFELSSDGRTCODI 109
DB 117 CTCKPQWQGEKCEPDINECKDPSNNGSCSQCIDNTPGSYHCCKNGFVMSLNKKDKDV 176

QY 110 DECA-DSBACGSEARCNLPGSYSLCDDGFAYSOKEACRDVDECLQGRQGVQVNSPQS 168
DB 177 DECSLKPSICGTAVCKNIGLGFCECPGGRYRNLSKSCEDIDECSNNCAQLCVNYPGG 236

QY 169 YTHCDGRGGLKLSQDMTCEDILPCVFPFSAKSVKSLYLGRMFSGTPVIRLRFK 223
DB 237 HTCYCDGKKGPKLAQDKSCEVWSVCLPLNLDTKYELLYLAEQAGV-VLYLKER 290

RESULT 38
ID ADD48900 standard; protein; 650 AA.
XX
XX
AC ADD48900;
XX

DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Human Protein AAA60181, SEQ ID NO 14611.
DE
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI: 2003-268312/26.
XX GENBANK; AAA60181.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a human protein (described in Table 3
XX of the specification) which is differentially expressed during pain.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 650 AA;

Query Match 45.2%; Score 586.5; DB 7; Length 650;
Best Local Similarity 42.6%; Pred. No. 2.7e-33;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRYLDICINKY-----GSPYTKNS--GFATCVQNLDPDOCTPNPCDRKGTQACQDLMGNF 52
DB 57 KYLVCLRSFQTGLFTAAARSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 116

QY 53 CLKAGWGRGLCDKDVNEC-----SQENGGLQICHNKPGRFHCSCHSFELSDDGRTQDI 109
Db 117 CTCKPGWQGEKCFEDINECKDFSNINGGCSQICDNTPGSYHCCKNGFVMLSNNKDKDV 176
QY 110 DSCA-DSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
Db 177 DCSLKPSTCGTAVCKNIUGDFECEPEGYRNLKSKSCEDIDECENNAQQLCVNYPPG 236
QY 169 YTHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYLGRMFSGTPIRLRFK 223
Db 237 HTCYCDGKGGFKLAQDKQKSEVSVCLPLNLTQVLYLLAEQFAGV-VLYLKFR 290
RESULT 39
ID ADD48898 standard; protein; 675 AA.
XX
AC ADD48898;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAC60704, SEQ ID NO 14609.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI: 2003-268312/26.
DR GENBANK; AAC60704.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide and the compound that
CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 675 AA;
Query Match 45.1%; Score 585.5; DB 7; Length 675;
Best Local Similarity 43.0%; Pred. No. 3.2e-33; Indels 13; Gaps 5;
Matches 101; Conservative 41; Mismatches 80;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLPDQCTPNPCDRKGTQACQDLMGHFF 52
Db 83 PKYLGLGAFRVGAFSAARQSANAYPDLRSCVNAIPDQCDMPNCNEDGVLSCKDQGAFT 142
QY 53 CLKAGWGRGLCDKDVNEC-----SQENGGLQICHNKPGRFHCSCHSFELSDDGRTQDI 109
Db 143 CTCKPGWQGEKCFEDINECKDFSNINGGCSQICDNTPGSYHCCKNGFVMLSNNKDKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYSCLCDEGFAYSSOEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSTCGTAVCKNIUGDFECEPEGYRNLKSKSCEDIDECENNAQQLCVNYPPG 262
QY 169 YTHCDGRGGLKLSQMDTCEDILPCVPFSAKSVKSLYLGRMFSGTPIRLRFK 223
Db 263 YSCYCDGKGGFKLAQDKQKSEVSVCLPLNLTQVLYLLAEQFAGV-VLYLKFR 316
RESULT 40
AAP70083
ID AAP70083 standard; protein; 676 AA.
XX
AC AAP70083;
XX
DT 25-MAR-2003 (revised)
DT 20-JAN-1991 (first entry)
XX
DE Human recombinant protein-S.
XX
KW Protein-S; plasma; anticoagulant; blood; ss.
XX
OS Homo sapiens.
XX
PN EP247843-A.
XX
PD 02-DEC-1987.
XX
PF 27-MAY-1987; 87EP-00304676.
XX
PR 27-MAY-1986; 86US-00866662.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Hoskins JA, Long GL;
XX
DR WPI: 1987-336481/48.
DR N-PSDB; AAN70080.
XX
PT Recombinant human protein S - a plasmin protein regulator of hemostasis
PT obtd. from a cDNA clone prepd. from human liver mRNA.
XX
PS Disclosure; Page 8; 100pp; English.
XX
CC The protein may be used in antithrombolytic therapy. It may be given as
CC i.v. infusions to patients with recurrent deep-vein thrombosis-pulmonary
CC embolism. It may also be used to treat: i. acquired protein-S deficiency
CC during pregnancy; ii. lupus erythematosus; iii. nephrotic syndrome; and
CC iv. other autoimmune and infectious diseases. (Updated on 25-MAR-2003 to
CC correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX

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SQ Sequence 676 AA;
Query Match 44.5%; Score 577.5; DB 1; Length 676;
Best Local Similarity 42.1%; Pred. No. 1.2e-32;
Matches 99; Conservative 45; Mismatches 78; Indels 13; Gaps 5;

Qy 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLMGNF 52
Db 83 PKYLVLRLSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDYMSCKDGKASFT 142
Qy 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSCHSGFELSSDGRTCQDI 109
Db 143 CTCKPGWQGEKCFDINECKDPSNINEGCSQICDNTPGSYHCSCXNGFVLSNKKDKDV 202
Qy 110 DECA--DSEACGEARCKNLPGSYCLCDGEGFAYSSOEKACRDVDECLQRCQVQCNVSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
Qy 169 YTCHCDGRGGLKLSQDMDTCEIILPCVPFVSVAKSVKSLYLGRMFSGTVIRLRFK 223
Db 263 YTCYCDGKKEFLAQDQKSCVSVCLPLNDTKVELLYLAEQAGV-VLYLKFR 316

RESULT 41
AAR70731
ID AAR70731 standard; protein; 244 AA.
XX
AC AAR70731;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Human protein S deletion mutant 243-C-terminus.
XX
KW Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
KW deletion mutant 243-C-terminus.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..41
FT Disulfide-bond 56..61 /note= "pre-pro leader sequence"
FT Domain 59..70 /note= "GLA domain"
FT Domain 86..243
FT Disulfide-bond 86..111 /note= "growth factor domains"
FT Disulfide-bond 119..132
FT Disulfide-bond 124..141
FT Disulfide-bond 143..152
FT Disulfide-bond 159..173
FT Disulfide-bond 169..182
FT Disulfide-bond 184..197
FT Disulfide-bond 203..215
FT Disulfide-bond 210..224
FT Disulfide-bond 226..239
XX
FN WO9501433-A1.
XX
PD 12-JAN-1995.
XX
PF 28-JUN-1994; 94WO-NL000149.
XX
PR 30-JUN-1993; 93EP-00201906.
XX
PA (UYLE-) RIJKSUNIV LEIDEN.
XX
PI Bouma BN, Bertina RM;
XX
DR WPI; 1995-060997/08.
XX
PT New deletion mutants of protein S retaining anticoagulant activity - are
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PT not neutralised by C4b binding protein, useful in treating thrombosis,
XX sepsis etc.
XX
PS Claim 5; Fig 5; 31pp; English.
XX
CC AAR70728 is the human protein S, from which the new deletion mutants
CC described in AAR70729-R70733 were derived. The mutants retain the
CC anticoagulant activity of the wild type protein, useful for the treatment
CC of thrombosis, protein S deficiency, sepsis, cancer and inflammation, but
CC lack the 2 putative C4b binding protein domains of the sex hormone
CC binding globulin domain of the wild type protein. As the mutants are
CC resistant to neutralisation by C4b binding protein they can provide
CC increased plasma levels of free protein S, and higher potency per unit
CC wt. of protein compared to the wild type protein. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
SQ Sequence 244 AA;
Query Match 32.2%; Score 418; DB 2; Length 244;
Best Local Similarity 43.3%; Pred. No. 8.1e-22;
Matches 71; Conservative 30; Mismatches 51; Indels 12; Gaps 4;

Qy 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTOACQDLMGNF 52
Db 81 PKYLVLRLSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDYMSCKDGKASFT 140
Qy 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSCHSGFELSSDGRTCQDI 109
Db 141 CTCKDQWQGEKCFDINECKDPSNINEGCSQICDNTPGSYHCSCXNGFVLSNKKDKDV 200
Qy 110 DECA--DSEACGEARCKNLPGSYCLCDGEGFAYSSOEKACRDVDE 152
Db 201 DECSLKPSICGTAVCKNIPGDFECEPEGYRYNLKSKSCEDIDE 244

RESULT 42
AAR70733
ID AAR70733 standard; protein; 244 AA.
XX
AC AAR70733;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Human protein S deletion mutant 243-C-terminus, 49, 60, 70.
XX
KW Human protein S; anticoagulant; thrombosis; cancer; sepsis; inflammation;
KW deletion mutant 243-C-terminus; 49, 60, 70 substitution.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..41
FT Misc-difference 49 /note= "pre-pro leader sequence"
FT Disulfide-bond 56..61 /note= "may be substituted"
FT Domain 59..70 /note= "GLA domain"
FT Misc-difference 60 /note= "may be substituted"
FT Misc-difference 70 /note= "may be substituted"
FT /note= "may be substituted; at least one of the three
FT possible substitutions must occur"
FT Domain 86..243
FT Disulfide-bond 86..111 /note= "growth factor domains"
FT Disulfide-bond 119..132
FT Disulfide-bond 124..141
FT Disulfide-bond 143..152
FT Disulfide-bond 159..173
FT Disulfide-bond 169..182
FT Disulfide-bond 184..197
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ADT49855;
16-DEC-2004 (first entry)
Murine FBLN1 partial sequence/betacellulin antibody SEQ ID NO:62.
FBLN1; BTC; betacellulin; antidiabetic; antilipemic;
antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
cytostatic; antiinflammatory; immunosuppressive; osteopathic;
antiarthritic; neuroprotective; antitropic; gene therapy;
diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
retinopathy; cardiovascular disease; cancer; fibrosis;
autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
Alzheimer's disease; neurodegenerative disorder;
cell proliferative disorder.
Mus musculus.
WO2004083241-A2.
30-SEP-2004.
18-MAR-2004; 2004WO-JP003699.
19-MAR-2003; 2003US-0456007P.
02-APR-2003; 2003US-0459944P.
(TAKE) TAKEDA CHEM IND LTD.
Sakamoto T, Takeda S;
WPI; 2004-691021/67.
New protein complexes comprising BTC and a second protein (e.g.
mLOC243548, mDLK1 or mPACE4) useful for diagnosing, preventing or
treating disorders such as diabetes mellitus, nephropathy, cardiovascular
disease or cancer.
Disclosure; SEQ ID NO 62; 493pp; English.
The invention relates to an isolated protein complex having a first
protein which is betacellulin (BTC) or its homologue, derivative or
fragment, interacting with a second protein selected from mLOC243548,
mDLK1, mPACE4, mBC032073 (1598), mTHB52, mFBLN5, mAK009011, mHRMT1L2,
mMATN3, mNID1, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
CAMLG, or homologue, derivative or fragment. A complex of the invention
has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
ophthalmological, cardiovascular-gen., cytostatic, antiinflammatory,
immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
nootropic activity, and may have a use in gene therapy. The composition
and methods are useful for treating physiological disorders associated
with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
disease, neurodegenerative disorder or cell proliferative disorder. These
may also be used for diagnosing or preventing the disorders cited above,
or for screening for agents that may be used to prevent or treat those
disorders. The present sequence is used in the exemplification of the
invention.
Sequence 397 AA;
Query Match 28.2%; Score 365.5; DB 8; Length 397;
Best Local Similarity 35.9%; Pred. No. 6.2e-18;
Matches 88; Conservative 28; Mismatches 74; Indels 55; Gaps 13;
6 CINKYGSPTKNSGPATCVQNLPT-----DQCTP--NPDRKGTOACQ 45
122 CINTEGS-----YTCQKVPNGRGYHLNBEGRTRCVQVDECSPPAEPG-KG-HHCL 171
46 DLMGNFFCLCKAGWG-----GRLCDKDVNCSQENG-G-CLQICHNKPFSFHCSHGSELS 100
172 NSPGSRCECKAGFYFDGISRTC-VDINECQYFGRLCGRKCENTPGSFHCSAGFRLS 230

QY 101 SDGRTCODIDECADSEACGEARCKNLPKSYSCLEGFAYSSQE-KACRDVDECLQGR-- 157
DB 231 VDRGSCEDVNECLNSPCSQE--CANVYGSQCYCRRGYQLSDVDGVTCEDIDECALPTGG 288
QY 158 --CSQVCVNSPGSYTCHDGRGGLKLSQDMDTCEDILPCVP-----FSVAKSVK 204
DB 289 HICSYRCINIPGSPQCSCPS-SGYRLAPNGRNCQDIDECVTGIHNCINETCFNIQGSFR 347
QY 205 SLYLG 209
DB 348 CLSFG 352
RESULT 45
ABO84707
ID ABO84707 standard; protein; 705 AA.
XX AC ABO84707;
XX DT 18-NOV-2004 (first entry)
XX DE Mouse cancer-associated protein MP21-032.1.
XX KW Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;
XX KW Lymphoma; CAP.
XX OS Mus musculus.
XX PN WO2004074320-A2.
XX PD 02-SEP-2004.
XX PF 17-FEB-2004; 2004WO-US004730.
XX PR 14-FEB-2003; 2003US-00367094.
XX PR 14-MAR-2003; 2003US-00388838.
XX PR 15-APR-2003; 2003US-00417375.
XX PR 13-JUN-2003; 2003US-00461862.
XX PR 15-SEP-2003; 2003US-00663431.
XX PR 15-DEC-2003; 2003US-00737318.
XX PA (SAGR-) SAGRES DISCOVERY INC.
XX PI Morris DW, Morris DW, Malandro MS;
XX DR WPI; 2004-652914/63.
XX DR N-PSDB; ABD33008.
XX PT New isolated cancer-associated polynucleotides and polypeptides useful
XX PT for diagnosing, preventing or treating cancers, especially lymphoma and
XX PT leukemia, or in screening for agents that modulate cancer.
XX PS disclosure; seqid 781; 310pp; English.
XX CC The invention relates to an isolated nucleic acid comprising at least 10
XX CC contiguous nucleotides of any of the 233 polynucleotide sequences given
XX CC in the specification, or its complement. The nucleic acids encode cancer-
XX CC associated proteins. Also included are an expression vector comprising
XX CC the isolated nucleic acid cited above, a host cell comprising the above
XX CC recombinant nucleic acid or expression vector, a microarray for detecting
XX CC a cancer-associated (CA) nucleic acid comprising at least one probe
XX CC comprising at least 10 contiguous nucleotides of any of the above-
XX CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
XX CC an open reading frame of a CA sequence selected from any of the 95
XX CC polynucleotide sequences as mentioned in the specification, or its
XX CC complement), an isolated antibody, (or its antigen binding fragment) that
XX CC binds to the above polypeptide, a hybridoma that produces the above
XX CC monoclonal antibody, a pharmaceutical composition comprising the above
XX CC antibody and a pharmaceutical excipient, a kit for detecting cancer
XX CC cells (comprising the antibody cited above, methods for diagnosing cancer
XX CC or for detecting the presence or absence of cancer cells in an
XX CC individual, a method for inhibiting growth of cancer cells in an

XX
 1234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991

XX

PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-00388838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX (SAGR-) SAGES DISCOVERY INC.
 PA
 PI Morris DW, Morris DW, Malandro MS;
 XX
 PI WPI; 2004-652914/63.
 DR N-PSDB; ABD32567.
 XX
 PT New isolated cancer-associated polynucleotides and polypeptides useful
 PT for diagnosing, preventing or treating cancers, especially lymphoma and
 PT leukemia, or in screening for agents that modulate cancer.
 XX
 PS claim 18; seqid 54; 310pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising at least 10
 CC contiguous nucleotides of any of the 233 polynucleotide sequences given
 CC in the specification, or its complement. The nucleic acids encode cancer-
 CC associated proteins. Also included are an expression vector comprising
 CC the isolated nucleic acid cited above, a host cell comprising the above
 CC recombinant nucleic acid or expression vector, a microarray for detecting
 CC a cancer-associated (CA) nucleic acid comprising at least one probe
 CC comprising at least 10 contiguous nucleotides of any of the above-
 CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
 CC an open reading frame of a CA sequence selected from any of the 95
 CC polynucleotide sequences as mentioned in the specification, or its
 CC complement), an isolated antibody, (or its antigen binding fragment) that
 CC binds to the above polypeptide, a hybridoma that produces the above
 CC monoclonal antibody, a pharmaceutical composition comprising the above
 CC antibody and a pharmaceutical excipient, a kit for detecting cancer
 CC cells (comprising the antibody cited above, methods for diagnosing cancer
 CC or for detecting the presence or absence of cancer cells in an
 CC individual, a method for inhibiting a growth of cancer cells in an
 CC individual, a method for delivering a therapeutic agent to cancer cells
 CC in an individual, an electronic library comprising the above
 CC polynucleotide or polypeptide (or their fragments), methods of screening
 CC for anticancer activity or for a bioactive agent capable of modulating
 CC the activity of a CA protein (CAP), methods for detecting cancer
 CC associated with expression of a polypeptide in a test cell sample, a
 CC method for treating cancers and a method for inhibiting the expression of
 CC CA gene in a cell. The composition and methods are useful for detecting,
 CC diagnosing, preventing and treating cancers, especially lymphoma and
 CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a human CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 518 AA;
 Query Match 27.8%; Score 361; DB 8; Length 518;
 Best Local Similarity 35.7%; Pred. No. 1.6e-17;
 Matches 81; Conservative 0; Mismatches 0; Indels 146; Gaps 1;
 Qy 1 PRYLDICINKYSPYTKNSGFATCVQNLDPQCTPNPDRKGTQACODLMGNPFCLCKAGWG 60
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 76 PRYLDICINKYSPYTKNSGFATCVQNLDPQCTPNPDRKGTQACODLMGNPFCLCKAGWG 118
 Qy 61 GRLCDKDVNECSQENGGLQICHNKPFGSCHSGFELSSDGRCTQDIDECADSEACGE 120
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 119 ----- 118
 Qy 121 ARCKNLPGSYSLCDEGPAYSSOEKACRDVDECLQRCQVCVNSPGSYTCHCDGRGLK 180
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 119 ----- 118
 Qy 181 LSQDMQTCEDILPCVPFVSVAKSVKSLYLGFMFGTVPVIRLRFKRLQP 227
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 119 -----DILPCVPFVSVAKSVKSLYLGFMFGTVPVIRLRFKRLQP 156
 RESULT 48
 ADT49854
 ID ADT49854 standard; protein; 258 AA.
 XX
 AC ADT49854;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Murine FBLN1 partial sequence/betacellulin antibody SEQ ID NO:61.
 XX
 KW FBLN1; BTC; betacellulin; antidiabetic; antilipemic;
 KW antiarteriosclerotic; nephrotropic; ophthalmological; cardiovascular;
 KW cytosstatic; antiinflammatory; immunosuppressive; osteopathic;
 KW aniaarthritic; neuroprotective; nootropic; gene therapy;
 KW diabetes mellitus; hyperlipemia; arteriosclerosis; nephropathy;
 KW retinopathy; cardiovascular disease; cancer; fibrosis;
 KW autoimmune disease; inflammatory disease; osteoarthritis; osteoporosis;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW cell proliferative disorder.
 XX
 OS Mus musculus.
 XX
 FN WO2004083241-A2.
 XX
 PD 30-SEP-2004.
 XX
 XX 18-MAR-2004; 2004WO-JP003699.
 PF
 XX 19-MAR-2003; 2003US-0456007P.
 PR
 XX 02-APR-2003; 2003US-0459944P.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 FA
 XX Sakamoto T, Takeda S;
 PI WPI; 2004-691021/67.
 DR
 XX New protein complexes comprising BTC and a second protein (e.g.
 PT mLOC243548, MDLKI or mPACE4) useful for diagnosing, preventing or
 PT treating disorders such as diabetes mellitus, nephropathy, cardiovascular
 PT disease or cancer.
 XX
 PS Disclosure; SEQ ID NO 61; 493pp; English.
 XX
 CC The invention relates to an isolated protein complex having a first
 CC protein which is betacellulin (BTC) or its homologue, derivative or
 CC fragment, interacting with a second protein selected from mLOC243548,
 CC MDLKI, mPACE4, mBC032073(1598), mTHBS2, mPELNS, mAK009011, mHRMT1L2,
 CC mMATN3, mNIDI, mTASP(459), mINPP5B, mTAKEDA008, UBB, mTREX1, mSGT and
 CC CAMLG, or homologue, derivative or fragment. A complex of the invention
 CC has antidiabetic, antilipemic, antiarteriosclerotic, nephrotropic,
 CC ophthalmological, cardiovascular-gen., cytosstatic, antiinflammatory,
 CC immunosuppressive, osteopathic, antiarthritic, neuroprotective, and
 CC nootropic activity, and may have a use in gene therapy. The composition
 CC and methods are useful for treating physiological disorders associated
 CC with diabetes mellitus, hyperlipemia, arteriosclerosis, nephropathy,
 CC retinopathy, cardiovascular disease, cancer, fibrosis, autoimmune
 CC disease, inflammatory disease, osteoarthritis, osteoporosis, Alzheimer's
 CC disease, neurodegenerative disorder or cell proliferative disorder. These
 CC may also be used for diagnosing or preventing the disorders cited above,
 CC or for screening for agents that may be used to prevent or treat those
 CC disorders. The present sequence is used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 258 AA;
 Query Match 27.7%; Score 359; DB 8; Length 258;
 Best Local Similarity 37.7%; Pred. No. 1.2e-17;
 Matches 83; Conservative 25; Mismatches 68; Indels 44; Gaps 12;

```
QY 6 CINKYSPYTKNGFATCVQNLPP-----DQCTP--NPCDRKGTQACQ 45
Db 17 CINTGSS-----YTCQNFVNCGRGYHLNEBTRCVDVDECSPAPPCQ-KG-HHCL 66
QY 46 DLWGNFFCLCKAGWG---GRLCDVNVCSOENG-CLQICHNKPFGSFHCSHSGFELS 100
Db 67 NSPGRFCRCEKAGFFDGIISRT-CVDINECQYPRGLCGHKCENTPGSFHCSAGFRLS 125
QY 101 SGRTCCQIDECADSEACGEARCKNLPLSGSYCLCDGFPAYSQE-KACRDVDECIQGR-- 157
Db 126 VDRGSCEDVNECLNSPCSQE--CANVGSYQCYCRGYQLSDVDGVTCEDIDECALPTGG 183
QY 158 --CEQVCNPSGYSYCHCDGRGGLKLSQDMTCEBILPCV 195
Db 184 HICSYRCINIPGNFOCSCPS-SGCRAPSGRNCQIDECV 222

RESULT 49
ABP56756
ID ABP56756 standard; protein; 911 AA.
XX AC ABP56756;
XX DT 31-MAR-2003 (first entry)
XX DE Mouse EGF-like 1 protein SEQ ID NO:4.
XX KW Human; secreted protein; epidermal growth factor protein subfamily;
XX KW epidermal growth factor; EGF; gene therapy; therapeutic; drug screening;
XX KW biological activity; immune response.
XX OS Mus musculus.
XX PN WO2002101080-A2.
XX PD 19-DEC-2002.
XX PF 07-MAY-2002; 2002WO-US022278.
XX PR 16-MAY-2001; 2001US-00855824.
XX PA (PEKE ) PE CORP NY.
XX PA (GONG/) GONG F.
XX PA (DFRA/) DI FRANCESCO V.
XX PI Gong F, Di Francesco V, Yan C, Beasley EM;
XX DR WPI; 2003-167407/16.
XX PT New isolated human secreted peptides, useful for diagnosing or treating a
XX PT disease characterized by an absence of, inappropriate or unwanted
XX PT expression of the secreted protein, and in drug screening assays.
XX PS Disclosure; Fig 2D-E; 185pp; English.
XX CC The present sequence encodes a human secreted peptide (I) related to the
XX CC epidermal growth factor (EGF) protein subfamily. (I) can be used in gene
XX CC therapy. (I) and the nucleic acid molecules encoding (I) can be used as
XX CC models for the development of human therapeutic targets, to aid in the
XX CC identification of therapeutic proteins, and to serve as targets for the
XX CC development of human therapeutic agents. (I) may be used in drug
XX CC screening assays, in assays to determine the biological activity of the
XX CC protein, to raise antibodies or to elicit another immune response, as a
XX CC reagent in assays designed to quantitatively determine levels of the
XX CC protein in biological fluids, or as markers for tissues in which the
XX CC corresponding protein is preferentially expressed. (I) can also be used
XX CC for diagnosing or treating a disease or disorder characterised by an
XX CC absence of, inappropriate or unwanted expression of the protein. (I) is
XX CC located to human chromosome 22. The present sequence represents mouse EGF
XX CC -like 1 protein which is given in comparison with (I) in the
XX CC exemplification of the present invention
XX SQ Sequence 911 AA;
```

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Query Match 27.6%; Score 357.5; DB 6; Length 911;
Best Local Similarity 38.6%; Pred. NO. 4.8e-17;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
QY 14 YTKSGFATCVQNLPDQCTPN--PCDRKGTQACQDLMGNFFCLCKAGW---GGFLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR---TCKDXTATGVRCSPVGTLPQDGKTC-KD 282
QY 68 VNECSQENGGCLQICHNKPFGSFHCSHSGFELSSDGRTCQIDECADSEACGEARCKNLPL 127
Db 283 INECLMNNGGCDHCRNTVGSFEGCGCKGKLLDTERTCQIDECSPERTCDHI-CINSP 341
QY 128 GSYSLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCNPSGYSYCHCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGYTLGYTTH--CGDVDECSMNNGSCBQGCVNTRGSEYECVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFPAVSKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRKASAKAQAQLSCGKV 424

RESULT 50
AD127635
ID AD127635 standard; protein; 961 AA.
XX AC AD127635;
XX DT 22-APR-2004 (first entry)
XX DE Mouse SCUBE1 protein.
XX KW human; SCUBE; secretory signal region; EGF-like domain chain; CUB domain;
XX KW endothelial cell; chromosome 22q13; antiarteriosclerotic; vasotropic;
XX KW thrombolytic; atherosclerosis; ischaemia; coagulation disorder;
XX KW thrombosis; mouse; murine; SCUBE1.
XX OS Mus musculus.
XX PN US2003219813-A1.
XX PD 27-NOV-2003.
XX PF 03-APR-2003; 2003US-00406073.
XX PR 05-APR-2002; 2002US-0369876P.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Yang R, Ng CKD, Tomlinson JS, Komuves LG, Topper JN, Robison KB;
XX DR WPI; 2004-097334/10.
XX PT New isolated polypeptide such as SCUBE1, SCUBE2 and SCUBE3, useful for
XX PT identifying an agent which modulates an activity of the new polypeptide.
XX PS Example 1; SEQ ID NO 13; 86pp; English.
XX CC The invention relates to a novel isolated human SCUBE polypeptide having
XX CC a sequence of 784, 386, 919, 914 or 993 amino acids and their encoding
XX CC nucleic acids. The invention specifically relates to SCUBE1, SCUBE2, and
XX CC SCUBE3. The SCUBE family has genes containing a secretory signal region,
XX CC a chain of EGF-like domains, and a CUB domain, that can be differentially
XX CC expressed in human endothelial cells compared to other human cell types.
XX CC The SCUBE1 gene has been found on human chromosome 22q13. The novel SCUBE
XX CC polypeptides have antiarteriosclerotic, vasotropic, and thrombolytic
XX CC activities. The isolated human SCUBE polypeptide is useful for
XX CC identifying an agent which modulates the expression of a nucleic acid
XX CC encoding the human SCUBE polypeptide. The human SCUBE polynucleotides are
XX CC useful for diagnosing a disease state in a subject which involves
XX CC determining the level of expression of the human SCUBE polynucleotides.
XX CC The human SCUBE polynucleotides and polypeptides are useful in a method
XX CC for treating a disorder such as atherosclerosis, ischaemia, coagulation
```

CC disorder or thrombosis, in a subject. This sequence represents a mouse
CC SCUBE1 protein of the invention.

XX
SQ Sequence 961 AA;
Query Match 27.6%; Score 357.5; DB 8; Length 961;
Best Local Similarity 38.6%; Pred. No. 5e-17;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
Qy 14 YTKNSGFATCVQNLDPDQTPN--PCDRKGTQACQDLGMGNFFCLCKAGW-----GGRLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR----TCKDTATGVRCSFVGFLLQPDGKTC-KD 282
Qy 68 VNECSQENGGLQICHNKPGSFHCSHGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNNGGCDHFCRNTVGSFECCQKGKLLTDERTCQDIDECSPERTCDHI-CINSP 341
Qy 128 GSYSCLCDGFA-YSSQKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGVTLTGTH--CGDVDECSMNGSCQGGCVNTRGSEYECVCP--PGRRLHWN 397
Qy 185 MDTCEDILPCVPFFSVAKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

Search completed: July 7, 2005, 09:31:35
Job time : 416.39 secs

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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:51:19 ; Search time 303.706 Seconds
(without alignments)
382.745 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRLDCINKYSGPYTKNSGF.....LGRMFGTPIRLPKRLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_spport.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1265.5	97.6	721	1	GAS6_HUMAN
2	1117	86.1	674	1	GAS6_RAT
3	1117	86.1	674	1	G6IRL1
4	1113	85.8	674	1	GAS6_MOUSE
5	810	62.5	668	2	O6PAE0
6	810	62.5	669	2	O6DFA5
7	647	49.9	648	2	Q773H4
8	609.5	47.0	649	1	PRTS_MACMU
9	601.5	46.4	497	2	Q72715
10	601.5	46.4	676	1	PRTS_HUMAN
11	596.5	46.0	675	1	PRTS_BOVIN
12	591.5	45.6	675	1	PRTS_MOUSE
13	586.5	45.2	646	1	PRTS_RABIT
14	586.5	45.2	650	2	Q16519
15	586.5	45.2	650	2	Q29NSD0
16	585.5	45.1	648	2	Q29094
17	585.5	45.1	675	1	PRTS_RAT
18	376	29.0	907	2	Q68EF9
19	363	28.0	705	1	FBL1_MOUSE
20	358.5	27.6	992	2	Q6C9Q4
21	358	27.6	1018	2	Q6NZL8
22	357.5	27.6	961	2	Q9BQC6
23	356	27.4	1666	1	LTB4_MOUSE
24	355	27.4	708	2	P87363
25	354.5	27.3	1577	2	Q9V589
26	354.5	27.3	1587	2	Q00508
27	353.5	27.3	997	2	Q9JJ50
28	353.5	27.3	1222	2	Q7PPC0
29	353.5	27.3	1511	2	O75412
30	351.5	27.1	3857	2	O88840
31	350.5	27.0	2872	2	Q9WUH8

32	349.5	26.9	2871	1	FBN1_BOVIN
33	349	26.9	988	2	Q81WY4
34	348.5	26.9	1365	2	Q75N88
35	348.5	26.9	2871	1	FBN1_HUMAN
36	348.5	26.9	2871	1	Q75N87
37	345	26.6	971	2	Q6ZW11
38	345	26.6	999	2	Q9NQ36
39	345	26.6	2871	1	FBN1_MOUSE
40	344.5	26.6	798	1	FBL1_CABEL
41	342.5	26.4	2809	1	FBN3_HUMAN
42	342	26.4	704	1	FBL1_CHICK
43	339	26.1	638	2	Q8NEH6
44	339	26.1	703	2	FBL1_HUMAN
45	339	26.1	1174	2	Q99K58
46	339	26.1	1221	1	FBL2_MOUSE
47	338	26.1	576	2	Q9Y3V7
48	337	26.0	1184	1	FBL2_HUMAN
49	337	26.0	1184	2	Q86V58
50	337	26.0	1231	2	Q81UI0
51	337	26.0	1231	2	Q81UI1
52	336.5	25.9	517	2	Q9NP01
53	334.5	25.8	1302	1	LTB3_HUMAN
54	334.5	25.8	1664	2	Q9TVQ2
55	333	25.7	880	2	Q8NAU9
56	333	25.7	1289	2	Q75JU6
57	331.5	25.6	893	2	Q8MJK0
58	331.5	25.6	1167	2	Q6KAT1
59	331.5	25.6	2911	1	FBN2_HUMAN
60	331	25.5	1398	2	Q8AXM6
61	331	25.5	1399	2	Q8JFZ4
62	331	25.5	2871	1	FBN1_PIG
63	330.5	25.5	1394	1	LTB3_HUMAN
64	330.5	25.5	1595	1	LTB1_HUMAN
65	328.5	25.3	2906	2	Q9WUH9
66	327	25.2	598	1	FBL1_CERAE
67	327	25.2	993	2	Q8IX30
68	326.5	25.2	1095	2	Q60784
69	326.5	25.2	2907	1	FBN2_MOUSE
70	325	25.1	827	2	Q68FG9
71	325	25.1	992	2	Q86UZ9
72	325	25.1	993	2	Q66PV1
73	324.5	25.0	1062	2	Q60789
74	323.5	24.9	443	2	Q9H3D5
75	323.5	24.9	682	2	Q6ZMN9
76	323	24.9	448	1	FBL5_HUMAN
77	323	24.9	448	1	FBL5_RAT
78	323	24.9	545	2	Q86TV4
79	322	24.8	937	2	Q66FT5
80	322	24.8	1016	2	Q8NDE6
81	321	24.7	448	1	FBL5_MOUSE
82	321	24.7	493	1	FBL3_HUMAN
83	321	24.7	493	2	Q7YQD7
84	320.5	24.7	1260	2	Q72YV5
85	320	24.7	493	1	FBL3_RAT
86	320	24.7	493	2	Q6AXN2
87	319.5	24.6	1712	1	LTB1_RAT
88	319.5	24.6	1821	1	LTB2_HUMAN
89	319.5	24.6	1821	2	Q6AZ94
90	319	24.6	387	2	Q8K0J4
91	319	24.6	448	2	Q6UWA3
92	319	24.6	477	2	Q8Y3N6
93	319	24.6	493	2	Q8NBP5
94	318	24.5	451	2	Q8N2G3
95	318	24.5	589	2	Q7ZX63
96	318	24.5	915	2	Q6UWA5
97	318	24.5	956	1	MTN2_HUMAN
98	318	24.5	3775	2	Q7PMF9
99	317.5	24.5	741	2	Q96K89
100	317.5	24.5	1244	2	Q69YJ3
101	317	24.4	1268	1	LTB3_MOUSE
102	316.5	24.4	443	1	FBL4_CRICR
103	316.5	24.4	937	2	Q9BLJ1
104	316.5	24.4	1246	1	EFL3_HUMAN

P98133	bos taurus
Q81wy4	homo sapien
Q75n88	homo sapien
P35555	homo sapien
Q75n87	homo sapien
Q6zw11	homo sapien
Q9nq36	homo sapien
Q15554	mus musculus
Q77469	caenorhabdi
Q75n90	homo sapien
Q73775	gallus gall
Q8bhb6	homo sapien
P23142	homo sapien
Q99K58	mus musculus
P37889	mus musculus
Q9y3v7	homo sapien
P98095	homo sapien
Q86v58	homo sapien
Q81ui0	homo sapien
Q81ui1	homo sapien
Q9np01	homo sapien
Q9na15	homo sapien
Q9tvq2	caenorhabdi
Q8nau9	homo sapien
Q75ju6	dictyosteli
Q6kat1	mus musculus
Q8mjko	cercopithe
P35556	homo sapien
Q8axm6	xenopus lae
Q8jfa4	xenopus lae
Q9t3v6	sus scrofa
P22064	homo sapien
Q14766	homo sapien
Q9wuh9	rattus norv
Q8nj9	cercopithe
Q8ax30	homo sapien
Q60784	mus musculus
Q61555	mus musculus
Q68fg9	mus musculus
Q86uz9	homo sapien
Q66pv1	mus musculus
Q60789	mus musculus
Q9h3d5	homo sapien
Q6zmn9	homo sapien
Q9ubx5	homo sapien
Q9wvh8	rattus norv
Q86tv4	homo sapien
Q86ft5	homo sapien
Q8nde6	homo sapien
Q9wvh9	mus musculus
Q12805	homo sapien
Q7ygd7	macaca fasc
Q7zrv5	oncorhynch
Q35568	rattus norv
Q6axn2	rattus norv
Q00918	rattus norv
Q14767	homo sapien
Q6az94	homo sapien
Q8k0j4	mus musculus
Q6uwa3	homo sapien
Q6y3n6	mus musculus
Q8bpb5	mus musculus
Q8n2g3	homo sapien
Q7zx63	xenopus lae
Q6uwa5	homo sapien
Q00339	homo sapien
Q7pmf9	anopheles g
Q96k89	homo sapien
Q69y33	homo sapien
Q61810	mus musculus
O55058	cricetulus
Q9blj1	ciona intes
Q75095	homo sapien

105	316.5	24.4	1389	1	LTBS_MOUSE	Q8G18 mus musculus	178	270.5	20.9	2470	1	NTC2_MOUSE	O35516 mus musculus
106	316.5	24.4	1713	1	LTBL_MOUSE	Q8G19 mus musculus	179	270	20.8	2037	2	O7QF52	O7qfs2 anopheles g
107	316	24.4	486	2	Q8SYF5	Q8syf5 drosophila	180	270	20.8	2437	1	NTC1_BRARE	P46530 brachydanio
108	315.5	24.3	715	2	Q7Z5X1	Q7z5x1 homo sapien	181	270	20.8	2656	2	O9GNUM3	Q9gm30 paracentrot
109	314.5	24.2	443	1	FBL4_HUMAN	Q95967 homo sapien	182	269	20.7	652	1	CD93_HUMAN	Q8wpl1 oikopleura
110	314.5	24.2	443	2	Q96TF5	Q96tf5 homo sapien	183	268.5	20.7	1972	2	O8WPL1	Q7psv8 anopheles g
111	314.5	24.2	443	2	Q6FH22	Q6fh22 homo sapien	184	268.5	20.7	2652	2	O7PSV8	O25253 lucilia cup
112	314.5	24.2	2428	2	O816X6	Q816x6 boophilus m	185	268.5	20.7	2653	2	O25253	O75440 homo sapien
113	313	24.1	886	1	EMR1_HUMAN	Q14246 homo sapien	186	268	20.7	161	2	O75440	O42401 gallus gall
114	312.5	24.1	528	2	Q9CKD8	Q9ckd8 mus musculus	187	268	20.7	452	1	MTN3_CHICK	O81xk1 homo sapien
115	312	24.1	839	2	Q6P3N7	Q6p3n7 xenopus tro	188	268	20.7	652	2	O81XK1	Q6mg89 rattus norv
116	311.5	24.0	872	2	Q6ZNB8	Q6znb8 homo sapien	189	268	20.7	1961	1	O6MG89	P31695 mus musculus
117	311.5	24.0	1842	1	LTB2_BOVIN	Q28019 bos taurus	190	266	20.5	1961	1	NTC4_MOUSE	P78504 homo sapien
118	310.5	23.9	443	1	FBL4_MOUSE	Q9wvj9 mus musculus	191	265.5	20.5	1218	1	JAG1_HUMAN	Q90y57 brachydanio
119	310.5	23.9	443	2	Q9UM06	Q9um06 mus musculus	192	265.5	20.5	1242	1	JAG1_BRARE	Q9gw30 rattus norv
120	310.5	23.9	1574	1	EFLJ3_RAT	Q8j281 rattus norv	193	265.5	20.5	2471	1	NTC2_RAT	Q90y54 brachydanio
121	309.5	23.8	2189	2	Q9BI05	Q9bi05 eimeria ten	194	264.5	20.4	1213	1	JAG3_BRARE	Q90y52 xenopus lae
122	308.5	23.8	1813	1	LTB2_MOUSE	O89999 mus musculus	195	264	20.4	1214	2	O90YD2	P10040 drosophila
123	307.5	23.7	1764	1	LTB2_RAT	O35806 rattus norv	196	264	20.4	2139	1	CRB_DROME	O9vc97 drosophila
124	304	23.4	2360	2	O7YZP0	Q7yzp0 eimeria max	197	264	20.4	2146	2	O9VC97	O16004 lytechinus
125	302.5	23.3	681	1	FBL1_BRARE	O42182 brachydanio	198	264	20.4	2531	2	O16004	Q9gye5 mus musculus
126	302.5	23.3	23015	2	Q8IQ18	Q8iq18 drosophila	199	263.5	20.3	1247	1	JAG2_MOUSE	P21783 xenopus lae
127	302	23.3	917	2	Q9V4B8	Q9v4b8 drosophila	200	263.5	20.3	2524	1	NOTC_XENLA	P46531 homo sapien
128	301	23.2	823	2	O7PSQ4	Q7psq4 anopheles g	201	263.5	20.3	2556	1	NTC1_HUMAN	O70244 rattus norv
129	300	23.1	65	2	O77692	O77692 oryctolagus	202	263.5	20.3	3623	2	O70244	O76809 hydra atten
130	300	23.1	2673	2	Q96SC3	Q96sc3 homo sapien	203	262.5	20.2	1081	2	O76809	Q01705 mus musculus
131	299.5	23.1	733	2	Q35678	Q25678 podocoryne	204	262.5	20.2	2531	1	NTC1_MOUSE	Q04721 homo sapien
132	299.5	23.1	2321	1	NTC3_HUMAN	Q9um47 homo sapien	205	261.5	20.2	2471	1	NTC2_HUMAN	Q7tcq52 mus musculus
133	299	23.1	5636	2	Q96RW7	Q96rw7 homo sapien	206	261.5	20.2	2516	2	O7TQ52	Q7tcq51 mus musculus
134	298.5	23.0	2319	1	NTC3_RAT	Q9r172 rattus norv	207	261.5	20.2	2526	2	O7TQ51	O8k428 mus musculus
135	297.5	22.9	643	1	CD93_RAT	Q9et61 rattus norv	208	261.5	20.2	2531	2	O8K428	O7LQ50 mus musculus
136	297	22.9	2524	2	Q9GPAS	Q9gpas branchiosto	209	261.5	20.2	2531	2	O7TQ50	O15232 homo sapien
137	294	22.7	396	2	Q6LCD7	Q6lcd7 mus musculus	210	261	20.1	486	1	MTN3_HUMAN	Q96aa0 homo sapien
138	294	22.7	931	1	EMR1_MOUSE	Q61549 mus musculus	211	260.5	20.1	537	2	O96AA0	Q61q50 homo sapien
139	292	22.5	867	2	Q6ZMN0	Q6zmn0 homo sapien	212	260.5	20.1	1317	2	O6IQ50	P10079 strongyloce
140	291.5	22.5	787	2	O8K061	Q8k061 mus musculus	213	259.5	20.0	1064	1	FBL1_STRPU	Q7008 rattus norv
141	291.5	22.5	1519	2	Q8WPN0	Q8wpn0 oikopleura	214	259.5	20.0	2531	1	NTC1_RAT	Q962w9 podocoryne
142	291.5	22.5	2318	1	NTC3_MOUSE	Q61982 mus musculus	215	258.5	19.9	713	2	O962W9	Q8i499 cupiennius
143	291	22.4	810	2	Q8C435	Q8c435 mus musculus	216	257.5	19.9	420	2	O8I499	Q08743 mus musculus
144	291	22.4	956	2	Q8R542	Q8r542 mus musculus	217	257	19.8	297	2	O08743	Q8bjb5 mus musculus
145	291	22.4	956	2	Q99K64	Q99k64 mus musculus	218	257	19.8	491	2	O8BJB5	Q15306 mus musculus
146	291	22.4	1115	2	O7QB67	Q7qb67 anopheles g	219	257	19.8	577	1	TRBM_MOUSE	Q8mx5 drosophila
147	289.5	22.3	729	2	O8BNH3	Q8bnh3 mus musculus	220	256.5	19.8	487	2	O8MSX5	Q68qf3 lithobius f
148	289	22.3	956	1	MTN2_MOUSE	O8746 mus musculus	221	256	19.7	463	2	O68QF3	Q6ux19 homo sapien
149	287	22.1	347	2	Q86T16	Q86t16 homo sapien	222	255	19.7	509	2	O6UX19	Q91v86 mus musculus
150	284.5	21.9	2528	2	Q8AXP0	Q8axp0 cynops pyrr	223	255	19.7	561	2	O91V88	Q80v54 mus musculus
151	283	21.8	590	2	Q8C088	Q8c088 mus musculus	224	255	19.7	608	2	O6NV58	O95460 homo sapien
152	282.5	21.8	304	2	O88744	O88744 mus musculus	225	255	19.7	619	1	MTN4_HUMAN	Q80ya8 mus musculus
153	279.5	21.5	2468	2	O800E4	Q800e4 brachydanio	226	255	19.6	1208	2	O80YA8	Q8hz48 oryctolagus
154	279	21.5	821	2	O6PYX2	Q6pyx2 brachydanio	227	254.5	19.5	580	2	O8HZA8	Q8r590 mus musculus
155	278	21.4	2585	2	Q33587	Q23587 caenorhabdi	228	253	19.5	1403	2	Q8R5G0	Q8cf3 mus musculus
156	277.5	21.4	191	2	Q9DED0	Q9ded0 gallus gall	229	253	19.5	1403	2	O8R5G0	Q8es77 mus musculus
157	277.5	21.4	832	2	Q8MQJ4	Q8mqj4 drosophila	230	253	19.5	3567	2	O9ES77	O6p424 xenopus tro
158	277.5	21.4	870	2	Q81QG6	Q81qg6 drosophila	231	253	19.5	904	2	O6P424	Q96dn2 homo sapien
159	277	21.4	669	2	O75441	Q75441 homo sapien	232	252.5	19.5	955	2	O96DN2	Q80wy0 homo sapien
160	275.5	21.2	647	2	Q8P3V5	Q8p3v5 mus musculus	233	252.5	19.5	1316	2	O96JU7	Q7q737 anopheles g
161	275.5	21.2	950	2	Q8MQN5	Q8mqn5 drosophila	234	252.5	19.5	1294	2	O96JU7	Q17494 caenorhabdi
162	275.5	21.2	1114	2	Q75WG2	Q75wg2 penaeus jap	235	252	19.4	1294	2	O8C622	Q95ln0 macaca fasc
163	275.5	21.2	1407	2	Q9VB65	Q9vb65 drosophila	236	252	19.4	1376	1	CRBH_HUMAN	Q95ln0 macaca fasc
164	275.5	21.2	1408	1	SERR_DROME	P18166 drosophila	237	252	19.4	1403	2	O7TQF0	Q1412 homo sapien
165	275.5	21.2	2003	1	NTC4_HUMAN	Q99466 homo sapien	238	252	19.4	1406	2	O8WY0	Q88322 mus musculus
166	275	21.2	644	1	CD93_MOUSE	O89103 mus musculus	239	252	19.4	3646	2	O17494	O9daws m mus muscu
167	274.5	21.2	481	1	MTN3_MOUSE	O35701 mus musculus	240	251.5	19.4	1106	2	Q17494	Q9puc8 gallus gall
168	274.5	21.2	481	2	Q6IR12	Q6ir12 mus musculus	241	251	19.4	376	2	O95LNO	Q80wv7 mus musculus
169	274.5	21.2	2447	2	O13149	O13149 figu rubrip	242	251	19.4	578	2	O912D3	P14543 homo sapien
170	273.5	21.1	255	2	O80845	O80845 mus musculus	243	251	19.4	1375	1	NID2_HUMAN	Q88322 mus musculus
171	273	21.0	1193	2	Q90819	Q90819 gallus gall	244	251	19.4	1403	1	NID2_MOUSE	O9daws m mus muscu
172	272	21.0	2703	2	NOTC_DROME	P07207 drosophila	245	250.5	19.3	439	2	O9DAW5	Q9puc8 gallus gall
173	271.5	20.9	1218	1	JAG1_MOUSE	Q9qxx0 mus musculus	246	250	19.3	135	2	O9PUC8	Q80wv7 mus musculus
174	271.5	20.9	1219	1	JAG1_RAT	Q63722 rattus norv	247	250	19.3	339	2	O80MW7	P14543 homo sapien
175	271	20.9	176	2	Q9PUC7	Q9puc7 gallus gall	248	250	19.3	1247	1	NIDO_HUMAN	Q8n9g0 homo sapien
176	271	20.9	827	2	O702I4	Q702i4 bos taurus	249	249.5	19.2	439	2	O8N9G0	Q8c9p6 mus musculus
177	270.5	20.9	2352	2	O61240	O61240 halocynthia	250	249.5	19.2	961	2	O8C9P6	

251	249.5	19.2	978	2	Q8BQI3	Q8bqi3 mus musculus	324	228	17.6	816	1	NEL2_HUMAN	Q99435 homo sapien
252	249.5	19.2	1176	2	Q6ZW16	Q6zw16 homo sapien	325	228	17.6	1202	1	JAG2_RAT	P97607 rattus norv
253	249.5	19.2	1245	1	NIDO_MOUSE	P10493 mus musculus	326	228	17.6	1905	2	Q76LJ2	Q76luj2 rattus norv
254	249.5	19.2	1245	2	Q8C3U8	Q8c3u8 mus musculus	327	227.5	17.5	347	2	Q9DDR4	Q9ddr4 gallus gall
255	249.5	19.2	529	2	Q25058	Q25058 heliocidari	328	227.5	17.5	811	1	LDLR_PIG	Q28832 sus scrofa
256	249.5	19.2	575	1	TRBM_HUMAN	P07204 homo sapien	329	227.5	17.5	837	2	Q9UH51	Q9uh51 homo sapien
257	249.5	19.2	575	1	TRBM_SALSC	Q71u07 salmiri sci	330	227.5	17.5	860	1	LDLR_HUMAN	P01130 homo sapien
258	249.5	19.2	577	2	Q81V29	Q81v29 homo sapien	331	227.5	17.5	1687	2	Q61204	Q61204 mus musculus
259	249.5	19.2	577	2	Q35370	Q35370 rattus norv	332	227	17.5	721	2	Q81902	Q81902 xenopus lae
260	249.5	19.2	1032	2	Q75WG1	Q75wg1 penaeus jap	333	226.5	17.5	1455	2	Q86FJ9	Q86fj9 caenorhabdi
261	248.5	19.2	356	2	Q706R6	Q706r6 anopheles g	334	226	17.4	739	1	ELT1_MOUSE	Q923x1 mus musculus
262	248.5	19.1	461	2	P97883	P97883 rattus norv	335	225.5	17.4	236	2	Q7Z3S9	Q7z3s9 homo sapien
263	248.5	19.1	624	1	MTM4_MOUSE	Q89029 mus musculus	336	225.5	17.4	853	2	Q6S4M2	Q6s4m2 macaca mula
264	246	19.0	891	2	Q71TX3	Q71tx3 gallus gall	337	225.5	17.4	1531	1	SLT1_RAT	Q88279 rattus norv
265	246	19.0	1315	2	Q71JF2	Q71jf2 mus musculus	338	224.5	17.3	297	2	Q7YUE5	Q7yue5 herdmania c
266	246	19.0	3871	2	Q20911	Q20911 caenorhabdi	339	224.5	17.3	1531	1	SLT1_MOUSE	Q80cr4 mus musculus
267	245.5	18.9	752	2	Q42374	Q42374 brachydanio	340	224.5	17.3	1537	2	Q8WY29	Q8wy29 homo sapien
268	245	18.9	969	2	Q81V28	Q81v28 homo sapien	341	224	17.3	726	2	Q8AM87	Q8am87 cynops pyrr
269	245	18.9	1216	2	Q90Y55	Q90y55 brachydanio	342	224	17.3	869	2	Q42126	Q42126 xenopus lae
270	245	18.9	1254	2	Q90Y56	Q90y56 brachydanio	343	224	17.3	869	2	Q6NS01	Q6ns01 xenopus lae
271	245	18.9	1254	2	Q9YHU2	Q9yhu2 brachydanio	344	224	17.3	1295	1	GLP1_CAEEL	P13508 caenorhabdi
272	244.5	18.9	722	1	DL11_MOUSE	Q61483 mus musculus	345	224	17.3	1847	2	Q76952	Q76952 aedes aegypt
273	244.5	18.9	722	2	Q6PFV7	Q6pfv7 mus musculus	346	223.5	17.2	261	2	Q7PRJ2	Q7prj2 anopheles g
274	244	18.8	508	2	Q6DHG1	Q6dhg1 brachydanio	347	223.5	17.2	911	2	Q7ZZT0	Q7zzt0 brachydanio
275	242.5	18.7	714	1	DL11_RAT	P97677 rattus norv	348	223	17.2	642	2	P79941	P79941 xenopus lae
276	242.5	18.7	3687	2	Q9W332	Q9w332 drosophila	349	223	17.2	772	2	Q6DI48	Q6di48 brachydanio
277	242	18.7	468	2	Q9UC32	Q9uc32 homo sapien	350	223	17.2	802	2	O57462	O57462 brachydanio
278	242	18.7	1238	1	JAG2_HUMAN	Q9Y219 homo sapien	351	222.5	17.2	338	2	Q6UXJ1	Q6uxj1 homo sapien
279	241.5	18.6	1534	1	SLT1_HUMAN	Q75093 homo sapien	352	222.5	17.2	553	2	Q81UX8	Q81ux8 homo sapien
280	241.5	18.6	1551	2	Q9NGV4	Q9ngv4 drosophila	353	222.5	17.2	553	2	Q8NBV0	Q8nbv0 homo sapien
281	241.5	18.6	3396	2	Q9VM55	Q9vm55 drosophila	354	222.5	17.2	554	2	Q9NZL7	Q9nzt7 homo sapien
282	241	18.6	1403	2	Q70E20	Q70e20 mus musculus	355	222.5	17.2	1216	2	Q9BEA0	Q9bea0 canis famil
283	240.5	18.5	1212	2	O42347	O42347 gallus gall	356	222.5	17.2	4599	1	LR1B_HUMAN	Q9nzt2 homo sapien
284	240.5	18.5	1569	2	Q7Q3I9	Q7q3i9 anopheles g	357	222.5	17.2	339	2	Q9BIJ2	Q9bij2 toxoplasma
285	240	18.5	1065	2	Q810H2	Q810h2 mus musculus	358	222	17.1	473	1	F22_MITGA	Q22464 mytilus gal
286	239	18.4	389	2	Q9DDR5	Q9ddr5 gallus gall	359	222	17.1	728	1	Q90656	Q90656 gallus gall
287	239	18.4	544	2	Q8AVH7	Q8avh7 xenopus lae	360	222	17.1	558	2	Q9UFK6	Q9ufk6 homo sapien
288	239	18.4	1530	2	Q90WZ3	Q90wz3 xenopus lae	361	221.5	17.1	219	2	Q7Z7L6	Q7z7l6 homo sapien
289	239	18.4	3620	2	Q9TU53	Q9tu53 canis famil	362	221	17.0	237	2	Q81VT0	Q81vt0 homo sapien
290	238.5	18.4	636	2	Q8N2S1	Q8n2s1 homo sapien	363	221	17.0	642	2	Q7ZXT4	Q7zxt4 xenopus lae
291	238.5	18.4	835	1	CD97_HUMAN	P48960 homo sapien	364	221	17.0	287	2	Q8MVJ7	Q8mvj7 boletia vi
292	238	18.4	816	1	NEL_CHICK	Q90827 gallus gall	365	220.5	17.0	356	1	TRBM_BOVIN	P06579 bos taurus
293	238	18.4	1405	2	Q8VHS2	Q8vhs2 mus musculus	366	220.5	17.0	542	2	Q7Q0Z8	Q7q0z8 anopheles g
294	237.5	18.3	761	2	Q6ST50	Q6st50 mus musculus	367	220.5	17.0	1210	2	Q95ND4	Q95nd4 felis silve
295	237	18.3	1515	2	Q9DE37	Q9de37 brachydanio	368	220.5	17.0	824	2	Q66S04	Q66s04 oikopleura
296	237	18.3	3494	2	Q71LC53	Q71lc53 homo sapien	369	220	17.0	1200	2	Q8VD07	Q8vd07 mus musculus
297	237	18.3	3623	2	Q60494	Q60494 homo sapien	370	220	17.0	1217	1	EGF_MOUSE	P01132 mus musculus
298	235.5	18.2	450	2	Q869J7	Q869j7 glomeris ma	371	220	17.0	996	1	LRP8_MOUSE	Q924x6 mus musculus
299	235.5	18.2	592	2	Q91XL5	Q91xl5 mus musculus	372	220	17.0	1476	2	Q90285	Q90285 carassius a
300	235.5	18.2	609	2	Q923T5	Q923t5 mus musculus	373	219.5	16.9	239	2	Q7Z618	Q7z618 homo sapien
301	234	18.0	570	1	FBP3_STRPU	P49013 strongyloce	374	219.5	16.9	816	1	NEL2_RAT	Q62918 rattus norv
302	233.5	18.0	406	2	Q25059	Q25059 heliocidari	375	219	16.9	819	2	Q8417	Q8r417 rattus norv
303	233	18.0	342	2	Q6PL92	Q6pl92 homo sapien	376	219	16.9	858	2	Q80UM5	Q80um5 mus musculus
304	233	18.0	366	2	Q9DDR6	Q9ddr6 gallus gall	377	219	16.9	784	2	Q8BM43	Q8bm43 m mus muscu
305	233	18.0	778	2	Q91BGA	Q91bga xenopus lae	378	219	16.9	816	1	NEL2_MOUSE	Q61220 mus musculus
306	233	18.0	2019	2	Q68FE0	Q68fe0 mus musculus	379	219	16.9	816	1	NEL2_RAT	Q62918 rattus norv
307	232.5	17.9	585	2	Q90UE2	Q90ue2 tribolium c	380	219	16.9	819	2	Q80UM5	Q80um5 mus musculus
308	232	17.9	1372	2	P91526	P91526 caenorhabdi	381	219	16.9	858	2	Q8BM06	Q8bm06 mus musculus
309	232	17.9	1905	1	LRP4_MOUSE	Q8vi56 mus musculus	382	218.5	16.8	1207	1	EGF_HUMAN	P01133 homo sapien
310	231.5	17.8	823	1	EMR2_HUMAN	Q9ubx3 homo sapien	383	217.5	16.8	783	2	Q90XG2	Q90xg2 gallus gall
311	231	17.8	269	2	Q8NC23	Q8nc23 homo sapien	384	217.5	16.8	950	2	Q90Z44	Q90z44 gallus gall
312	231	17.8	1282	2	Q8TER0	Q8ter0 homo sapien	385	217.5	16.8	1132	2	Q6P6T8	Q6p6t8 rattus norv
313	231	17.8	1305	1	LRP4_RAT	Q9gyp1 rattus norv	386	217	16.7	757	2	Q9HCU0	Q9hcu0 homo sapien
314	231	17.8	3523	2	Q70CF4	Q70cf4 anopheles g	387	217	16.7	1114	2	Q6VQ0A	Q6vqa2 brachydanio
315	230.5	17.8	814	2	Q7ZXL5	Q7zxl5 xenopus lae	388	216.5	16.7	546	2	Q8R4V5	Q8r4v5 mus musculus
316	230	17.7	356	2	Q96FY1	Q96fy1 homo sapien	389	216.5	16.7	717	2	P87357	P87357 brachydanio
317	229.5	17.7	723	1	DL11_HUMAN	Q00548 homo sapien	390	216.5	16.7	720	2	Q8UWJ4	Q8uwj4 brachydanio
318	229	17.7	1950	1	LRP4_HUMAN	Q75096 homo sapien	391	216.5	16.7	1429	1	L112_CAEEL	P14585 caenorhabdi
319	228.5	17.6	236	2	Q8WUQ9	Q8wuq9 homo sapien	392	216	16.7	684	2	Q81498	Q81498 cupiennius
320	228.5	17.6	271	2	Q8CJG6	Q8cjpg6 rattus norv	393	215.5	16.6	664	2	Q91AT6	Q9iat6 brachydanio
321	228.5	17.6	327	2	Q8BPM8	Q8bpm8 mus musculus	394	215.5	16.6	917	1	LRP8_CHICK	Q98931 gallus gall
322	228.5	17.6	355	2	Q9JUZ5	Q9jjz5 mus musculus	395	215.5	16.6	1521	1	SLT2_MOUSE	Q9rib9 mus musculus
323	228	17.6	815	2	Q96J52	Q96j52 homo sapien	396	215	16.6	738	1	ELT1_RAT	Q9esc1 rattus norv

397	214.5	16.5	546	2	Q6V0K7	Q6v0k7 rattus norv	470	201	15.5	1529	2	Q7ZXI2	Q7zxi2 xenopus lae
398	214.5	16.5	546	2	Q811T0	Q811t0 mus musculus	471	201	15.5	4544	1	LRP1_HUMAN	Q07954 homo sapien
399	214.5	16.5	546	2	Q8C9U1	Q8c9u1 mus musculus	472	200	15.4	689	2	Q80VA2	Q80va2 mus musculus
400	214.5	16.5	991	2	Q7SWG0	Q7swg0 penaeus jap	473	200	15.4	738	2	Q90Z45	Q90z45 gallus gall
401	214	16.5	318	2	Q8CJG7	Q8cjg7 rattus norv	474	200	15.4	1209	2	Q80XT9	Q80xt9 mus musculus
402	214	16.5	604	2	Q6T3J7	Q6t3j7 drosophila	475	199.5	15.4	644	2	Q642D6	Q642d6 rattus norv
403	214	16.5	833	1	DL_DROME	P10041 drosophila	476	199.5	15.4	3183	1	Q652C2	Q652c2 caenorhabdi
404	214	16.5	1245	1	Q6PPB4	P6ppb4 gallus gall	477	199.5	15.4	3767	1	MUA3_CAEEL	P34576 caenorhabdi
405	214	16.5	2571	1	SN1_MOUSE	Q8r4y4 mus musculus	478	199	15.3	650	2	Q7Q0M5	Q7q0m5 anopheles g
406	212.5	16.4	500	2	Q864U4	Q864u4 bos taurus	479	199	15.3	881	2	Q8WY31	Q8wy31 homo sapien
407	212.5	16.4	765	2	Q91V98	Q91v98 mus musculus	480	199	15.3	1060	2	Q968S4	Q968s4 drosophila
408	212.5	16.4	765	2	Q91ZV1	Q91zv1 mus musculus	481	199	15.3	1060	2	Q9VM97	Q9vm97 drosophila
409	212	16.3	340	2	Q7QKC9	Q7qkc9 anopheles g	482	199	15.3	1286	2	Q7QCT2	Q7qct2 anopheles g
410	212	16.3	678	2	Q68EY0	Q68ey0 xenopus lae	483	199	15.3	1523	1	SLT3_HUMAN	Q75094 homo sapien
411	212	16.3	1441	2	Q867Q2	Q867q2 caenorhabdi	484	199	15.3	4753	1	LRP_CAEEL	Q04833 caenorhabdi
412	211.5	16.3	674	2	Q8N027	Q8n027 homo sapien	485	198.5	15.3	454	2	Q8TB42	Q8tb42 homo sapien
413	211.5	16.3	810	1	NEL1_HUMAN	Q92832 homo sapien	486	198.5	15.3	545	2	Q8WMZ8	Q8wmz8 homo sapien
414	211.5	16.3	810	1	Q6NSY8	Q6nsy8 homo sapien	487	198.5	15.3	674	2	Q8T4N9	Q8t4n9 strongyloce
415	211.5	16.3	1059	2	Q9VQ47	Q9vq47 drosophila	488	198.5	15.3	737	2	Q8NFT8	Q8nft8 homo sapien
416	211.5	16.3	1101	2	Q7KU08	Q7ku08 drosophila	489	197.5	15.2	382	1	EFL9_MOUSE	Q8kl83 mus musculus
417	211.5	16.3	1529	1	SLT2_HUMAN	O94813 homo sapien	490	197.5	15.2	644	1	UROM_RAT	P27590 rattus norv
418	211.5	16.3	3222	2	Q6V0I7	Q6v0i7 homo sapien	491	197.5	15.2	4543	1	LRPI_CHICK	P98157 gallus gall
419	211	16.3	2025	2	Q8CJA0	Q8cja0 mus musculus	492	197	15.2	474	2	Q8WYG3	Q8wyg3 homo sapien
420	211	16.3	642	2	Q91X17	Q91x17 mus musculus	493	197	15.2	863	1	LDVR_CHICK	P98165 gallus gall
421	211	16.3	1133	1	EGF_RAT	P07522 rattus norv	494	196.5	15.2	383	1	EFL9_HUMAN	Q6uy11 homo sapien
422	210.5	16.2	97	2	Q91WZ4	Q91wz4 mus sp. fib	495	196.5	15.2	737	2	Q81VT0	Q81vt0 homo sapien
423	210.5	16.2	492	2	P37806	P37806 mus musculus	496	196.5	15.2	739	2	Q8IGR9	Q8igr9 drosophila
424	210.5	16.2	4599	1	LR1B_MOUSE	Q9j1l8 mus musculus	497	196.5	15.2	818	1	CD97_MOUSE	Q9z0m6 mus musculus
425	210	16.2	615	2	O57409	O57409 brachydanio	498	196.5	15.2	883	2	Q9VBN1	Q9vbn1 drosophila
426	209.5	16.2	879	1	LDLR_RAT	P35952 rattus norv	499	196.5	15.2	996	2	Q6NP71	Q6np71 drosophila
427	209.5	16.2	1214	2	Q9BD00	Q9bd00 sus scrofa	500	196.5	15.2	1031	2	Q9VBN0	Q9vbn0 drosophila
428	209	16.1	854	1	LDLR_CRICR	P35950 cricetus	501	196.5	15.2	1037	2	Q6NP66	Q6np66 drosophila
429	209	16.1	1270	2	Q9GPN0	Q9gpn0 caenorhabdi	502	196.5	15.2	1952	2	Q95SN5	Q95sn5 drosophila
430	209	16.1	4569	2	Q7PFS35	Q7pfs35 anopheles g	503	196.5	15.2	4547	2	Q9W343	Q9w343 drosophila
431	208.5	16.1	810	1	NEL1_RAT	Q62919 rattus norv	504	196	15.1	4545	2	Q91ZX7	Q91zx7 mus musculus
432	208	16.0	792	2	Q90Z43	Q90z43 gallus gall	505	196	15.1	4545	2	Q61291	Q61291 mus musculus
433	208	16.0	838	2	Q3VQA9	Q3vqa9 drosophila	506	196	15.1	4545	2	Q61291	Q61291 mus musculus
434	208	16.0	1095	2	Q90XG4	Q90xg4 gallus gall	507	195.5	15.1	192	2	Q9UDM2	Q9udm2 homo sapien
435	208	16.0	1984	1	YL_DROME	P98163 drosophila	508	195.5	15.1	737	2	Q8VD97	Q8vd97 mus musculus
436	208	16.0	2570	1	SN1_HUMAN	Q9ny15 homo sapien	509	195	15.0	738	2	Q7QK75	Q7qk75 anopheles g
437	207.5	16.0	732	2	Q95L62	Q95l62 sus scrofa	510	195	15.0	749	2	Q7QK77	Q7qk77 anopheles g
438	207.5	16.0	1308	2	Q9GPM8	Q9gpm8 caenorhabdi	511	195	15.0	845	2	Q91XY0	Q91xy0 mus musculus
439	207.5	16.0	4610	2	Q9AXB7	Q9axb7 brachydanio	512	195	15.0	873	1	LDVR_MOUSE	P98156 mus musculus
440	207	16.0	1809	2	Q8AMP02	Q8amp02 periplaneta	513	195	15.0	887	2	Q9U1T9	Q9u1t9 caenorhabdi
441	206	15.9	1523	1	SLT3_MOUSE	Q9rvb4 mus musculus	514	195	15.0	909	1	LDL1_XENLA	Q93087 xenopus lae
442	205	15.8	237	2	Q804J3	Q804j3 gallus gall	515	195	15.0	4655	1	LRP2_HUMAN	P98164 homo sapien
443	205	15.8	862	2	Q9UF98	Q9uf98 homo sapien	516	195	15.0	4655	2	Q7Z5C0	Q7z5c1 homo sapien
444	205	15.8	1410	2	Q20204	Q20204 caenorhabdi	517	195	15.0	4655	2	Q7Z5C1	Q7z5c1 homo sapien
445	205	15.8	1523	1	SLT3_RAT	O88280 rattus norv	518	194.5	15.0	762	2	O42373	O42373 brachydanio
446	205	15.8	2551	1	SN2_HUMAN	Q8vwq8 h stabilin	519	194.5	15.0	837	1	LDLR_RABIT	P20063 cryctolagus
447	204.5	15.8	642	2	Q822B5	Q822b5 mus musculus	520	194.5	15.0	891	2	Q7VM57	Q7vm57 aedes aegypt
448	204.5	15.8	643	1	UROM_BOVIN	P48733 bos taurus	521	194	15.0	471	2	Q804X6	Q804x6 gallus gall
449	204	15.7	1512	2	Q9DE36	Q9de36 brachydanio	522	194	15.0	857	2	P79708	P79708 chiloscyll
450	204	15.7	1722	2	Q19350	Q19350 caenorhabdi	523	193.5	14.9	308	2	O46370	O46370 bos taurus
451	204	15.7	4589	2	Q9WU10	Q9wu10 rattus norv	524	193.5	14.9	455	2	Q7SY86	Q7sy86 xenopus lae
452	203.5	15.7	611	2	Q91YG0	Q91yg0 homo sapien	525	193	14.9	225	2	Q7PFO7	Q7pfg7 anopheles g
453	203.5	15.7	640	1	UROM_HUMAN	P07911 homo sapien	526	193	14.9	873	1	LDVR_RABIT	P35953 cryctolagus
454	203.5	15.7	826	2	Q86B77	Q86b77 drosophila	527	193	14.9	873	1	LDVR_RAT	P98166 rattus norv
455	203.5	15.7	861	2	Q7YT26	Q7yt26 drosophila	528	193	14.9	4590	1	FATH_HUMAN	Q14517 homo sapien
456	203.5	15.7	1064	2	Q7YU01	Q7yu01 drosophila	529	192	14.8	261	2	Q9GM41	Q9gm41 macaca fasc
457	203.5	15.7	1069	2	Q9VBN2	Q9vbn2 drosophila	530	192	14.8	813	2	Q6ZK10	Q6zkl0 oryza sativ
458	203	15.7	306	2	Q8C6U7	Q8c6u7 mus musculus	531	192	14.8	883	2	O46131	O46131 locusta mig
459	203	15.7	796	2	Q8MY77	Q8my77 branchiosto	532	191.5	14.8	433	2	Q804X5	Q804x5 gallus gall
460	203	15.7	1782	2	Q8X0I2	Q8x0i2 solenopsis	533	191.5	14.8	722	2	Q9DC42	Q9dc42 mus musculus
461	202.5	15.6	734	1	CD97_BOVIN	Q8sq44 bos taurus	534	191	14.7	798	2	Q75WV8	Q75wv8 branchiosto
462	202	15.6	1859	2	Q7PFS28	Q7pfs28 anopheles g	535	190.5	14.7	353	2	Q86UC0	Q86uc0 homo sapien
463	201.5	15.5	389	2	Q8R226	Q8r226 mus musculus	536	190	14.6	122	2	Q869J5	Q869j5 archispiros
464	201.5	15.5	737	2	Q8JZM4	Q8jzm4 mus musculus	537	190	14.6	199	2	O6SPF9	O6spf9 tribolium c
465	201.5	15.5	737	2	Q8R4T6	Q8r4t6 mus musculus	538	190	14.6	752	2	Q8NAN7	Q8nan7 homo sapien
466	201.5	15.5	862	2	Q9VCT0	Q9vct0 mus musculus	539	190	14.6	873	1	LDVR_HUMAN	P98155 homo sapien
467	201.5	15.5	862	2	Q91ZJ1	Q91zj1 mus musculus	540	190	14.6	873	2	Q6S4M1	Q6s4m1 macaca mula
468	201.5	15.5	864	1	LDLR_MOUSE	P35951 mus musculus	541	190	14.6	892	1	LDL2_XENLA	Q99088 xenopus lae
469	201.5	15.5	2559	1	SN2_MOUSE	Q8r4u0 mus musculus	542	189.5	14.6	353	2	Q6UXH1	Q6uxh1 homo sapien

543	189.5	14.6	794	2	Q8T4P0	Q8t4p0 lytechinus	616	177.5	13.7	456	1	PRTC_CANFA
544	189.5	14.6	963	1	LRPE_HUMAN	Q14114 homo sapien	617	177	13.6	241	2	Q8CI01
545	189.5	14.6	1156	2	Q963T3	Q963t3 aedis aegyp	618	177	13.6	241	2	Q8CI01
546	189	14.6	663	2	Q44247	Q44247 hemiceintrot	619	176.5	13.6	344	2	Q9CVK2
547	189	14.6	747	2	Q6UWL2	Q6uwl2 homo sapien	620	176	13.6	350	2	Q9CVA0
548	189	14.6	747	2	Q6DJD9	Q6djd9 xenopus lae	621	175.5	13.5	459	1	PRTC_PTG
549	188.5	14.5	227	2	Q7RXP6	Q7rpx6 lucilia cup	622	175.5	13.5	273	1	EPFL7_HUMAN
550	188.5	14.5	341	2	Q75XFK	Q75xfk brachydanio	623	175.5	13.5	321	2	Q9BU47
551	188.5	14.5	686	1	DLH4_MOUSE	Q9j171 mus musculus	624	175.5	13.5	383	2	Q7O534
552	188.5	14.5	807	2	Q8MP01	Q8mp01 halocynthia	625	175.5	13.5	383	2	Q7O534
553	188	14.5	845	2	Q77505	Q77505 bos taurus	626	175.5	13.5	482	1	FA10_RAT
554	187.5	14.5	498	2	Q66NE4	Q66ne4 bombyx mori	627	175.5	13.5	770	2	Q9U2D5
555	187.5	14.5	587	2	Q8NBS4	Q8nbs4 homo sapien	628	175	13.5	1170	1	TSP1_BOVIN
556	187.5	14.5	758	2	Q6GNE3	Q6gne3 bombyx mori	629	175	13.5	438	2	Q8I497
557	187	14.4	721	2	Q95YGO	Q95ygo ciona savig	630	174.5	13.5	591	1	BMPI_MOUSE
558	186.5	14.4	383	2	Q669Y6	Q669y6 homo sapien	631	174.5	13.5	584	2	Q73920
559	186.5	14.4	574	2	Q62759	Q62759 sus scrofa	632	174.5	13.5	589	1	DL33_RAT
560	186.5	14.4	4660	1	LRP2_RAT	Q62759 sus scrofa	633	174.5	13.5	619	2	Q73921
561	186	14.3	553	2	Q8HXE2	Q8hxe2 macaca fasc	634	174.5	13.5	775	2	Q6P550
562	185.5	14.3	376	1	FL10_TROCA	P81428 tropidechis	635	174.5	13.5	986	1	BMPI_MOUSE
563	185.5	14.3	383	1	DLK_HUMAN	Q80370 homo sapien	636	174.5	13.5	991	2	Q6NZM2
564	185.5	14.3	585	2	Q8W06	Q80w06 mus musculus	637	174.5	13.5	584	2	Q73920
565	185.5	14.3	592	1	DL33_MOUSE	Q8516 mus musculus	638	174	13.4	1012	2	Q9WVM6
566	185.5	14.3	686	2	Q9DBU9	Q9dbu9 mus musculus	639	173	13.3	1504	1	SLIT_DROME
567	185.5	14.3	2104	2	Q21281	Q21281 caenorhabdi	640	172.5	13.3	737	2	Q6IR63
568	185.5	14.3	2104	2	Q664N4	Q664n4 caenorhabdi	641	172.5	13.3	684	2	Q9BIM7
569	185	14.3	138	2	Q6UTY0	Q6uty0 bos taurus	642	172.5	13.3	559	2	Q9V244
570	185	14.3	1431	1	SBN2_RAT	Q80f66 rattus norv	643	172	13.2	947	2	Q8BKK7
571	185	14.3	5175	2	Q810L3	Q810l3 caenorhabdi	644	171.5	13.2	1140	2	Q80T91
572	185	14.3	5198	2	Q76518	Q76518 caenorhabdi	645	171.5	13.2	952	2	Q62TA9
573	184.5	14.2	348	2	Q60438	Q60438 cricetus	646	171.5	13.2	463	2	Q6IT10
574	184	14.2	475	1	FA10_CHICK	P25155 gallus gall	647	171	13.2	475	2	Q804W9
575	183.5	14.1	490	1	FA10_RABIT	Q19045 oryctolagus	648	171	13.2	504	2	Q6DUF5
576	183	14.1	340	2	Q8OY26	Q80y26 mus musculus	649	171	13.2	156	2	Q6D661
577	183	14.1	481	1	FA10_MOUSE	Q8947 mus musculus	650	171	13.2	422	2	Q619X5
578	182.5	14.1	443	2	Q8JHC9	Q8jhc9 brachydanio	651	170.5	13.1	974	2	Q9UAG0
579	182.5	14.1	450	2	Q8KOH9	Q8kho9 mus musculus	652	170.5	13.1	261	2	Q8IY13
580	182.5	14.1	685	1	DLH4_HUMAN	Q9nr61 homo sapien	653	170.5	13.1	598	2	Q6PEN1
581	182.5	14.1	844	2	Q7TSG9	Q7tsg9 mus musculus	654	170.5	13.1	4705	1	FAT2_DROME
582	182.5	14.1	844	2	Q6Y857	Q6y857 morone amer	655	169.5	13.1	432	2	Q6GNA2
583	182	14.0	292	2	Q86SM0	Q86sm0 homo sapien	656	169.5	13.1	219	2	Q90W22
584	182	14.0	296	2	Q727K9	Q727k9 homo sapien	657	169.5	13.1	403	2	O18375
585	182	14.0	439	2	Q6EY72	Q6epj72 homo sapien	658	169.5	13.1	417	2	Q9Y409
586	182	14.0	733	2	Q6P7G8	Q6p7g8 xenopus lae	659	169.5	13.1	420	2	Q8NFT4
587	181.5	14.0	444	1	FA7_RABIT	P98139 oryctolagus	660	169.5	13.1	808	2	Q7YU36
588	181	14.0	138	2	Q7O6T4	Q7q6t4 anopheles g	661	169.5	13.1	1067	1	TLT_DROME
589	181	14.0	263	2	Q8KYU6	Q8kyu6 homo sapien	662	169	13.0	936	2	Q81FX2
590	181	14.0	623	2	Q93484	P93484 pisum sativ	663	169	13.0	977	2	Q91925
591	180.5	13.9	618	1	DL33_HUMAN	Q9ny17 homo sapien	664	169	13.0	1070	2	P91972
592	180	13.9	238	2	Q8QGG9	Q8qgg9 gallus gall	665	168.5	13.0	1075	2	Q9NC90
593	180	13.9	263	2	Q99740	Q99740 homo sapien	666	168.5	13.0	462	2	Q6IT09
594	180	13.9	397	1	PROZ_MOUSE	Q9ccw3 mus musculus	667	168.5	13.0	492	1	FA10_BOVIN
595	180	13.9	909	2	Q9XTS9	Q9xts9 caenorhabdi	668	168.5	13.0	1013	2	Q623B1
596	179.5	13.8	272	2	Q9SLI9	Q9sl19 mus musculus	669	168	13.0	3616	2	Q7PPF9
597	179.5	13.8	290	2	Q9DAU5	Q9daus mus musculus	670	168	13.0	452	1	FA9_CANFA
598	179.5	13.8	385	1	DLK_MOUSE	Q90163 mus musculus	671	168	13.0	458	1	PRTC_RABIT
599	179.5	13.8	385	2	Q925U3	Q925u3 mus musculus	672	168	13.0	1666	2	Q8MXG2
600	179.5	13.8	488	1	FA10_HUMAN	Q90742 homo sapien	673	167.5	12.9	1949	2	Q8MXG3
601	179	13.8	360	2	Q9AWB4	Q9awb4 physcomitre	674	167	12.9	616	2	Q20852
602	179	13.8	407	1	FAT7_BOVIN	P22457 bos taurus	675	167	12.9	433	2	Q90YK1
603	179	13.8	456	1	PRTC_BOVIN	P00745 bos taurus	676	167	12.9	459	1	FA9_MOUSE
604	179	13.8	642	2	Q86Z23	Q86z23 canis famil	677	167	12.9	460	1	PRTC_MOUSE
605	178.5	13.8	513	2	Q90YA5	Q90ya5 anguilla ja	678	167	12.9	623	2	P93026
606	178.5	13.8	847	2	Q90W12	Q90w12 oncorhynch	679	167	12.9	623	2	P94037
607	178	13.7	420	2	Q91XD7	Q91xd7 mus musculus	680	166.5	12.8	623	2	Q94AC0
608	178	13.7	446	1	FAT7_RAT	Q8kx36 rattus norv	681	166.5	12.8	267	2	Q8BXY5
609	178	13.7	844	2	Q7ZTG7	Q7ztg7 orochromis	682	166.5	12.8	476	2	Q6G1L7
610	178	13.7	1081	2	Q8T4N8	Q8t4n8 penaeus sem	683	166.5	12.8	1007	2	Q6J128
611	178	13.7	1650	2	Q9QV76	Q9qvt6 rattus sp.	684	166.5	12.8	1019	2	O57382
612	178	13.7	4569	2	Q7EPV66	Q7epv66 anopheles g	685	166	12.8	4587	2	Q9QX43
613	177.5	13.7	373	2	Q90YA4	Q90ya4 conger myri	686	166	12.8	305	2	Q9N028
614	177.5	13.7	376	1	FA10_HOPST	P83370 hoplocephal	687	166	12.8	356	2	Q19267
615	177.5	13.7	446	1	FAT7_MOUSE	P70375 mus musculus	688	166	12.8	356	2	Q73A1
										626	2	Q7XHX6

689	166	12.8	1278	2	Q7Q440	Q7q440 anopheles g	762	158.5	12.2	838	2	Q27422	Q27422 caenorhabdi
690	165.5	12.8	462	2	Q6PAG2	Q6pag2 xenopus lae	763	158.5	12.2	890	2	Q7Q41	Q7q41 anopheles g
691	165.5	12.8	504	2	Q6PGW7	Q6pgw7 brachydanio	764	158.5	12.2	925	2	Q9UB95	Q9ub95 caenorhabdi
692	165	12.7	434	2	Q7T3B6	Q7t3b6 brachydanio	765	158.5	12.2	942	2	Q7QYW9	Q7qyw9 giardia lam
693	165	12.7	466	1	FA7_HUMAN	P08709 homo sapien	766	158.5	12.2	951	2	Q20176	Q20176 caenorhabdi
694	165	12.7	624	2	O48662	O48662 cucurbita c	767	158.5	12.2	961	2	Q86TG2	Q86tg2 homo sapien
695	165	12.7	679	2	Q6PQ8	Q6ppq8 homo sapien	768	158.5	12.2	1147	2	O6DIB5	O6dib5 mus musculu
696	165	12.7	1051	2	Q8TA75	O8ta75 caenorhabdi	769	158.5	12.2	3712	1	LMA_DROME	Q00174 drosophila
697	165	12.7	1090	2	Q95QP6	Q95qp6 caenorhabdi	770	158.5	12.2	3712	2	Q9VFW0	Q9vrw0 drosophila
698	164.5	12.7	537	2	Q804W8	Q804w8 fugu rubrip	771	158	12.2	138	2	Q28994	Q28994 sus scrofa
699	164.5	12.7	591	2	Q6LBN5	Q6lbn5 homo sapien	772	158	12.2	252	2	Q9NTF1	Q9ntf1 homo sapien
700	164.5	12.7	949	1	TSP4_BRARE	Q81gw0 brachydanio	773	158	12.2	692	2	Q6PDN4	Q6pdn4 mus musculu
701	164.5	12.7	1022	1	TLD_BRARE	O57460 brachydanio	774	158	12.2	1045	2	Q8T3A6	Q8t3a6 caenorhabdi
702	164	12.6	338	2	Q7QGV2	Q7qgv2 anopheles g	775	158	12.2	1070	2	Q8T3A7	Q8t3a7 caenorhabdi
703	164	12.6	433	2	Q8JHD0	Q8jhd0 brachydanio	776	158	12.2	1111	2	Q9XWD6	Q9xwd6 caenorhabdi
704	164	12.6	461	1	PRTC_HUMAN	P04070 homo sapien	777	158	12.2	1235	2	Q65YF9	Q65yf9 ciona intes
705	164	12.6	582	2	Q7QPM3	Q7qpm3 giardia lam	778	158	12.2	1501	2	Q75JAS	Q75jas dictyostell
706	163.5	12.6	626	2	Q8ND91	Q8nd91 homo sapien	779	158	12.2	1615	2	Q7QZU9	Q7qzu9 giardia lam
707	163.5	12.6	726	2	Q7SY09	Q7sy09 brachydanio	780	157.5	12.1	406	2	Q6UXH8	Q6uxh8 homo sapien
708	163.5	12.6	969	2	Q96KG6	Q96kg6 homo sapien	781	157.5	12.1	418	2	Q8TF19	Q8tf19 homo sapien
709	163.5	12.6	1827	2	Q20535	Q20535 caenorhabdi	782	157.5	12.1	1810	2	Q90824	Q90824 gallus gall
710	163	12.6	461	2	Q68FY8	Q68fy8 rattus norv	783	157	12.1	768	1	LEM3_MOUSE	Q01102 mus musculu
711	163	12.6	574	2	Q86R18	Q86r18 ilyanassa o	784	157	12.1	841	2	Q6R8U4	Q6r8u4 brachydanio
712	163	12.6	628	2	O80979	O80979 arabidopsis	785	157	12.1	935	2	Q6R8J3	Q6r8j3 brachydanio
713	163	12.6	630	2	P93027	P93027 arabidopsis	786	157	12.1	977	2	Q6R8J2	Q6r8j2 brachydanio
714	163	12.6	820	2	Q96NT6	Q96nt6 homo sapien	787	157	12.1	1004	2	Q8CGA7	Q8cga7 mus musculu
715	163	12.6	1170	1	TSP1_MOUSE	P35441 mus musculu	788	157	12.1	1170	1	TSP1_HUMAN	P07996 homo sapien
716	163	12.6	1171	2	Q80YQ1	Q80yq1 mus musculu	789	157	12.1	1584	2	Q93791	Q93791 caenorhabdi
717	163	12.6	1171	2	Q8CGB2	Q8cgb2 mus musculu	790	156.5	12.1	155	2	Q6YIL9	Q6yil9 drosophila
718	163	12.6	1731	2	Q8WY30	Q8wy30 homo sapien	791	156.5	12.1	155	2	Q7YSR5	Q7ysr5 drosophila
719	162.5	12.5	424	2	Q7Q3P0	Q7q3p0 anopheles g	792	156.5	12.1	155	2	Q7ZIJ0	Q7zlj0 drosophila
720	162.5	12.5	1013	2	O43897	O43897 homo sapien	793	156.5	12.1	567	2	Q8WUL3	Q8wul3 homo sapien
721	162.5	12.5	1013	2	Q9NQS4	Q9nqs4 homo sapien	794	156.5	12.1	909	2	Q7JP81	Q7jpb1 caenorhabdi
722	162	12.5	628	2	O80977	O80977 arabidopsis	795	156.5	12.1	911	2	Q7JP80	Q7jpb0 caenorhabdi
723	162	12.5	832	2	Q80YX0	Q80yx0 mus musculu	796	156.5	12.1	1140	2	Q96KG7	Q96kg7 homo sapien
724	162	12.5	1008	2	Q7DER7	Q7der7 gallus gall	797	156.5	12.1	1140	2	Q68DE5	Q68de5 homo sapien
725	162	12.5	1170	2	O71SA3	O71sa3 rattus norv	798	156.5	12.1	1768	2	Q7QEK9	Q7qek9 anopheles g
726	162	12.5	1532	2	Q90994	Q90994 gallus gall	799	156	12.0	512	2	Q95RQ1	Q95rq1 drosophila
727	162	12.5	1714	2	Q90995	Q90995 gallus gall	800	155.5	12.0	374	2	Q9VFP0	Q9vpf0 drosophila
728	162	12.5	1808	1	TENA_CHICK	P10039 gallus gall	801	155.5	12.0	685	2	Q7QWD9	Q7qwd9 giardia lam
729	162	12.5	2019	2	Q64706	Q64706 mus musculu	802	155.5	12.0	915	2	O02364	O02364 caenorhabdi
730	162	12.5	2019	2	Q80YX2	Q80yx2 mus musculu	803	155.5	12.0	927	2	Q7JKS6	Q7jks6 caenorhabdi
731	162	12.5	2110	2	Q80YX1	Q80yx1 mus musculu	804	155.5	12.0	980	1	TSP4_RAT	P49744 rattus norv
732	161.5	12.5	469	2	Q9GMD9	Q9gmd9 ornithorhyn	805	155.5	12.0	1015	2	Q9Y6L7	Q9y6l7 homo sapien
733	161.5	12.5	752	2	Q93473	Q93473 caenorhabdi	806	155.5	12.0	1078	2	Q9UQ00	Q9uq00 homo sapien
734	161.5	12.5	1097	2	Q8TDW7	Q8tdw7 homo sapien	807	155.5	12.0	3672	1	LML2_CAEEL	Q21313 caenorhabdi
735	161.5	12.5	2811	2	Q7Q434	Q7q434 anopheles g	808	155.5	12.0	3704	2	F91904	P91904 caenorhabdi
736	161.5	12.5	4555	2	Q8R508	Q8r508 rattus norv	809	155.5	12.0	5147	1	FAT_DROME	P33450 drosophila
737	161	12.4	441	2	Q804X2	Q804x2 fugu rubrip	810	155	12.0	337	2	Q8NHD3	Q8nhd3 homo sapien
738	161	12.4	461	1	PRTC_RAT	P31394 rattus norv	811	155	12.0	342	2	Q8NHD5	Q8nhd5 homo sapien
739	161	12.4	1027	2	Q7QK54	Q7qk54 anopheles g	812	155	12.0	466	2	O6SA95	O6sa95 felis silve
740	161	12.4	4699	2	Q9V383	Q9v383 drosophila	813	155	12.0	515	2	Q7QYS0	Q7qys0 giardia lam
741	160.5	12.4	211	2	Q6H8Q4	Q6h8q4 canis fami	814	155	12.0	528	2	Q9ULF8	Q9ulf8 caenorhabdi
742	160.5	12.4	280	2	Q7ZXT0	Q7zxt0 xenopus lae	815	155	12.0	569	2	Q8NHD4	Q8nhd4 homo sapien
743	160.5	12.4	362	2	Q9U483	Q9u483 neospora ca	816	155	12.0	744	2	Q8NHD2	Q8nhd2 homo sapien
744	160.5	12.4	474	2	Q8JTHC8	Q8jthc8 brachydanio	817	155	12.0	830	1	SREC_HUMAN	Q14162 homo sapien
745	160.5	12.4	625	2	Q8L7E3	Q8l7e3 arabidopsis	818	155	12.0	1117	2	Q6E0K3	Q6e0k3 didelphis m
746	160.5	12.4	1464	2	Q23995	Q23995 drosophila	819	155	12.0	1353	2	Q00546	Q00546 gallus gall
747	160.5	12.4	1464	2	Q24132	Q24132 drosophila	820	155	12.0	2517	2	Q7QLI9	Q7qli9 anopheles g
748	160.5	12.4	1464	2	Q9VC47	Q9vc47 drosophila	821	155	12.0	3695	1	LMAS_HUMAN	O15230 homo sapien
749	160	12.3	378	2	Q21756	Q21756 caenorhabdi	822	155	12.0	3695	1	Q8TDF8	Q8tdf8 homo sapien
750	160	12.3	2201	1	TENA_HUMAN	P24821 homo sapien	823	154.5	11.9	220	2	Q63404	Q63404 rattus norv
751	159.5	12.3	220	2	Q8TCT8	Q8tct8 homo sapien	824	154.5	11.9	277	2	Q6QH77	Q6qh77 brachydanio
752	159.5	12.3	400	1	PRTZ_HUMAN	P22891 homo sapien	825	154.5	11.9	618	2	O64758	O64758 arabidopsis
753	159.5	12.3	628	2	Q7Q0C4	Q7q0c4 anopheles g	826	154.5	11.9	747	2	Q8VHF4	Q8vhf4 mus musculu
754	159.5	12.3	961	1	TSP4_HUMAN	P35443 homo sapien	827	154.5	11.9	963	1	TSP4_MOUSE	Q9z12 mus musculu
755	159.5	12.3	1581	2	Q73809	Q73809 fugu rubrip	828	154.5	11.9	1034	2	Q8VHL7	Q8vhl7 mus musculu
756	159	12.3	442	2	Q804X1	Q804x1 fugu rubrip	829	154.5	11.9	1034	2	Q8VIK5	Q8vik5 mus musculu
757	159	12.3	1746	1	TENA_PIG	Q92116 sus scrofa	830	154	11.9	144	2	O12973	O12973 gallus gall
758	158.5	12.2	408	2	Q8BFW1	Q8bfw1 m mus muscu	831	153.5	11.8	488	2	Q8N2M7	Q8n2m7 homo sapien
759	158.5	12.2	408	2	Q8BMT1	Q8bmt1 mus musculu	832	153.5	11.8	540	2	Q8N2M5	Q8n2m5 homo sapien
760	158.5	12.2	600	2	Q8N369	Q8n369 homo sapien	833	153.5	11.8	1089	2	Q8T3A0	Q8t3a0 ciona intes
761	158.5	12.2	838	2	Q18761	Q18761 caenorhabdi	834	153	11.8	416	1	FA9_BOVIN	P00741 bos taurus

835	153	11.8	502	2	017692	017692 caenorhabdi	908	145.5	11.2	360	2	Q7Q114	Q7q114 anopheles g
836	153	11.8	516	2	Q6YID6	Q6yid6 penaeus mon	909	145.5	11.2	2515	2	Q24551	Q24551 drosophila
837	153	11.8	679	2	Q93X09	Q93x09 vigna mungo	910	145.5	11.2	2731	2	Q18366	Q18366 drosophila
838	153	11.8	647	2	Q7LZ69	Q7lZ69 notophthalm	911	145.5	11.2	2731	2	Q61307	Q61307 drosophila
839	153	11.8	925	2	Q44191	Q44191 caenorhabdi	912	145.5	11.2	2731	2	Q3VNU6	Q3vnu6 drosophila
840	153	11.8	925	2	Q9U4E4	Q9u4e4 caenorhabdi	913	145.5	11.2	2972	2	P30891	P30891 caenorhabdi
841	153	11.8	925	2	Q9UB94	Q9ub94 caenorhabdi	914	145	11.2	1036	2	Q97378	Q97378 strongyloce
842	152.5	11.8	624	2	Q91LR3	Q91lr3 triticum ae	915	145	11.2	1136	1	TIE1_BOVIN	TIE1_BOVIN
843	152.5	11.8	647	2	Q8MLX3	Q8mlx3 caenorhabdi	916	144.5	11.1	124	2	Q659B4	Q659B4 homo sapien
844	152.5	11.8	647	2	Q8NM25	Q8nm25 caenorhabdi	917	144.5	11.1	474	2	Q919K4	Q919k4 gallus gall
845	152.5	11.8	647	2	Q8MV49	Q8mv49 caenorhabdi	918	144.5	11.1	637	2	Q655Y8	Q655Y8 oryza sativ
846	152.5	11.8	647	2	Q8MV50	Q8mv50 caenorhabdi	919	144.5	11.1	664	2	Q8WS87	Q8ws87 hyalomma an
847	152.5	11.8	647	2	Q8MV51	Q8mv51 caenorhabdi	920	144.5	11.1	1935	2	Q6QHS3	Q6qhs3 lytechinus
848	152.5	11.8	647	2	Q8MV52	Q8mv52 caenorhabdi	921	144.5	11.1	2643	2	Q01552	Q01552 caenorhabdi
849	152.5	11.8	647	2	Q8MV53	Q8mv53 caenorhabdi	922	143.5	11.1	631	2	Q94HD5	Q94hd5 oryza sativ
850	152.5	11.8	661	2	Q9TVY6	Q9tvY6 caenorhabdi	923	143.5	11.1	643	2	Q8H8K1	Q8h8k1 oryza sativ
851	152.5	11.8	954	2	Q75UQ6	Q75uq6 achaearanaea	924	143.5	11.1	650	1	BM86_BOOMI	P20736 boophilus m
852	152.5	11.8	2009	2	Q9VXM0	Q9vxm0 drosophila	925	143.5	11.1	754	2	Q6DFX1	Q6dfx1 mus musculu
853	152	11.7	594	2	Q6U0Y5	Q6u0y5 homo sapien	926	143.5	11.1	3170	2	Q7PN80	Q7pn80 anopheles g
854	152	11.7	765	2	Q9NL50	Q9nl50 sarcophaga	927	143	11.0	300	2	Q9BIM6	Q9bim6 toxoplasma
855	152	11.7	803	2	Q7QSK8	Q7qsk8 giardia lam	928	143	11.0	474	2	Q68BF1	Q68ef1 mus musculu
856	152	11.7	3718	1	LMA5_MOUSE	Q61001 mus musculu	929	143	11.0	681	2	Q7ZT70	Q7zt70 lampetra ja
857	151.5	11.7	155	2	Q7Z1J1	Q7z1j1 drosophila	930	143	11.0	748	1	AD10_HUMAN	Q14672 homo sapien
858	151.5	11.7	638	2	Q7PM27	Q7pm27 anopheles g	931	142.5	11.0	278	1	EFL7_MOUSE	Q9qxt5 mus musculu
859	151.5	11.7	849	2	Q96SQ3	Q96sq3 homo sapien	932	142.5	11.0	317	2	Q9NGD3	Q9ngd3 drosophila
860	151	11.6	656	1	EFL3_MOUSE	Q8ov70 mus musculu	933	142.5	11.0	317	2	Q9NGD4	Q9ngd4 drosophila
861	151	11.6	835	2	Q69ZY6	Q69zy6 mus musculu	934	142.5	11.0	317	2	Q9NGD5	Q9ngd5 drosophila
862	151	11.6	860	2	Q7QAH1	Q7qah1 anopheles g	935	142.5	11.0	317	2	Q9NGD7	Q9ngd7 drosophila
863	150.5	11.6	866	1	SRC2_HUMAN	Q96gp6 homo sapien	936	142.5	11.0	317	2	Q9NGD9	Q9ngd9 drosophila
864	150	11.6	279	1	EFL7_RAT	Q6az60 rattus norv	937	142.5	11.0	806	1	ITB7_MOUSE	P26011 mus musculu
865	150	11.6	299	2	Q8BX64	Q8bx64 mus musculu	938	142.5	11.0	833	1	SRC2_MOUSE	P59222 mus musculu
866	150	11.6	461	1	FA9_HUMAN	P00740 homo sapien	939	142.5	11.0	979	2	Q9CVB78	Q9cvb78 drosophila
867	150	11.6	461	1	FA9_PANTR	Q95nd7 pan troglod	940	142	10.9	403	2	Q14549	Q14549 homo sapien
868	150	11.6	461	1	Q95ND6	Q95nd6 pan troglod	941	142	10.9	430	2	Q804X0	Q804x0 fugu rubrip
869	150	11.6	574	2	Q7R5J3	Q7r5j3 giardia lam	942	142	10.9	648	2	Q9NKD7	Q9nkd7 drosophila
870	150	11.6	881	2	Q7Q1J5	Q7q1j5 anopheles g	943	142	10.9	648	2	Q9VJU4	Q9vju4 drosophila
871	150	11.6	881	2	Q9W0A0	Q9w0a0 drosophila	944	142	10.9	701	2	Q86BL2	Q86bl2 drosophila
872	150	11.6	1107	1	YLK2_CAEEL	P41950 caenorhabdi	945	142	10.9	2765	1	TSP3_BRARE	Q81jhw2 brachydanio
873	150	11.6	1350	2	Q9V5J7	Q9v5j7 drosophila	946	142	10.9	962	1	Q9R1K2	Q9rlk2 rattus norv
874	150	11.6	1370	2	Q7KQX6	Q7kqx6 drosophila	947	142	10.9	5141	2	Q700K0	Q700k0 rattus norv
875	150	11.6	1451	2	Q7R2Y9	Q7r2y9 giardia lam	948	141.5	10.9	384	2	Q9W630	Q9w630 cyprinus ca
876	149.5	11.5	112	2	Q9H557	Q9h557 homo sapien	949	141.5	10.9	1823	2	Q7PRP5	Q7prp5 anopheles g
877	149.5	11.5	293	1	EFL8_MOUSE	Q6guq1 mus musculu	950	141	10.9	494	2	Q8VDV0	Q8vdv0 mus musculu
878	149	11.5	396	1	PRTZ_BOVIN	P00744 bos taurus	951	141	10.9	494	2	Q8BMS0	Q8bms0 mus musculu
879	149	11.5	592	2	Q7Q799	Q7q799 giardia lam	952	141	10.9	808	2	Q9XXU1	Q9xxul caenorhabdi
880	149	11.5	663	2	Q7X6L7	Q7x6l7 oryza sativ	953	141	10.9	810	2	Q9NL29	Q9nl29 caenorhabdi
881	149	11.5	892	2	Q25243	Q25243 lucilia cup	954	141	10.9	1358	2	Q15568	Q15568 homo sapien
882	149	11.5	956	1	TSP3_HUMAN	P49746 homo sapien	955	141	10.9	1358	2	Q92752	Q92752 homo sapien
883	148.5	11.4	673	2	Q7PPD2	Q7ppd2 anopheles g	956	141	10.9	4998	2	Q8CG65	Q8cg65 mus musculu
884	148.5	11.4	4135	2	O18977	O18977 bos taurus	957	141	10.9	5086	2	Q7Q3K5	Q7q3k5 anopheles g
885	148	11.4	320	2	Q8N780	Q8n780 homo sapien	958	140.5	10.8	569	2	Q9Y0V1	Q9y0v1 boophilus m
886	148	11.4	626	2	Q49438	Q49438 arabidopsis	959	140.5	10.8	640	2	Q09182	Q09182 rattus norv
887	148	11.4	1751	2	Q7PXP5	Q7pxf5 anopheles g	960	140	10.8	40	2	Q8IXC8	Q8ixc8 homo sapien
888	148	11.4	1827	2	Q8UHV6	Q8jnv6 brachydanio	961	140	10.8	40	2	Q86Z10	Q86z10 homo sapien
889	147.5	11.4	259	2	Q9SDR8	Q9sdr8 prunus dulc	962	140	10.8	494	2	Q9S965	Q9s965 homo sapien
890	147.5	11.4	219	2	Q8BMI5	Q8bmi5 mus musculu	963	140	10.8	625	2	Q22925	Q22925 arabidopsis
891	147.5	11.4	1521	2	Q7QYW5	Q7qyw5 giardia lam	964	140	10.8	784	2	Q97702	Q97702 canis fami
892	147	11.3	109	2	Q15972	Q15972 homo sapien	965	140	10.8	784	2	Q9TUN7	Q9tun7 canis fami
893	147	11.3	291	1	EFL8_RAT	Q6mg84 rattus norv	966	139.5	10.8	317	2	Q9NGD6	Q9ngd6 drosophila
894	147	11.3	425	2	Q8Q4X7	Q804x7 gallus gall	967	139.5	10.8	317	2	Q9NGD8	Q9ngd8 drosophila
895	147	11.3	884	2	Q7QT01	Q7qt01 giardia lam	968	139.5	10.8	799	1	ITBN_DROME	Q27591 drosophila
896	147	11.3	956	1	TSP3_MOUSE	Q05895 mus musculu	969	139.5	10.8	1162	2	Q8WTP0	Q8wtp0 halocynthia
897	147	11.3	956	1	TSP3_MOUSE	Q7tn15 mus musculu	970	139.5	10.8	2633	2	Q7OK12	Q7ok12 anopheles g
898	147	11.3	13133	2	Q71A42	Q71a42 caenorhabdi	971	139.5	10.8	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
899	146.5	11.3	448	2	Q9VJU8	Q9vju8 drosophila	972	139	10.7	266	2	Q9R1K1	Q9rlk1 rattus norv
900	146.5	11.3	647	2	Q8MV54	Q8mv54 caenorhabdi	973	139	10.7	544	1	AD10_RAT	Q10743 rattus norv
901	146.5	11.3	1581	1	LMG3_MOUSE	Q9x0b6 mus musculu	974	139	10.7	852	2	Q75S85	Q75s85 halocynthia
902	146	11.3	220	2	Q8MVP0	Q8mvp0 boltenia vi	975	139	10.7	1125	1	TIE2_BOVIN	Q66807 bos taurus
903	146	11.3	421	2	Q9NKE1	Q9nke1 drosophila	976	138.5	10.7	744	2	Q7Q7D9	Q7q7d9 anopheles g
904	146	11.3	766	2	Q7XVH9	Q7xvh9 oryza sativ	977	138.5	10.7	837	2	Q75S84	Q75s84 halocynthia
905	146	11.3	1356	2	Q05546	Q05546 rattus norv	978	138.5	10.7	1639	1	LMG1_DROME	P15215 drosophila
906	146	11.3	1358	2	Q8BY19	Q8by19 mus musculu	979	138.5	10.7	2212	2	Q7Q112	Q7q112 anopheles g
907	145.5	11.2	293	1	EFL8_HUMAN	Q99944 homo sapien	980	138.5	10.7	2764	2	Q9WTS5	Q9wts5 mus musculu

981 138.5 10.7 3005 2 Q6BFG4
 982 138 10.6 211 2 Q6TPK5
 983 138 10.6 400 2 Q5QP8
 984 138 10.6 504 2 Q7QMR4
 985 138 10.6 721 2 Q818V6
 986 138 10.6 1299 2 Q7R4A6
 987 138 10.6 2427 2 Q8MQ36
 988 138 10.6 2705 2 Q9W6V6
 989 138 10.6 4006 2 Q35452
 990 138 10.6 4114 2 Q34796
 991 138 10.6 4288 2 Q3NPX9
 992 138 10.6 4289 1 TENX_HUMAN
 993 137.5 10.6 639 1 BMPH_STRPU
 994 137.5 10.6 891 1 Q6NNG1
 995 137.5 10.6 955 1 TSP4_XENLA
 996 137.5 10.6 1039 2 Q9VQB1
 997 137.5 10.6 1050 2 Q71G60
 998 137.5 10.6 2330 1 EFL4_MOUSE
 999 137 10.6 337 2 Q9R1K0
 1000 137 10.6 798 1 ITB5_MOUSE

ALIGNMENTS

RESULT 1

ID GAS6_HUMAN STANDARD; PRT; 721 AA.
 AC Q14393; Q7Z7N3;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth-arrest-specific protein 6 precursor (GAS-6).
 GN Name=GAS6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=93330291; PubMed=8336730;
 RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
 RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
 RT member of the vitamin K-dependent proteins related to protein S, a
 RT negative coregulator in the blood coagulation cascade.";
 RL Mol. Cell. Biol. 13:4976-4985(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Munoz X., Sunoy L., de Frutos P., Sala N.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Uterus;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiroaka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togawa S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shionhara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Takakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Kitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RN Nat. Genet. 36:40-45(2004).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal lung, and fetal spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler N.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo A.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-85 FROM N.A.
 RA Marée A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP RECEPTOR INTERACTION.
 RX PubMed=7854420; DOI=10.1038/373623a0;
 RA Varnum B.C., Young C., Elliott G., Garcia A., Bartley T.D.,
 RA Fridell Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,
 RA Yanagihara D., Bennett L., Sylber M., Merewether L.A., Tseng A.,
 RA Escobar E., Liu E.T., Yamane H.K.;
 RT "Axl receptor tyrosine kinase stimulated by the vitamin K-dependent
 RT protein encoded by growth-arrest-specific gene 6.";
 RL Nature 373:623-626(1995).
 RN [7]
 RP RECEPTOR INTERACTION.
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;
 RA Stitt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,
 RA Mattson K., Fisher J., Gies D.R., Jones P.F., Masiakowski P.,
 RA Ryan T.E., Tobkes N.J., Chen D.H., DiStefano P.S., Long G.L.,
 RA Basilico C., Goldfarb M.P., Lemke G., Glass D.J., Yancopoulos G.D.;
 RT "The anticoagulation factor protein S and its relative, Gas6, are
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";
 RL Cell 80:661-670(1995).
 RN [8]
 RP ALTERNATIVE SPLICING (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;
 RA Marcandalli P., Gostissa M., Varnum B., Goruppi S., Schneider C.;
 RT "Identification and tissue expression of a splice variant for the
 RT growth arrest-specific gene gas6.";
 RL FEBS Lett. 415:56-58(1997).
 RN [9]
 RP RECEPTOR INTERACTION.
 RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
 RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
 RA Mizuno K.;

RT Identification of the product of growth arrest-specific gene 6 as a
RT common ligand for Axl, Sky, and Mer receptor tyrosine kinases.,"
RL J. Biol. Chem. 271:30022-30027(1996).
[10]
RN RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND PROCESSING.
RX PubMed=9326369; DOI=10.1016/S0014-5793(97)01093-4; AND
RA Goruppi S., Yamane H., Marchandalli P., Garcia A., Clogston C.,
RA Gostissa M., Varnum B., Schneider C.;
RT "The product of a gas6 splice variant allows the release of the domain
RT responsible for Axl tyrosine kinase receptor activation.,"
RL FEBS Lett. 415:59-63(1997).
[11]
RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 261-721 (ISOFORM 2), AND
RP MUTAGENESIS OF PHE-530; LEU-663 AND TYR-703.
RX PubMed=8621659; DOI=10.1074/jbc.271.16.9785;
RA Mark M.R., Chen J., Hammonds R.G., Sadick M., Godowski P.J.;
RT "Characterization of Gas6, a member of the superfamily of G domain-
RT containing proteins, as a ligand for Rse and Axl.,"
RL J. Biol. Chem. 271:9785-9789(1996).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
CC and MER whose signaling is implicated in cell growth and survival,
CC cell adhesion and cell migration. Plays a role in thrombosis by
CC amplifying platelet aggregation and secretion in response to known
CC agonists (by similarity).
CC -!- SUBUNIT: Monomer (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Name=1; Synonyms=gag6SV;
CC IsoId=Q14393-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q14393-2; Sequence=VSP_010494;
CC Name=3;
CC IsoId=Q14393-3; Sequence=VSP_010492, VSP_010493, VSP_010494;
CC Note-No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Plasma. Isoform 1 and isoform 2 are widely
CC expressed. Isoform 1 is the predominant form in spleen.
CC -!- PTM: Isoform 1 is proteolytically processed after secretion to
CC yield a N-terminal 36 kDa protein and a C-terminal 50 kDa protein
CC including the laminin G-like domains which activates AXL.
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
CC dependent carboxylation. These residues are essential for the
CC binding of calcium (by similarity).
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L13720; AAA58494.1; -
DR EMBL; AY256843; AAO84057.1; -
DR EMBL; AY256830; AAO84057.1; JOINED.
DR EMBL; AY256831; AAO84057.1; JOINED.
DR EMBL; AY256832; AAO84057.1; JOINED.
DR EMBL; AY256833; AAO84057.1; JOINED.
DR EMBL; AY256834; AAO84057.1; JOINED.
DR EMBL; AY256835; AAO84057.1; JOINED.
DR EMBL; AY256836; AAO84057.1; JOINED.
DR EMBL; AY256837; AAO84057.1; JOINED.
DR EMBL; AY256838; AAO84057.1; JOINED.
DR EMBL; AY256839; AAO84057.1; JOINED.
DR EMBL; AY256840; AAO84057.1; JOINED.
DR EMBL; AY256841; AAO84057.1; JOINED.
DR EMBL; AY256842; AAO84057.1; JOINED.
DR EMBL; AK125533; BAC6580.1; -
DR EMBL; BC038984; AAH38984.1; -

DR EMBL; AY170372; AAO41859.1; -
DR PIR; B48089; B48089.
DR PDB; 1H30; X-ray; A=257-678.
DR Genew; HGNC:4168; GAS6.
DR MIM; 600441; -
DR GO; GO:0005102; P:receptor binding; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.

Query Match 97.6%; Score 1265.5; DB 1; Length 721;
Best Local Similarity 84.1%; Pred. No. 2.6e-96;
Matches 227; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 PRYLDICNKYSPTKNSGPAFCVQNLDPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 60
DB 90 PRYLDICNKYSPTKNSGPAFCVQNLDPDQCTPNPCDRKGTQACQDLNMGFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSSGFSLSGDRGTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGGCLQICHNKPFSFHCSSGFSLSGDRGTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYCLCDEGFPAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGLK 180
DB 210 ARCKNLPGSYCLCDEGFPAYSSQEKACRDVDECLQRCCEQVCVNSPGSYTCHCDGRGLK 269

QY 181 LSQMDMTCE-----DILPCVPFF 197
DB 270 LSQMDMTCELEAGWPCPRRRRDSGPAARPGAGQSRSEGHIPDRRGRPRWQDILPCVPFF 329

QY 198 SVAKSVKSLYLGRMFSGTPTVIRLRFKRLQ 227
DB 330 SVAKSVKSLYLGRMFSGTPTVIRLRFKRLQ 359

RESULT 2
GAS6_RAT STANDARD; PRT; 674 AA.
AC Q63772;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-arrest-specific protein 6 precursor (GAS-6) (Growth-
DE potentiating factor) (GFP).
GN Name=GAS6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95197586; PubMed=7890695; DOI=10.1074/jbc.270.11.5702;
RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura K., Fujita H.,
RA Ohara O., Arita H.;
RT "Vascular smooth muscle cell-derived, Gla-containing growth-
RT potentiating factor for Ca(2+)-mobilizing growth factors.,"
RL J. Biol. Chem. 270:5702-5705(1995).
RN [2]
RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX PubMed=7559388; DOI=10.1074/jbc.270.39.22681;
RA Ohashi K., Nagata K., Toshima J., Nakano T., Arita H., Teuda H.,
RA Suzuki K., Mizuno K.;
RT "Stimulation of sky receptor tyrosine kinase by the product of growth
RT arrest-specific gene 6.,"
RL J. Biol. Chem. 270:22681-22684(1995).
RN [3]
RP RECEPTOR INTERACTION.
RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
RA Mizuno K.;
RT "Identification of the product of growth arrest-specific gene 6 as a
RT common ligand for Axl, Sky, and Mer receptor tyrosine kinases.,"
RL J. Biol. Chem. 271:30022-30027(1996).
RN [4]

RP GAMMA-CARBOXYGLUTAMIC ACIDS.

RA PubMed-9163328;

RT Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.;

RT "Requirement of gamma-carboxyglutamic acid residues for the biological

RT activity of Gas6; contribution of endogenous Gas6 to the proliferation

RT of vascular smooth muscle cells.";

RL Biochem. J. 323:387-392(1997).

CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3

CC and MER whose signaling is implicated in cell growth and survival,

CC cell adhesion and cell migration. Plays a role in thrombosis by

CC amplifying platelet aggregation and secretion in response to known

CC agonists (By similarity).

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K

CC dependent carboxylation. These residues are essential for the

CC binding of calcium (Probable).

CC -!- SIMILARITY: Contains 4 EGF-like domains.

CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)

CC domain.

CC -!- SIMILARITY: Contains 2 laminin G-like domains.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

DR EMBL; D42148; BAA0719.1; -.

DR PIR; I55476; I55476.

DR HSP; P00740; ICFH.

DR RGD; 61913; Gas6.

DR InterPro; IPR000152; Asx hydroxyl S.

DR InterPro; IPR008985; ConA like_lec_gl.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF-Ca.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002383; GLA blood.

DR InterPro; IPR001791; Laminin G.

DR InterPro; IPR003129; TSP N.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00054; Laminin G; 2.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01186; EGF 2; 3.

DR PROSITE; PS00026; EGF 3; 4.

DR PROSITE; PS01187; EGF CA; 3.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS00998; GLA_2; 1.

DR PROSITE; PS00025; LAM G DOMAIN; 2.

KW Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid;

KW Growth regulation; Repeat; Signal; Vitamin K.

FT SIGNAL 1 27 Potential.

FT CHAIN 28 674 Growth-arrest-specific protein 6.

FT DOMAIN 50 91 Gla.

FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).

FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).

FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).

FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).

FT DOMAIN 295 467 Laminin G-like 1.

FT DOMAIN 474 666 Laminin G-like 2.

FT METAL 326 326 Calcium (By similarity).

FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).

FT	METAL	437	437	Calcium (via carbonyl oxygen) (By similarity).
FT	METAL	652	652	Calcium (By similarity).
FT	DISULFID	117	130	By similarity.
FT	DISULFID	122	139	By similarity.
FT	DISULFID	141	150	By similarity.
FT	DISULFID	157	168	By similarity.
FT	DISULFID	164	177	By similarity.
FT	DISULFID	179	192	By similarity.
FT	DISULFID	198	209	By similarity.
FT	DISULFID	204	218	By similarity.
FT	DISULFID	220	233	By similarity.
FT	DISULFID	239	248	By similarity.
FT	DISULFID	244	257	By similarity.
FT	DISULFID	259	274	By similarity.
FT	DISULFID	280	566	By similarity.
FT	DISULFID	441	467	By similarity.
FT	DISULFID	639	666	By similarity.
FT	CARBOHYD	189	189	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	417	417	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	488	488	N-linked (GlcNAc. . .) (Potential).
SQ	SEQUENCE	674 AA;	74637 MW;	FBF8F6B8664D6F2E CRC64;

Query Match 86.1%; Score 1117; DB 1; Length 674;
 Best Local Similarity 82.8%; Pred. No. 4.5e-84;
 Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

Qy 1 PRYDCINKYGPSYTKNSGFATCVQNLPDQCTNPCKDKGTQACODLMGNFFCLCKAGWG 60
 Db 87 PRYQECMRKGRPEDKNPNFATCVKNLPDQCTNPCKDKGTQACODLMGNFFCLCKDGWG 146

Qy 61 GRLCDKDVNECSQENGGCLQICHNKGSPHCSHSGFELSSDGRTCODIDECADSEACGE 120
 Db 147 GRLCDKDVNECSQENGGCSQVCHNKGSPQACSHGFSLOSDNKSQDIDECTDSDTCGD 206

Qy 121 ARCKNLFGSYSCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
 Db 207 ARCKNLFGSYSCLDCKGYTYSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCNGRGLK 266

Qy 181 LSQDMDCEDILPCVPFSPVAKSVKSLYLGMFSGTTPVIRLRFKRLQ 227
 Db 267 LSPDMDCEDILPCVPFSPVAKSVKSLYLGMFSGTTPVIRLRFKRLQ 313

RESULT 3

Q6IRL1 ID Q6IRL1 PRELIMINARY; PRT; 674 AA.

AC Q6IRL1; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Gas6 protein.

GN Name=Gas6;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

XP [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Lung;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumman J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC070881; AAH70881.1; -;
DR HSSP; P00736; IAPQ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR003129; TSP N.
DR InterPro; IPR000294; Vit_k_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_Ca; 2.
DR Pfam; PF00594; GLA; 1.
DR Pfam; PF02210; Laminin G 2; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_Ca; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_Ca; 3.
DR PROSITE; PS00011; GLA 1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 674 AA; 74671 MW; CC9A5EBD04480AE7 CRC64;

Query Match 86.1%; Score 1117; DB 2; Length 674;
Best Local Similarity 82.8%; Pred. No. 4.5e-84;
Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGGCLQICHNKPGSPHCSCGSEFSSDGRCTQDIDECADSEACGE 120
DB 87 PRYQECMRKYGRPEDKNPNFATCVNKLDPQCTPNFCDRKGTQACQDLNMGNFFCLCKGNG 146
QY 61 GLRLCDKDVNECSQENGGCLQICHNKPGSPHCSCGSEFSSDGRCTQDIDECADSEACGE 120
DB 147 GLRLCDKDVNECSQENGGCLQICHNKPGSPHCSCGSEFSSDGRCTQDIDECADSEACGE 206
QY 121 ARCKNLPGSYSLCDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSLCDGEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTCDIEDILPCVPFFSVAKSVKSLYLGRMPSGTPTVIRLKRLOP 227
DB 267 LSPDMDTCDIEDILPCVPFFSVAKSVKSLYLGRMPSGTPTVIRLKRLOP 313

RESULT 4
GAS6_MOUSE STANDARD; PRT; 674 AA.

AC Q61592; Q99K57;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-arrest-specific protein 6 precursor (GAS-6).
GN Name=GAS6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93330291; PubMed=8336730;
RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
member of the vitamin K-dependent proteins related to protein S, a
negative co-regulator in the blood coagulation cascade.";
RL Mol. Cell. Biol. 13:4976-4985(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumman J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX PubMed=11175853; DOI=10.1038/94667;
RA Angelillo-Scherer A., de Frutos P., Aparicio C., Melis E., Savi P.,
RA Lupu F., Arnout J., Dewerchin M., Hoylaerts M., Herbert J., Collen D.,
RA Dahlback B., Carmeliet P.;
RT "Deficiency or inhibition of Gas6 causes platelet dysfunction and
protects mice against thrombosis.";
RL Nat. Med. 7:215-221(2001).
CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3
and MER whose signaling is implicated in cell growth and survival,
cell adhesion and cell migration (By similarity). Plays a role in
thrombosis by amplifying platelet aggregation and secretion in
response to known agonists.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K
dependent carboxylation. These residues are essential for the
binding of calcium (By similarity).
CC -!- MISCELLANEOUS: GAS6 deficient mice show protection against
thrombosis, but no spontaneous bleeding.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.ebi.ac.uk/ebis/sib.ch/announce/>)

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X59846; CAA42507.1; -.
DR EMBL; BC005444; AAH05444.1; -.
DR PIR; A48089; A48089.
DR HSSP; P00740; 1CFH.
DR MGD; MGI:95660; Gas6.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin_G; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW Calcium-binding; EGF-Like domain; Gamma-carboxyglutamic acid;
KW Growth regulation; Repeat; Signal; Vitamin K.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 674 Growth-arrest-specific protein 6.
FT DOMAIN 50 91 Gla.
FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 295 467 Laminin G-like 1.
FT DOMAIN 474 666 Laminin G-like 2.
FT METAL 326 326 Calcium (via carbonyl oxygen).
FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).
FT METAL 437 437 Calcium (via carbonyl oxygen) (By similarity).
FT METAL 652 652 Calcium (By similarity).
FT DISULFID 117 130 Calcium (By similarity).
FT DISULFID 122 139 By similarity.
FT DISULFID 141 150 By similarity.
FT DISULFID 157 168 By similarity.
FT DISULFID 164 177 By similarity.
FT DISULFID 179 192 By similarity.
FT DISULFID 198 209 By similarity.
FT DISULFID 204 218 By similarity.
FT DISULFID 220 233 By similarity.
FT DISULFID 239 248 By similarity.
FT DISULFID 244 257 By similarity.
FT DISULFID 259 274 By similarity.
FT DISULFID 280 566 By similarity.
FT DISULFID 441 467 By similarity.
FT DISULFID 639 666 By similarity.
FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).
FT CONFLICT 530 530 Missing (in Ref. 1).
SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;
Query Match 85.8%; Score 1113; DB 1; Length 674;
Best Local Similarity 82.8%; Pred. No. 9.6e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;
QY 1 PRYLDCKNGSPYTKNGSFATCVQNLDPQCTPNPCDKGTHICQDLMGNFCTDGGW 60
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Db 87 PRYQECRKYGRPEKNPDPFAKCVQNLDPQCTPNPCDKGTHICQDLMGNFCTDGGW 146
Qy 61 GRLCDKDVNCSQNGCLOICHNKGPSFCHSGFSLSSDGRTCODIDECADSEACGE 120
Db 147 GRLCDKDVNCSQNGCLOICHNKGPSFCHSGFSLSSDGRTCODIDECADSEACGE 206
Qy 121 ARCKNLPGSYSCLCDEGFAYSSOFKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSCLCDEGTYTSSKEKTCQDVDEQCDRCETCVNSPGSYTCHCDGRGLK 266
Qy 181 LSQDMDTCEDILPCVPFSAKSVKSLYLGRMFGTGPVIRLRFKRLQ 227
Db 267 LSPDMDTCEDILPCVPFSAKSVKSLYLGRMFGTGPVIRLRFKRLQ 313

RESULT 5
Q6PAE0
ID Q6PAE0 PRELIMINARY; PRT; 668 AA.
AC Q6PAE0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68463 protein.
GN Name=MGC68463;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Klein S., Strausberg R.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC060355; AAH0355.1; -.
DR HSSP; P00743; IAP0.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
```



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Db 85 PKYIECNRRY-RHLNKDSLTTIHHNI PDQSSAPCYREGSLHCTDLHGDFFFCHCKPGWT 143
Qy 61 GRLCDKDVNECSQENGGLQICHNPKGSPFCHSGFELSSDGRCTQDIDECADS-EACG 119
Db 144 GKTCSDRINECATENGNSHCINKPGTHQCLCRSGYRLHTNNKLCIDIDECAPSPNFCG 203
Qy 120 EARKCNKLPGSYCLDEGFAYSSQKACRDVDECLQRCQVNVNPGSYTCHCDGRGGL 179
Db 204 TAQCKNVLSTVYCLCEGGRYDETSKQDIDECCKEGRCEQTQVNSPGSYTCHCDGRGGV 263
Qy 180 KLSQMDMTCEDILPCVPFVSAKSVKSLYLGRMFSGTPIVIRLFRKLP 227
Db 264 KLSQNMNTCEDILPCLPASEKRSNLSYLGRMFSGTPIVIRLFRKQKP 311
RESULT 7
ID Q7T3H4 PRELIMINARY; PRT; 648 AA.
AC Q7T3H4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Growth arrest specific 6.
GN ORFNames=zgc:63860;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio;
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBDJ databases.
DR EMBL; BC053117; AAH53117.1; -.
DR HSSP; Q14393; 1H30.
DR ZFIN; ZDB-GENE-030131-7773; zgc:63860.
DR GO; GO:0005576; Extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR002453; Beta tubulin.
DR InterPro; IPR008985; Cona-like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
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DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF_1.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF02210; Laminin_G_2.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; Lamg; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 648 AA; 72625 MW; E2935F42AF21CF64 CRC64;
Query Match 49.9%; Score 647; DB 2; Length 648;
Best Local Similarity 49.8%; Pred. No. 2.9e-45;
Matches 112; Conservative 31; Mismatches 80; Indels 2; Gaps 2;
Qy 1 PLYLDICINKYSPYTKNSGFATCYQNLPDQCTNPDCRKGTOACQDLMGNFCLCKAGWG 60
Db 79 PKYQACMERFGDSKKQDLITCVHNIPDQCSNPVCYHYGTVRCEDKKGFCHCFTGWS 138
Qy 61 GRLCDKDVNECSQENGGLQICHNPKGSPFCHSGFELSSDGRCTQDIDECADS-EACG 119
Db 139 GATCQNDVDEICSGNGGCEHVCNNTMGSKCSBDGYRLSGH-HSCLDVDCEVTPDVCG 197
Qy 120 EARKCNKLPGSYCLDEGFAYSSQKACRDVDECLQRCQVNVNPGSYTCHCDGRGGL 179
Db 198 SARCSNLIGGLECLCDGFIYDNISRCVVDDECTHVCCEECVNTGSCFCDCGRGLK 257
Qy 180 KLSQMDMTCEDILPCVPFVSAKSVKSLYLGRMFSGTPIVIRLFRK 224
Db 258 RLSSDMSCSEIGLDRLDVRNRSRLYLGRMFSGIPVLRFR 302
RESULT 8
PRTS MACMU
ID PRTS MACMU STANDARD; PRT; 649 AA.
AC Q28520;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor (fragment).
GN Name=PROS1; Synonyms=PROS;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95134217; PubMed=7832752;
RA Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;
RA "Identification of candidate residues for interaction of protein S
RA with C4b binding protein and activated protein C.";
RL Biochem. J. 305:397-403 (1995).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
CC activated protein C in the degradation of coagulation factors Va
CC and VIIa. It help to prevent coagulation and stimulating
CC fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
```

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CC EMBL; L31380; AAA70376.1; ALT_INIT.
CC HSSP; P00740; 1CFH.
CC InterPro; IPR000152; Asx hydroxyl S.
CC InterPro; IPR0008985; ConA_like_lec_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001791; Laminin G.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00594; Gla; 1.
CC Pfam; PF00054; Laminin G; 1.
CC PRINTS; PR00001; GLABLOOD.
CC PROSITE; PS00010; ASX HYDROXYL; 4.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS00026; EGF_3; 4.
CC PROSITE; PS01187; EGF_Ca; 3.
CC PROSITE; PS00011; GLA_1; 1.
CC PROSITE; PS00998; GLA_2; 1.
CC PROSITE; PS00025; LAM_G_DOMAIN; 2.
CC Blood coagulation; Calcium; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Vitamin K; Zymogen.
FT NON_TER 1
FT PROPEP <1 14
FT CHAIN 15 649
FT DOMAIN 15 60
FT DOMAIN 61 89
FT DOMAIN 90 128
FT DOMAIN 130 173
FT DOMAIN 174 215
FT DOMAIN 216 236
FT DOMAIN 272 448
FT DOMAIN 457 639
FT MOD_RES 20 20
FT MOD_RES 21 21
FT MOD_RES 28 28
FT MOD_RES 30 30
FT MOD_RES 33 33
FT MOD_RES 34 34
FT MOD_RES 39 39
FT MOD_RES 40 40
FT MOD_RES 43 43
FT MOD_RES 46 46
FT MOD_RES 50 50
FT MOD_RES 109 109
FT DISULFID 94 107
FT DISULFID 99 116
FT DISULFID 118 127
FT DISULFID 134 148
FT DISULFID 144 157
FT DISULFID 159 172
FT DISULFID 178 190
FT DISULFID 185 199
FT DISULFID 201 214
FT DISULFID 220 229
FT DISULFID 225 238
FT DISULFID 240 255
FT CARBOHYD 472 482
FT CARBOHYD 482 492
FT CARBOHYD 503 503
SEQUENCE 649 AA; 72402 MW; 5C7C13D31CD7B6B CRC64;

Query Match 47.0%; Score 609.5; DB 1; Length 649;
Best Local Similarity 44.0%; Pred. No. 3.7e-42;
Matches 106; Conservative 39; Mismatches 71; Indels 25; Gaps 5;
QY 1 PRYLDICINKYSPYTKNSGFAT-----CYQNLDPDOCTPNPCDRKKGTOACOD 46
DB 56 PKYLVLCLRSF-----QSGLFTAAQSTDAYPDLSRCVNAIPDQCSPLPNCNEDGYMSCKD 109
QY 47 LMGNFFCLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPQSFHSCSHGFBLSDDG 103
DB 110 GKASFTCTCKPQWQGCERCEFDINECKDPNSINGGCSQICDNTPGSYHCSCKSGFVWLSNK 169
QY 104 RTCQDIDSCA-DSEACGEARKNUPGSYSCLCDEGFAYSSOEKACRDVDECLQGRCEQVC 162
DB 170 KDKDQVDECSLKNPMCGTAVCKNIPGDFECPEGYRNLKSKSCDVEDCESENCAQLC 229
QY 163 VNSPGSYTCHCDGRGGLKLSODMDTCEDILPCVPFSVAKSVKSLVLRMFSTPTVLRRF 222
DB 230 VNYPGGYTCYCDGRKGFKLAQDQKSCSAVSVCLPLNLDTKYELLYLABQFAGV-VLYLRF 288
QY 223 K 223
DB 289 R 289
RESULT 9
Q7Z715
ID Q7Z715 PRELIMINARY; PRT; 497 AA.
AC Q7Z715
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Protein S (Alpha) (Fragment).
GN Name=PROS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearn M.O., Kulandane S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY308744; AAP45054.1; -.
DR HSSP; P00740; 1CFH.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_Ca; 2.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin_G_1; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_Ca; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
KW EGF-like domain.
FT NON_TER 497 497
SEQUENCE 497 AA; 55563 MW; B05828AC43C59903 CRC64;

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Query Match          46.4%; Score 601.5; DB 2; Length 497;
Best Local Similarity 43.4%; Pred. No. 1.3e-41;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTCACQDLGMGNFF 52
DB 83 PKYLVLRLSFQTGLFTAAARQSTNAYPDLRLSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGRICDKDVNEC-----SQENGCLQICHNKPSPFCSCSHSGFELSSDGRCTCQDI 109
DB 143 CTCKPGWQGEKCFEINECKDPFNSINGCSQICDNTPGSYHCXKNGFVNLNSKKDCKDV 202
QY 110 DECA-DSEACGEARCKNLPGSVSLCDGFGAYSSOEKACRDVDECLQRCQVQCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDFECPGGRYNYLKSKEIIDECSNMCAQLCVNYPGG 262
QY 169 YTHCDGRGLKLSQMDTCEIDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFK 223
DB 263 YTCYCDGKPKLAQDKSCVSVCLPLNDLTKYELLYLAEQFAGV-VLYLKER 316

RESULT 10
PRTS HUMAN
ID PRTS HUMAN STANDARD; PRT; 676 AA.
AC P07225; O15518;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN Name=PROS1; Synonyms=PROS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87092407; PubMed=3467362;
RA Hoskins J., Norman D.K., Beckmann R.J., Long G.L.;
RT "Cloning and characterization of human liver cDNA encoding a protein S
RT precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:349-353(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88005138; PubMed=2820795; DOI=10.1016/0014-5793(87)80217-X;
RA Ploos van Amstel H.K., van der Zanden A.L., Reitsma P.H.,
RA Bertina R.M.;
RT "Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus
RT sequences for the post-translational processing.";
RL FEBS Lett. 222:186-190(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91084444; PubMed=2148110;
RA Schmidt D.K., Tatro A.V., Phelps L.G., Tomczak J.A., Long G.L.;
RT "Organization of the human protein S genes.";
RL Biochemistry 29:7845-7852(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91084445; PubMed=2148111;
RA Ploos van Amstel H.K., Reitsma P.H., der Logt C.P., Bertina R.M.;
RT "Intron-exon organization of the active human protein S gene PS alpha
RT and its pseudogene PS beta: duplication and silencing during primate
RT evolution.";
RL Biochemistry 29:7853-7861(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Stapleton M., Soares M.B., Bonaudo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting J., Helton E., Kettaman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
Fahy M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E.,
Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 27-676 FROM N.A.
RX MEDLINE=86313649; PubMed=2944113;
RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,
RA Stenflo J., Wydro R.;
RT "Isolation and sequence of the cDNA for human protein S, a regulator
RT of blood coagulation.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).
RN [7]
RP VARIANT HEERLEN PRO-501.
RX MEDLINE=90335440; PubMed=2143091;
RA Bertina R.M., Ploos van Amstel H.K., van Wijngaarden A., Coenen J.,
RA Leemhuis M.P., Deutz-Terlouw P.P., van der Linden I.K., Reitsma P.H.;
RT "Heerlen polymorphism of protein S, an immunologic polymorphism due to
RT dimorphism of residue 460.";
RL Blood 76:538-548(1990).
RN [8]
RP VARIANT PROS1 DEFICIENCY SER-258.
RX Cooper D.N.;
RL Unpublished observations (SEP-1993).
RN [9]
RP VARIANT PROS1 DEFICIENCY TOKUSHIMA GLU-196.
RX MEDLINE=94129009; PubMed=8298131;
RA Hayashi T., Nishioka J., Shigeakiyo T., Saito S., Suzuki K.;
RT "Protein S Tokushima: abnormal molecule with a substitution of Glu for
RT Lys-155 in the second epidermal growth factor-like domain of protein
RT S.";
RL Blood 83:683-690(1994).
RN [10]
RP VARIANTS PROS1 DEFICIENCY CYS-482; CYS-485 AND GLY-561, AND VARIANTS
RP PRO-501 AND MET-559.
RX MEDLINE=99374922; PubMed=10447256;
RX DOI=10.1002/(SICI)1098-1004(1999)14:1<30::AID-HUMU4>3.3.CO;2-O;
RA Espinosa-Parilla Y., Morell M., Souto J.C., Tirado I.,
RA Fontcuberta J., Estivill X., Sala N.;
RT "Protein S gene analysis reveals the presence of a cosegregating
RT mutation in most pedigrees with type I but not type III PS
RT deficiency.";
RL Hum. Mutat. 14:30-39(1999).
CC CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
CC activated protein C in the degradation of coagulation factors Va
CC and VIIIa. It helps to prevent coagulation and stimulating
CC fibrinolysis.
CC CC -!- SUBCELLULAR LOCATION: Secreted.
CC CC -!- TISSUE SPECIFICITY: Plasma.
CC CC -!- DISEASE: Defects in PROS1 are the cause of protein S deficiency
CC (PROS1 deficiency) [MIM:176880]. It is associated with an
CC increased risk to develop thrombotic disease (thrombophilia).
CC CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
CC domain.
CC CC -!- SIMILARITY: Contains 2 laminin G-like domains.
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DR EMBL; M13044; AAA30757.1; -.
DR EMBL; X12891; CAA31382.1; -.
DR PIR; A24759; KXBOS.
DR HSP; P00740; LCPH.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000985; ConA like lec_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin G; 1.
DR PRINTS; PR00001; GLABLOOD.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF 1; 1.
DR PROSITE; PS01186; EGF 2; 3.
DR PROSITE; PS00026; EGF 3; 3.
DR PROSITE; PS01187; EGF-Ca; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS00998; GLA_2; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
KW Blood coagulation; Calcium; Direct protein sequencing;
KW EGF-like domain; Gamma-carboxyglutamic acid; Glycoprotein;
KW Hydroxylation; Plasma; Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24
FT PROPEP 25 41
FT CHAIN 42 675
FT DOMAIN 42 87
FT DOMAIN 88 116
FT DOMAIN 117 155
FT DOMAIN 157 200
FT DOMAIN 201 242
FT DOMAIN 243 283
FT DOMAIN 299 475
FT DOMAIN 484 665
FT SITE 93 94
FT SITE 111 112
FT MOD_RES 47 47
FT MOD_RES 48 48
FT MOD_RES 55 55
FT MOD_RES 57 57
FT MOD_RES 60 60
FT MOD_RES 61 61
FT MOD_RES 66 66
FT MOD_RES 67 67
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 77 77
FT MOD_RES 136 136
FT MOD_RES 177 177
FT MOD_RES 219 219
FT MOD_RES 258 258
FT DISULFID 58 63
FT DISULFID 88 113
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FT DISULFID 205 217
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FT DISULFID 252 265
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FT DISULFID 267 282
FT DISULFID 288 567
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FT DISULFID 638 665
FT CARBOHYD 499 499
FT CARBOHYD 509 509
SQ SEQUENCE 675 AA; 75132 MW; CF7EC5BC1C318DEE CRC64;

Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best local Similarity 43.0%; Pred. No. 4.5e-41;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

Qy 1 PRYLDCKINKYGPSYTKNSGFAT-----CVQNLDPQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLGCLGSFRAGLFTFAARLSTNAYPDLRSCVNAISDCNPLPCNEDGFTCKDQATFT 142
Qy 53 CLCKAGWGRLCDKDVNECSQE---NGGCLQIQCHNKPGSFHCSCHSELSGDRTCODI 109
Db 143 CICKSGWQGEKCESDINECKDPVNINGCSQICENTPGSYHSCCKNGFVMSLNKKDKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCOEVCVNSPGS 168
Db 203 DECVLKPSICGTAVCKNIPGDFFCECAEGYKYNPVSCKDDVDECAENLCAQLCVNYPGG 262
Qy 169 YTHCDGRGGLKLSQMDTCTEDILPCVPFVSVAKSLSYLGRMFSFGTPVIRLRFK 223
Db 263 YSCYCDGKGFKAQDKSCSEAVPCLPLDLDDKNYELLYLAEQFVG-VLYLKER 316

RESULT 12
PRTS_MOUSE STANDARD; PRT; 675 AA.
AC Q08761; P43483;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN Name=Prosl; Synonyms=Pros;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94198297; PubMed=8148380; DOI=10.1016/0167-4781(94)90294-1;
RA Chu M.D., Sun J., Bird P.I.;
RT "Cloning and sequencing of a cDNA encoding the murine vitamin K-
dependent protein S.";
RL Biochim. Biophys. Acta 1217:325-328(1994).
[2]
RP SEQUENCE OF 33-675 FROM N.A.
RX MEDLINE=94302659; PubMed=8029814; DOI=10.1016/0049-3848(94)90006-X;
RA Lu D., Schmidel D.K., Long G.L.;
RT "Structure of mouse protein S as determined by PCR amplification and
DNA sequencing of cDNA.";
RL Thromb. Res. Suppl. 74:135-142(1994).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIII. It help to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
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CC -----
CC EMBL; Z25469; CAA80961.1; -.
CC DR EMBL; L27439; AAA40006.1; -.
CC DR PIR; S43504; KXMS.
CC DR HSSP; P00740; 1CFH.
CC DR MGI; MGI:1095733; Prosl.
CC DR InterPro; IPR000152; Asx_hydroxyl_s.
CC DR InterPro; IPR008985; ConA_like_lec_gl.
CC DR InterPro; IPR000742; EGF_2.
CC DR InterPro; IPR001881; EGF_Ca.
CC DR InterPro; IPR006209; EGF_like.
CC DR InterPro; IPR002383; GLA_blood.
CC DR InterPro; IPR009030; Grow_fac_recept.
CC DR InterPro; IPR001791; Laminin_G.
CC DR InterPro; IPR000294; Vitk_dep_GLA.
CC DR Pfam; PF00008; EGF; 3.
CC DR Pfam; PF00594; Gla; 1.
CC DR Pfam; PF00594; Gla; 1.
CC DR Pfam; PF00594; Gla; 1.
CC DR PRINTS; PR00054; Laminin_G; 1.
CC DR PRINTS; PR00001; GLABLOOD.
CC DR PROSITE; PS00010; ASX_HYDROXYL; 4.
CC DR PROSITE; PS00022; EGF_1; 1.
CC DR PROSITE; PS01186; EGF_2; 3.
CC DR PROSITE; PS00026; EGF_3; 4.
CC DR PROSITE; PS01187; EGF_Ca; 3.
CC DR PROSITE; PS00011; GLA_1; 1.
CC DR PROSITE; PS00998; GLA_2; 1.
CC DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
CC DR Blood coagulation; Calcium; EGF-like domain;
CC Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL; 1 24 By similarity.
FT PROPEP; 25 41 By similarity.
FT CHAIN; 42 675 Vitamin K-dependent protein S.
FT DOMAIN; 42 87 Gla.
FT DOMAIN; 88 116 Thrombin-sensitive.
FT DOMAIN; 117 135 EGF-like 1.
FT DOMAIN; 157 200 EGF-like 2, calcium-binding (Potential).
FT DOMAIN; 201 242 EGF-like 3, calcium-binding (Potential).
FT DOMAIN; 243 283 EGF-like 4, calcium-binding (Potential).
FT DOMAIN; 299 475 Laminin G-like 1.
FT DOMAIN; 484 665 Laminin G-like 2.
FT MOD_RES; 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES; 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES; 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES; 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES; 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES; 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES; 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES; 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES; 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES; 73 73 4-carboxyglutamate (By similarity).
FT MOD_RES; 77 77 4-carboxyglutamate (By similarity).
FT MOD_RES; 136 136 3-hydroxyaspartate (By similarity).
FT DISULFID; 121 134 By similarity.
FT DISULFID; 126 143 By similarity.
FT DISULFID; 145 154 By similarity.
FT DISULFID; 161 175 By similarity.
FT DISULFID; 171 184 By similarity.
FT DISULFID; 186 199 By similarity.
FT DISULFID; 205 217 By similarity.
FT DISULFID; 212 226 By similarity.
FT DISULFID; 228 241 By similarity.
FT DISULFID; 247 256 By similarity.
FT DISULFID; 252 265 By similarity.
FT DISULFID; 267 282 By similarity.
FT CARBOHYD; 499 509 N-linked (GlcNAc...) (Potential).
FT CONFLICT; 493 493 F -> L (in Ref. 2).
CC SEQUENCE 675 AA; 74934 MW; 79D51203E85AF31F CRC64;
Query Match 45.6%; Score 591.5; DB 1; Length 675;
Best Local Similarity 44.7%; Pred. No. 1.2e-40;
Matches 105; Conservative 35; Mismatches 82; Indels 13; Gaps 5;
QY 1 PRYLDCKINKY--GSPYTKNSG-----FATCVQNLPDQCTNPDCRKGTOACQDLMGNFF 52
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DB 83 PKYLGLGAFRVGSGFHAARQSANAYPDLRSVCVAISDQCDIPCNEDGYLACQDQAFT 142
QY 53 CLKAGWGRLCDKDVNEC-----SQENGGLQICHNKPGSFHCSHGSELSDDGRTQDI 109
DB :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
DB 143 CFCKPGWQDRQCYDVNECKDFSNVNGGSCQICDNTPGSYHCSCKRGFAMLPNKKDKDL 202
QY 110 DECA--DSEACGEARCKNLPGSYSCLCDEGFAYSQEKACRDVDECLQGRQGVQCVNSPGS 168
DB :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
DB 203 DECALKPSVCGTAVCKNIPGDFECPCPGYRIDPSSSKCKDVDESENMCAQLCVNFGG 262
QY 169 YTHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSYKSLYLGRMFSGTGVIRLRFK 223
DB :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
DB 263 YSCYCDGKKGKFLAQDQKSCGIPVCLSLDLDDKNVELLYLAEQFAGV-VLYLKFR 316
RESULT 13
PRTS_RABIT
ID PRTS_RABIT STANDARD; PRT; 646 AA.
AC P98118;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor (Fragment).
GN Name=PROS1; Synonyms=PROS;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94039141; PubMed=8223642;
RA He X., Dahlback B.;
RT "Molecular cloning, expression and functional characterization of
RL rabbit anticoagulant vitamin-K-dependent protein S.";
Eur. J. Biochem. 217:857-865(1993).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIIIa. It help to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBUNIT: Interacts with C4b-binding protein, a regulator of the
complex system. In rabbit plasma however, protein S appears to be
present only in free form.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
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Db 234 YSCYCDGKGFKAQDKKSCBAVPVCLPLDLDRYQLLYLAEQFVGA-VLYLKF 286

RESULT 14

Q16519 PRELIMINARY; PRT: 650 AA.

ID Q16519

AC Q16519; 01-NOV-1996 (TREMELrel. 01, Created)

DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)

DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)

DE Protein S precursor (Fragment).

GN Name=PROS1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_TaxID=9606;

RP SEQUENCE FROM N.A.

RX MEDLINE=86313649; PubMed=2944113;

RA Lundwall A., Dackowski W., Cohen E., Shaffer M., Mahr A., Dahlback B.,

RA Stenflo J., Wydro R.;

RT "Isolation and sequence of the cDNA for human protein S, a regulator

RT of blood coagulation."

RL Proc. Natl. Acad. Sci. U.S.A. 83:6716-6720(1986).

DR EMBL; M14338; AAA60181.1; -.

DR HSSP; P00740; 1CFH.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR000152; ASx_hydroxyl_S.

DR InterPro; IPR000985; ConA_like_lectin_S.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR001791; Laminin_G.

DR InterPro; IPR003129; TSP N.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF07645; EGF_Ca; 1.

DR Pfam; PF00594; Glia; 1.

DR Pfam; PF00054; Laminin_G_1; 1.

DR Pfam; PF02210; Laminin_G_2; 1.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF_CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 3.

DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

DR PROSITE; PS01186; EGF_2; 3.

DR PROSITE; PS00026; EGF_3; 2.

DR PROSITE; PS01187; EGF_CA; 2.

DR PROSITE; PS00011; GLA_1; 1.

DR PROSITE; PS00025; LAM_G_DOMAIN; 2.

KW EGF-like domain; Signal.

FT NON_TER 1 15 Potential.

FT SIGNAL 16 650 protein S.

FT CHAIN 650 AA; 72462 MW; 9A8C044C503BF474 CRC64;

SQ SEQUENCE

Query Match 45.2%; Score 586.5; DB 1; Length 646;

Best Local Similarity 43.2%; Pred. No. 2.9e-40;

Matches 101; Conservative 39; Mismatches 81; Indels 13; Gaps 5;

QY 1 PRLYDCINKYGSFY---TKNSG-----FATCVQNLPDQCTNPNCDRKGTGTCQDLMGNFF 52

Db 54 PRLYGLGSGFRKLFATARRSANGYPDLRSCVNAIPDQCNPLPCEBGLNCKDQGTFT 113

QY 53 CLCKAGWGRLCDKDVNEC---NGGCLQICHNKPSCFHCSCFELSSDGRTCQDI 109

Db 114 CLCKPQWGEKECEIDINECKDPTNNGGCSQICONTAGSYHCSCSKGFMVLANEKCKDM 173

QY 110 DECA-DSEACGEARKCNLPGSYCLCBGFAYSSOAKACRDVDECLQORCEQVCVNSPGS 168

Db 174 DECSVKPSVCGTAVCKNTPDGFECESGGRYNPTAKSCEDIDECSENWCAQLCVNYPGG 233

QY 169 YTHCDGRGLKLSDMDTCDEILPCVPFSPVAKSVKSLYLGRMFGTPVIRLRF 222

InterPro; IPR000294; VitK_dep_GLA.

Pfam; PF00008; EGF; 3.

Pfam; PF00594; Glia; 1.

Pfam; PF00054; Laminin_G; 1.

PRINTS; PR00001; GLABLOOD.

PROSITE; PS00010; ASX_HYDROXYL; 4.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 3.

PROSITE; PS00026; EGF_3; 3.

PROSITE; PS01187; EGF_CA; 3.

PROSITE; PS00011; GLA_1; 1.

PROSITE; PS00098; GLA_2; 1.

PROSITE; PS00025; LAM_G_DOMAIN; 2.

Blood coagulation; Calcium; EGF-like domain;

KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;

KW Repeat; Vitamin K; Zymogen.

FT NON_TER 1 12

FT PROPEP <1 12

FT CHAIN 13 646

FT DOMAIN 13 58

FT DOMAIN 59 87

FT DOMAIN 88 126

FT DOMAIN 128 171

FT DOMAIN 172 213

FT DOMAIN 214 254

FT DOMAIN 270 446

FT DOMAIN 455 636

FT MOD_RES 18 18

FT MOD_RES 19 19

FT MOD_RES 26 26

FT MOD_RES 28 28

FT MOD_RES 31 31

FT MOD_RES 32 32

FT MOD_RES 37 37

FT MOD_RES 38 38

FT MOD_RES 41 41

FT MOD_RES 44 44

FT MOD_RES 48 48

FT MOD_RES 107 107

FT DISULFID 92 105

FT DISULFID 97 114

FT DISULFID 116 125

FT DISULFID 132 146

FT DISULFID 142 155

FT DISULFID 157 170

FT DISULFID 176 188

FT DISULFID 183 197

FT DISULFID 199 212

FT DISULFID 218 227

FT DISULFID 223 236

FT DISULFID 238 253

FT CARBOHYD 470 470

FT CARBOHYD 480 480

SQ SEQUENCE 646 AA; 71969 MW; 131219C48891B2EC CRC64;

Query Match 45.2%; Score 586.5; DB 1; Length 646;

Best Local Similarity 43.2%; Pred. No. 2.9e-40;

Matches 101; Conservative 39; Mismatches 81; Indels 13; Gaps 5;

QY 1 PRLYDCINKYGSFY---TKNSG-----FATCVQNLPDQCTNPNCDRKGTGTCQDLMGNFF 52

Db 54 PRLYGLGSGFRKLFATARRSANGYPDLRSCVNAIPDQCNPLPCEBGLNCKDQGTFT 113

QY 53 CLCKAGWGRLCDKDVNEC---NGGCLQICHNKPSCFHCSCFELSSDGRTCQDI 109

Db 114 CLCKPQWGEKECEIDINECKDPTNNGGCSQICONTAGSYHCSCSKGFMVLANEKCKDM 173

QY 110 DECA-DSEACGEARKCNLPGSYCLCBGFAYSSOAKACRDVDECLQORCEQVCVNSPGS 168

Db 174 DECSVKPSVCGTAVCKNTPDGFECESGGRYNPTAKSCEDIDECSENWCAQLCVNYPGG 233

QY 169 YTHCDGRGLKLSDMDTCDEILPCVPFSPVAKSVKSLYLGRMFGTPVIRLRF 222

117	CTCKPGWQGEKCFEDINECKDP	PSNINGCCSQICDNTPGSYHC	SKRGFWMLSNKKDKDV	176
Db				
110	DECA-DSSACGEARCKMLPGS	YSLCDEGFAYSQEKACRDVDE	CLQGRCEQVCVNSPGS	168
Qy				
177	DECSLKPSICGTAVCKMLGDF	CECEPEGRYNLKSKSEDI	DECSNCAQLCVNYPGG	236
Db				
169	YTCDCDGGGLKLSQDMTCED	ILPCVPFVSVAKSVKSLYLGR	MFSCTPVIRLRFK	223
Qy				
237	HTYQCDGKKGFKLAODKSC	SEWSVCLPLNLTQYLLYLAE	OFAGV-VLYLKFGR	290
Db				

ID	Q29094	PRELIMINARY;	PRT;	648 AA.
Q29094	Q29094			
AC	Q29094;			
DT	01-NOV-1996 (TrEMBLrel. 01, Created)			
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Protein S (fragment).			
DE	Name=PROS;			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RC	MEDLINE=95134217; PubMed=78272752;			
RA	Greengard J.S., Fernandez J.A., Radtke K.P., Griffin J.H.;			
RT	"Identification of candidate residues for interaction of protein S			
RT	with C4b binding protein and activated protein C.;"			
RL	Biochem. J. 305:397-403(1995).			
EMBL	L31379; AAA70382.1; --			
DR	PIR; S53433; S53433.			
DR	HSP; P00740; ICFP.			
DR	GO; GO:0005576; C:extracellular; IEA.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	InterPro; IPR000152; Asx_hydroxyl_S.			
DR	InterPro; IPR008985; ConA_like_lec_gl.			
DR	InterPro; IPR000742; EGF_2.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF like.			
DR	InterPro; IPR002383; GLA_blood.			
DR	InterPro; IPR001791; Laminin G.			
DR	InterPro; IPR000294; VICK_dep_GLA.			
DR	Pfam; PF00008; EGF; 1.			
DR	Pfam; PF07645; EGF_CA; 3.			
DR	Pfam; PF00594; Gla; 1.			
DR	Pfam; PF00054; Laminin_G_1; 1.			
DR	PRINTS; PR00001; GLABLOOD.			
DR	SMART; SM00179; EGF_CA; 3.			
DR	SMART; SM00069; GLA; 1.			
DR	SMART; SM00282; LamG; 2.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 4.			
DR	PROSITE; PS00022; EGF_1; UNKNOWN_1.			
DR	PROSITE; PS01186; EGF_2; 3.			
DR	PROSITE; PS00026; EGF_3; 2.			
DR	PROSITE; PS01187; EGF_CA; 3.			
DR	PROSITE; PS00011; GLA_1; 1.			
DR	PROSITE; PS00025; LAM_G_DOMAIN; 1.			
KW	EGF-like domain.			
FT	NON TER			
FT	SEQUENCE 648 AA; 71914 MW; 4BDF9ABBI30872136 CRC64;			

Query Match 45.1%; Score 585.5; DB:2; Length 648;
 Best Local Similarity 43.8%; Pred. No. 3.5e-40;
 Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

QY 1 PRLCDINKYKSGPYTKNSGPT-----CQNLDPDQCTPNPCDKGTQACQDLMGNFF 52
 DB 56 PAYLACLGSGFRAGLFTAARLSTNAYPLVRS CVNAIPDQCNPLPNCNEDGFMFTCKDQGMFT 115
 QY 53 CLCKAGWGGRCLDKDVNECSQEN---CGCQLQI CNKPGSFHCSCHSGFELSSDCGRTQDI 109

```
Db 116 CICKSGWEGKELDINECKOPPNPIIGCSQICDNTPGSYHSCSKSGFIMLSNKKDKQDV 175
Qy 110 DECA-DSACGACRKNULPGSYSLCLDGGPAYSSQEKACRDVDECLQRCQVQCVNSPGS 168
Db 176 DECSVKPSICDTAVCNIPGDFECPCPGRYNPTLKSCDVEDCESENMCAQLCVNYPGG 235
Qy 169 YTHCDGRGGLKLSODMDTCDILPCVPFVSVAKSVLGLGRMFSGTPIRLRFK 223
Db 236 YSCYCDGRKGFKLADQKSCAEPVCLPLNDKNLYLLAEQFVG-VLYLKFR 289

RESULT 17
PRTS_RAT
ID_PRTS_RAT STANDARD; PRT; 675 AA.
AC P53813;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitamin K-dependent protein S precursor.
GN Name=Prosl; Synonyms=Prosl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=95332263; PubMed=7608128;
RA Yasuda F., Hayashi T., Tanitame K., Nishioka J., Suzuki K.;
RT "Molecular cloning and functional characterization of rat plasma
protein S.";
RL J. Biochem. 117:374-383(1995).
CC -!- FUNCTION: Anticoagulant plasma protein; it is a cofactor to
activated protein C in the degradation of coagulation factors Va
and VIIa. It help to prevent coagulation and stimulating
fibrinolysis.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla)
domain.
CC -!- SIMILARITY: Contains 2 laminin G-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S87444; AAC60704.1; -.
DR PIR; JC4180; KXRTS.
DR HSP; P00740; 1CFH.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA-like_lect_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR000294; Vtck_dep_GLA.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00054; Laminin G; 1.
DR PRINTS; PR00001; GLABLOD.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF 2; 3.
DR PROSITE; PS00026; EGF 3; 4.
DR PROSITE; PS01187; EGF_Ca; 3.
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DR PROSITE; PS00011; GLA 1; 1.
DR PROSITE; PS00998; GLA 2; 1.
DR PROSITE; PS50025; LAM_G DOMAIN; 1.
KW Blood coagulation; Calcium; EGF-like domain;
KW Gamma-carboxyglutamic acid; Glycoprotein; Hydroxylation; Plasma;
KW Repeat; Signal; Vitamin K; Zymogen.
FT SIGNAL 1 24 By similarity.
FT PROPEP 25 41 By similarity.
FT CHAIN 42 675 Vitamin K-dependent protein S.
FT DOMAIN 42 87 Gla.
FT DOMAIN 88 116 Thrombin-sensitive.
FT DOMAIN 117 155 EGF-like 1.
FT DOMAIN 157 200 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 201 242 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 243 283 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 299 475 Laminin G-like 1.
FT DOMAIN 484 665 Laminin G-like 2.
FT MOD_RES 47 47 4-carboxyglutamate (By similarity).
FT MOD_RES 48 48 4-carboxyglutamate (By similarity).
FT MOD_RES 55 55 4-carboxyglutamate (By similarity).
FT MOD_RES 57 57 4-carboxyglutamate (By similarity).
FT MOD_RES 60 60 4-carboxyglutamate (By similarity).
FT MOD_RES 61 61 4-carboxyglutamate (By similarity).
FT MOD_RES 66 66 4-carboxyglutamate (By similarity).
FT MOD_RES 67 67 4-carboxyglutamate (By similarity).
FT MOD_RES 70 70 4-carboxyglutamate (By similarity).
FT MOD_RES 73 73 4-carboxyglutamate (By similarity).
FT MOD_RES 77 77 4-carboxyglutamate (By similarity).
FT MOD_RES 136 136 3-hydroxyaspartate (By similarity).
FT DISULFID 121 134 By similarity.
FT DISULFID 126 143 By similarity.
FT DISULFID 145 154 By similarity.
FT DISULFID 161 175 By similarity.
FT DISULFID 176 184 By similarity.
FT DISULFID 181 199 By similarity.
FT DISULFID 205 217 By similarity.
FT DISULFID 212 226 By similarity.
FT DISULFID 228 241 By similarity.
FT DISULFID 247 256 By similarity.
FT DISULFID 252 265 By similarity.
FT DISULFID 267 282 By similarity.
FT CARBOHYD 499 499 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 509 509 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 675 AA; 74626 MW; B4338F756B486075 CRC64;

Query Match 45.18; Score 585.5; DB 1; Length 675;
Best Local Similarity 43.08; Pred. No. 3.7e-40;
Matches 101; Conservative 41; Mismatches 80; Indels 13; Gaps 5;

Qy 1 PRYLDCKINKY-----GSPYTKNS--GFATCVQLPQCTPNPCDRKGTQACQDLMGNNF 52
Db 83 PKYLGCLGAFRVGNFSAARQSANAYPDLRCVNAIPQCDMPFCNEDGYLSCKDQGAFT 142
Qy 53 CLCKAGWGRLCDKDVNEC---SQENGCGCIQI CHNKPFSFHCSCHSFELSSDGRTCQDI 109
Db 143 CICKPGWQDKCQDFDINECKDPSNNGGCSQTCNTPTGSHYSCCKIGFAMLTNKKDKQDV 202
Qy 110 DECA-DSEACGEARCKULPGSYSLCLDGGPAYSSQEKACRDVDECLQRCQVQCVNSPGS 168
Db 203 DECSLKPSSVCGTAVCKNIPGDFECPCPGRYNPTLKSCDVEDCESENMCAQLCVNYPGG 262
Qy 169 YTHCDGRGGLKLSODMDTCDILPCVPFVSVAKSVLGLGRMFSGTPIRLRFK 223
Db 263 YSCYCDGRKGFKLADQKSCAEPVCLPLNDKNLYLLAEQFAGV-VLYLKFR 316

RESULT 18
Q68EF9
ID Q68EF9 PRELIMINARY; PRT; 907 AA.
AC Q68EF9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
```

KW	Hypothetical protein.	RA	Birney E., Hayashizaki Y.;
SQ	SEQUENCE 907 AA; 99465 MW; 66F1F4CF664EA3A2 CRC64;	RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
	Query Match 29.0%; Score 376; DB 2; Length 907;	RL	Nature 420:563-573(2002).


```
DB 436 VDRSCEDVNECLNSPCSQE--CANYGYSQYCRRGYQLSDVGVTCEDIDECALPTGG 493
QY 158 --CEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDTLPCV 195
DB 494 HICSYRCINIPSPQSCSPS--SGYRLAPNGRNCQIDECV 532

RESULT 20
Q8C9Q4
ID Q8C9Q4 PRELIMINARY; PRT; 992 AA.
AC Q8C9Q4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
DE library, clone:A630023E24 product:signal peptide, CUB domain, EGF-like
DE 1, full insert sequence.
GN Name=Scubel;
OS Mus musculus. (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
[2]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[3]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[4]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[5]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[6]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuura T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK041590; BAC30996.1; -
DR HSSP: P35555; 1LMJ
DR MGD: MGI:189616; Scubel.
DR GO: GO:0008987; C:external side of plasma membrane; ISS.
DR GO: GO:0005509; F:calcium ion binding; ISS.
DR GO: GO:0046982; F:protein heterodimerization activity; ISS.
DR GO: GO:0042804; F:protein homooligomerization activity; ISS.
DR GO: GO:0007512; P:adult heart development; ISS.
DR GO: GO:0007596; P:blood coagulation; ISS.
DR GO: GO:0045446; P:endothelial cell differentiation; ISS.
DR GO: GO:0006954; P:inflammatory response; ISS.
DR GO: GO:0009791; P:post-embryonic development; ISS.
DR InterPro: IPR000152; Axx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR001491; Thrombomoduln.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00008; EGF; 6.
DR Pfam: PF07645; EGF_CA; 2.
DR PRINTS: PR00307; THROMBOMODULN.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00179; EGF_CA; 6.
DR PROSITE: PS00010; ASX_HYDROXYL; 6.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS01186; EGF_2; 6.
DR PROSITE: PS00026; EGF_3; 2.
DR PROSITE: PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 992 AA; 108569 MW; 42219D6679791FA1 CRC64;

Query Match 27.6%; Score 358.5; DB 2; Length 992;
Best Local Similarity 38.6%; Pred. No. 3e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTQACQDLMGNFCLCKAGH----GGRLCDKD 67
DB 232 YALHADGRTCIET----CAVNGGCDR----TKDTATGVRCSGPGFTLPDQKTC-KD 282
QY 68 VNECSQENGCGCLQICHNKPFGSHCSHSGFELSDGRTCDIDECADSEACGEARCKNLP 127
DB 283 INECLMNGGCDHFCRTNVGSGFCGQKGHKLLDERTCQDIDECSPERTCDHI-CINSP 341
QY 128 GSYSLCDDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGGLKLSQD 184
DB 342 GSFQCLCRRGYTLVGTTH--CGDVDECSMNGSCGQGVNTKGSVEVCVP--PGRRLHWN 397
QY 185 MDTEDILPCVPFVSVAKSLSLYLGRM 211
DB 398 QKDCVEMNGCLSRKSKASQAQQLSCGKV 424

RESULT 21
Q6NZL8
ID Q6NZL8 PRELIMINARY; PRT; 1018 AA.
AC Q6NZL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smaltz J., Myers R.M., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC066066; AAH6066.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain, Hypothetical protein.
SQ SEQUENCE 1018 AA; 111647 MW; 05F09FD42E4B6D42 CRC64;

Query Match 27.6%; Score 358; DB 2; Length 1018;
Best Local Similarity 37.5%; Pred. No. 3.4e-21;
Matches 84; Conservative 24; Mismatches 88; Indels 28; Gaps 10;
QY 6 CINKYGSPTXNSGATCVQN-----LPDQCTPN--PCDRKGTQACQDLGMNFFCL 54
DB 241 CLEKDEAIIERSQFNATSVADVDRKVRLLMETCAVNGGCDR----TKDGTATGVRCS 296
QY 55 CKAGH-----GGRLCDKVNESQENGGLQICHNPGSFHSGHSGFELSSDGRTCQDID 110
DB 297 CPVPGFTLPDQKTC-KDINECLMNGGDDHFCRNTVGSFEGCGQKHLLTDERTCQDID 355
QY 111 ECADSEACGEARCKNLPGSYSLCLDEGFA--YSSQEKACRDVDECL--QGRCEQCVNSPG 167
DB 356 ECSFERTCDHI-CINSPGFCLCRRGTYLYGTTH--CGDVDECSMNGSCGQCVNTKG 412
QY 168 SYTHCHDGRGGLKLSQMDTDEILPVPFSPVSAKSVKSLYLGRM 211

Db 413 SYECVCP--PGRRLHWNKDCVEMNMGCLSRSKASQAQLSCGKV 454
RESULT 22
Q9EQC6
ID Q9EQC6 PRELIMINARY; PRT; 961 AA.
AC Q9EQC6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE EGF-related protein SCUBE1.
GN Name=Scube1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3H1;
RX MEDLINE=20541712; PubMed=11087664; DOI=10.1006/geno.2000.6370;
RA Grimmond S., Lander R., Van Hateren N., Siggers P., Hulsebos T.J.M.,
RA Arkell R., Greenfield A.;
RT "Cloning, mapping, and expression analysis of a gene encoding a novel
RT mammalian EGF-related protein (SCUBE1).";
RL Genomics 70:74-81(2000).
DR EMBL; AF276425; AAG25939.1; -.
DR HSP; P35555; ILMJ.
DR MGD; MGI:1890616; Scube1.
DR GO; GO:0009897; C:external side of plasma membrane; ISS.
DR GO; GO:0005509; F:calcium ion binding; ISS.
DR GO; GO:0046982; F:protein heterodimerization activity; ISS.
DR GO; GO:0042804; F:protein homooligomerization activity; ISS.
DR GO; GO:0007512; P:adult heart development; ISS.
DR GO; GO:0007596; P:blood coagulation; ISS.
DR GO; GO:0045446; P:endothelial cell differentiation; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:000791; P:post-embryonic development; ISS.
DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001491; Thrbomoduln.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 6.
DR Pfam; PF07645; EGF_CA; 2.
DR PRINTS; PR00907; THRBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 961 AA; 103989 MW; 9C6726C4E9BD33E8 CRC64;

Query Match 27.6%; Score 357.5; DB 2; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
QY 14 YTKNSGATCVQNLPDQCTPN--PCDRKGTQACQDLGMNFFCLCKAGW----GGRLCDKD 67
DB 232 YALHADGRTCIET----CAVNGGCDR----TKDGTATGVRCSFVGFTLPDQKTC-KD 282
QY 68 VNECSQENGGLQICHNPGSFHSGHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
DB 283 INECLMNGGDDHFCRNTVGSFEGCGQKHLLTDERTCQDIDECFERTCDHI-CINSP 341
QY 128 GSYSLCLDEGFA--YSSQEKACRDVDECL--QGRCEQCVNSPGSYTHCHDGRGGLKLSQD 184
DB 342 GSFOCLCRRGTYLYGTTH--CGDVDECSMNGSCGQCVNTGRGSEYCVCP--PGRRLHWN 397

QY 185 MDTCEIDILCPVPSVAKSVKSLVGLRM 211
 DB 398 QKDCVEMNGCLSRKASQAQLSCGKV 424

RESULT 23
 ID LTB4_MOUSE
 AC Q8K4G1; Q8K4G0; STANDARD; PRT; 1666 AA.
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Latent transforming growth factor beta binding protein 4 precursor
 DE (LTBP-4).
 GN Name=LTBP4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=22198089; PubMed=12208449; DOI=10.1101/gad.229102;
 RA Sterner-Kock A., Thorey I.S., Koli K., Wenpe F., Ote J., Bangsow T.,
 RA Kuhlmeier K., Kirchner T., Jin S., Keski-Oja J., von Weichner H.;
 RT "Disruption of the gene encoding the latent transforming growth
 RT factor-beta binding protein 4 (LTBP-4) causes abnormal lung
 RT development, cardiomyopathy, and colorectal cancer.";
 RL Genes Dev. 16:2264-2273 (2002).
 RN [2]
 RP SEQUENCE OF 60-1666 FROM N.A. (ISOFORM 3).
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner F.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: May be involved in the assembly, secretion and targeting
 CC of TGFBI to sites at which it is stored and/or activated. May play
 CC critical roles in controlling and directing the activity of TGFBI.
 CC May have a structural role in the extra cellular matrix (ECM) (By
 CC similarity).
 CC -!- SUBUNIT: Forms part of the large latent transforming growth factor
 CC beta precursor complex; removal is essential for activation of
 CC complex. Binds to FBN1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=LTBP4L;
 CC IsoId=Q8K4G1-1; Sequence=Displayed;
 CC Name=2; Synonyms=LTBP4S;
 CC IsoId=Q8K4G1-2; Sequence=VSP_009248, VSP_009250;
 CC Name=3;
 CC IsoId=Q8K4G1-3; Sequence=VSP_009249;
 CC Note=Sequence incomplete.
 CC -!- DOMAIN: Associates covalently with small latent TGF-beta complex
 CC via Repeat C.

CC -!- PTM: Contains hydroxylated asparagine residues (By similarity).
 CC -!- SIMILARITY: Belongs to the LTBP family.
 CC -!- SIMILARITY: Contains 14 EGF-like domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF410798; AAN04661.1; -;
 CC EMBL; AF410799; AAN04662.1; -;
 CC EMBL; BC059016; AAN59016.1; -;
 CC HSSP; P35555; 1EMN.
 CC MGD; MGI:1321395; Ltbp4.
 CC GO; GO:0005578; C:extracellular matrix; ISS.
 CC GO; GO:0005509; F:calcium ion binding; ISS.
 CC GO; GO:0005539; F:glycosaminoglycan binding; ISS.
 CC GO; GO:0005178; F:integrin binding; ISS.
 CC GO; GO:0007275; P:development; ISS.
 CC GO; GO:0030252; P:growth hormone secretion; ISS.
 CC GO; GO:0046879; P:hormone secretion; IMP.
 CC GO; GO:0006457; P:protein folding; ISS.
 CC GO; GO:0045595; P:regulation of cell differentiation; ISS.
 CC GO; GO:0001558; P:regulation of cell growth; ISS.
 CC GO; GO:0030162; P:regulation of proteolysis and peptidolysis; ISS.
 CC GO; GO:0017015; P:regulation of transforming growth factor be...; ISS.
 CC InterPro; IPR000152; Axx_hydroxy_S.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001881; EGF Ca.
 CC InterPro; IPR006209; EGF like.
 CC InterPro; IPR002212; Fibril-assoc.
 CC InterPro; IPR009030; Grow_fac_recept.
 CC Pfam; PF00008; EGF; 16.
 CC Pfam; PF00683; TB; 3.
 CC SMART; SM00179; EGF_CA; 16.
 CC PROSITE; PS00010; ASX_HYDROXYL; 14.
 CC PROSITE; PS00022; EGF_1; 2.
 CC PROSITE; PS01186; EGF_2; 12.
 CC PROSITE; PS00026; EGF_3; 16.
 CC PROSITE; PS01187; EGF_CA; 17.
 CC Alternative splicing; EGF-like domain; Glycoprotein;
 CC Growth factor binding; Repeat; Signal.
 CC SIGNAL 1 24
 CC CHAIN 25 1666
 CC
 CC DOMAIN 148 180
 CC DOMAIN 356 396
 CC REPEAT 415 457
 CC Internal repeat 1.
 CC DOMAIN 588 629
 CC EGF-like 3.
 CC DOMAIN 630 671
 CC EGF-like 4.
 CC DOMAIN 672 713
 CC EGF-like 5.
 CC DOMAIN 714 751
 CC EGF-like 6.
 CC DOMAIN 753 794
 CC EGF-like 7.
 CC DOMAIN 795 836
 CC EGF-like 8.
 CC DOMAIN 877 919
 CC EGF-like 9.
 CC DOMAIN 920 961
 CC EGF-like 10.
 CC DOMAIN 962 1002
 CC EGF-like 11.
 CC DOMAIN 1091 1132
 CC EGF-like 12.
 CC REPEAT 1233 1276
 CC Internal repeat 2.
 CC DOMAIN 1295 1337
 CC EGF-like 13.
 CC DOMAIN 1338 1379
 CC EGF-like 14.
 CC REPEAT 1401 1443
 CC Internal repeat 3.
 CC DOMAIN 1575 1615
 CC EGF-like 15.
 CC DOMAIN 1616 1660
 CC EGF-like 16.
 CC Pro-rich.
 CC DOMAIN 477 608
 CC Cys-rich.
 CC DOMAIN 592 1160
 CC Pro-rich.
 CC DOMAIN 1161 1217
 CC Pro-rich.
 CC DOMAIN 1449 1534
 CC Pro-rich.
 CC DISULFID 152 162
 CC By similarity.
 CC DISULFID 156 168
 CC By similarity.

ID Q9V899 PRELIMINARY; PRT: 1577 AA.
AC Q9V899;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG7526-PA (CG7526-pb).
GN ORFNames=CG7526;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler C., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasner K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasmann D.A., Weinstein G.M., Weissenbach J., Ye J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003558; AAF50538.3; --
DR HSSP: P00736; 1AFO.
DR FlyBase: FBgn0035798; CG7526.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR InterPro: IPR00152; Asx hydroxyl S.
DR InterPro: IPR000742; EGF 2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR003410; HyalIn.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF07645; EGF_CA; 10.
DR Pfam: PF00084; Sushi; 3.
DR SMART: SM00032; CCP; 3.
DR SMART: SM00181; EGF; 13.
DR SMART: SM00179; EGF_CA; 12.
DR PROSITE: PS00010; ASX HYDROXYL; 8.
DR PROSITE: PS01186; EGF_2; 9.
DR PROSITE: PS50026; EGF_3; 4.
DR PROSITE: PS01187; EGF_CA; 10.
DR PROSITE: PS50825; HYR; 2.
DR PROSITE: PS50923; SUSHI; 1.
KW EGF-like domain.
SQ SEQUENCE 1577 AA; 172605 MW; 716DE6C311263E33 CRC64;
Query Match 27.3%; Score 354.5; DB 2; Length 1577;
Best Local Similarity 32.4%; Pred. NO. 1e-20;
Matches 72; Conservative 29; Mismatches 89; Indels 32; Gaps 5;
QY 1 PRYLDCKNGSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACODLWGNFCLCKAGW- 59
Db 610 PGGYGCICAAGYELKLDGIRGYCFDI--DECSQRTGCSQDQMLCNLNGSYTCLCPGYA 668
QY 60 -----GGRLCKDKNVCSQENGCGCLQICHNKPFGSCSCH 94
Db 669 LGLDNHIVTSLNSSFITDSTSETPSAHTC-LDIDECSLANGNCSHFQNGPFGQACAP 727
QY 95 SGFELSSDGRTCQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDSCL 154
Db 728 LGYALSDMRTCQDIDECSDNGQCSQLCNQPGGFACACETGFELPDGFGCADIDCS 787
QY 155 Q--GCEQVCVNSPGSYTCHCDGRGLKLSQDMTCDILPC 194
Db 788 QDYGNCSIDICNLGLGTHACACE--RGVELAKDKLSCLDVDEC 827
RESULT 26
Q00508
ID Q00508 PRELIMINARY; PRT: 1587 AA.
AC Q00508;

RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA001008960; EAA10730.2; --
DR HSSP; P00736; IAPQ.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003410; Hyalin.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF07645; EGF_CA; 12.
DR Pfam; PF02494; HYR; 1.
DR Pfam; PF00084; Sushi; 2.
DR PRINTS; PR00907; THROMBOMODULN.
DR PROSITE; PS00010; ASX_HYDROXYL; 13.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 11.
DR PROSITE; PS00825; HYR; 2.
DR PROSITE; PS00923; SUSHI; 1.
DR EGF-like domain.
KW NON_TER
FT NON_TER 1
SQ SEQUENCE 1222 1222 DECD795CGFF7D740 CRC64;
Query Match 27.3%; Score 353.5; DB 2; Length 1222;
Best Local Similarity 35.4%; Pred. No. 9.6e-21;
Matches 73; Conservative 24; Mismatches 66; Indels 43; Gaps 10;
QY 22 TCQNLPDOCT---PNPDRKGTQACQDLGMNFFCLCKAGW----GGRLCDKDVNEC--- 71
DB 452 TCVDR--DECANARGGCDHN----CHNTAGSYCTCHAGYKLAENARTC-MDVNDCCP 504
QY 72 -----SQNGGCLQICHNKGPSFHCSCHSFGLSSDGRTCQDIDE 111
DB 505 KGFQLDSEHQKTCVDVDEACASRGNGGCSHECVNSPGSYECRCPDYELRHRHACQDVDE 564
QY 112 C-ADSEACGEARKNLPKSGYSLCLDEGFAYSSQEKACRDVDECLQR--CEQVCVNSPGS 168
DB 565 CIVENGNCNSNI-CINLPGRHRCACEIGYSLQDDQRTCSVDVDEBNCNDGTHDCSHHCNVNPGA 623
QY 169 YTCDCDGRGGLKLSQDMTDCEDILPC 194
DB 624 YECECP--AGFKLGRNLSCEDVDEC 647
RESULT 29
O75412 PRELIMINARY; PRT; 1511 AA.
ID O75412
AC O75412
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Latent transforming growth factor-beta binding protein 4S.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Heart;
RC MEDLINE=98325059; PubMed=9660815; DOI=10.1074/jbc.273.29.18459;
RX Saharinen J., Taipale J., Monni O., Keski-Oja J.;

RT "Identification and characterization of a new latent transforming
RT growth factor--binding protein, LTBP-4.";
RL J. Biol. Chem. 273:18459-18469(1998).
DR EMBL; AF051344; AAC39879.1; --
DR HSSP; P35555; LEWN.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR GO; GO:0005509; F:calcium ion binding; NAS.
DR GO; GO:0005539; F:glycosaminoglycan binding; NAS.
DR GO; GO:0005178; F:integrin binding; NAS.
DR GO; GO:0050431; F:transforming growth factor beta binding; IDA.
DR GO; GO:0007275; P:development; TAS.
DR GO; GO:0030252; P:growth hormone secretion; TAS.
DR GO; GO:0006457; P:protein folding; TAS.
DR GO; GO:0045595; P:regulation of cell differentiation; TAS.
DR GO; GO:0001558; P:regulation of cell growth; TAS.
DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
DR GO; GO:0017015; P:regulation of transforming growth factor be...; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 16.
DR Pfam; PF00683; TB; 4.
DR SMART; SM00179; EGF_CA; 16.
DR PROSITE; PS00010; ASX_HYDROXYL; 14.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01186; EGF_2; 12.
DR PROSITE; PS00026; EGF_3; 13.
DR PROSITE; PS01187; EGF_CA; 17.
KW EGF-like domain.
SQ SEQUENCE 1511 AA; 161157 MW; C61AB757B256958D CRC64;
Query Match 27.3%; Score 353.5; DB 2; Length 1511;
Best Local Similarity 43.3%; Pred. No. 1.2e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;
QY 29 DOCTNP--CDRKGTTQACQDLGMNFFCLCKAGWGRGLCDKQVNECSQENGCG--LQICHNK 85
DB 560 DECTQSPGLC---GRGACKNLPKSGFRVCVCPAGFRGSACEEDVDECAQBPPCPGRCNDT 616
QY 86 PGSFHCSCHSFGLSSDGRTCQDIDEACDS--BACGEARKNLPKSGYSLCLDEGFAYSSQ 144
DB 617 AGSFHCACPAGFRSGPAGCPQDVDECARSPPTCYTCRCENTEGSFQCVCPMGFQFNAA 676
QY 145 KACRDVDECLQR--RCE--QVCVNSPGSYTCH--CDGRGGLKLSQ--DMTDCED--ILPCVP 196
DB 677 SECDVDEBNCNHLACPGQECVNSPGSFQCRACPSGHLHHRGCTDVEDCSGAPCGP 734
RESULT 30
O88840 PRELIMINARY; PRT; 3857 AA.
ID O88840
AC O88840
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mutant fibrillin-1.
GN Name=Fbn1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=B10.D2;
RX MEDLINE=98069008; PubMed=9405934;
RA Bona C.A., Murai C., Casares S., Kasturi K., Nishimura H., Honjo T.,
RA Matsuda F.;
RT "Structure of the mutant fibrillin-1 gene in the tight skin (TSK)
RT mouse.";
RL DNA Res. 4:267-271(1997).

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DR EMBL; AF007248; AAC62317.1; -.
DR HSP; P35555; 1LWJ.
DR MGI; MGI:95489; Fbn1.
DR GO; GO:0001527; C:micr of fibril; TAG.
DR InterPro; IPR00152; ASX hydroxyl S.
DR InterPro; IPR002557; Chitin_bind_PeRA.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00608; EGF_4.
DR Pfam; PF07645; EGF_CA; 59.
DR Pfam; PF00683; TB_12.
DR SMART; SM00494; TcBD2; 5.
DR SMART; SM00179; EGF_CA; 60.
DR PROSITE; PS00010; ASX HYDROXYL; 61.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 50.
DR PROSITE; PS50026; EGF_3; 56.
DR PROSITE; PS01187; EGF_CA; 61.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 3857 AA; 418303 MW; 5BC0618BC527E04C CRC64;

Query Match 27.1%; Score 351.5; DB 2; Length 3857;
Best Local Similarity 33.2%; Pred. No. 4.3e-20;
Matches 83; Conservative 26; Mismatches 94; Indels 47; Gaps 8;

QY 6 CINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAG 58
DB 2115 CHNTGYSRCPCPPGHQLSPNISACIDINECELSANLCPH---GRCVNLIGKYCACNPG 2171
QY 59 W---GGRLCDKDVNCSQENGGLQICHNKPGSFHCSHGFSFELSSDQRTQDIDECADS 115
DB 2172 YHPHTRDLFCVDIDECSIMNGGCETFTNSDGSYECSCQPGFALMPDQSRCTDIDECEDN 2231
QY 116 -EAGCARCKNLPGSYCLCDEGFAYSSQEKACRDVDE-----CLOGRCEQVCVNSPG 167
DB 2232 PNICDGGQCTNIPGYSYCLCYDGFMASEDMKTCVDVNECDLNPNICLSGTCE----NTKG 2287
QY 168 SYTHCHD---GRGLKLSQDMDTCE-----DILPCVPFVSVAKSYS 205
DB 2288 SFICHDMGYSKKGKTKGTCTDINECEIGAHCNDRHAVCTNTAGSPKCSQPGWIGDGKIC 2347
QY 206 LYLGRMFSGT 215
DB 2348 TDLDECSST 2357

RESULT 31
Q9WUH8 PRELIMINARY; PRT; 2872 AA.
AC Q9WUH8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fibrillin-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99032689; PubMed=9815129;
RA Kanwar Y.S.; Ota K.; Yang Q.; Kumar A.; Wada J.; Kashiwara N.;
RA Peterson D.R.;
RT "Isolation of rat fibrillin-1 cDNA and its relevance in metanephric
RT development."
RL Am. J. Physiol. 275:F710-F723 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Kanwar Y.S.;
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RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF135059; AAD34438.1; -.
DR HSP; P35555; 1APJ.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR00152; ASX hydroxyl S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR011398; Fibrillin.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF07645; EGF_CA; 41.
DR Pfam; PF00683; TB_9.
DR SMART; PIRSF036312; Fibrillin; 1.
DR SMART; SM00179; EGF_CA; 41.
DR PROSITE; PS00010; ASX HYDROXYL; 42.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS50026; EGF_3; 38.
DR PROSITE; PS01187; EGF_CA; 41.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 2872 AA; 312069 MW; 0C4F7F3B87A80280 CRC64;

Query Match 27.0%; Score 350.5; DB 2; Length 2872;
Best Local Similarity 36.9%; Pred. No. 3.9e-20;
Matches 76; Conservative 24; Mismatches 77; Indels 29; Gaps 7;

QY 6 CINKYG-----SPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAG 58
DB 1130 CHNTGYSRCPCPPGHQLSPNISACIDINECELSANLCPH---GRCVNLIGKYCACNPG 1186
QY 59 W---GGRLCDKDVNCSQENGGLQICHNKPGSFHCSHGFSFELSSDQRTQDIDECADS 115
DB 1187 YHPHTRDLFCVDIDECSIMNGGCETFTNSDGSYECSCQPGFALMPDQSRCTDIDECEDN 1246
QY 116 -EAGCARCKNLPGSYCLCDEGFAYSSQEKACRDVDE-----CLOGRCEQVCVNSPG 167
DB 1247 PNICDGGQCTNIPGYSYCLCYDGFMASEDMKTCVDVNECDLNPNICLSGTCE----NTKG 1302
QY 168 SYTHCHD---GRGLKLSQDMDTCE 189
DB 1303 SFICHDMGYSKKGKTKGTCTDINECE 1328

RESULT 32
FBN1_BOVIN STANDARD; PRT; 2871 AA.
AC P98133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor (WP340).
GN Name=FBN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RX MEDLINE=95137597; PubMed=7835900;
RA Tilstra D.J.; Potter K.A.; Byers P.H.;
RT "Sequence of the coding region of the bovine fibrillin cDNA and
RT localization to bovine chromosome 10."
RL Genomics 23:480-485 (1994).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=96132851; PubMed=8557636; DOI=10.1074/jbc.271.28.16662;
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FT DISULFID 1097 1111 By similarity.
FT DISULFID 1117 1129 By similarity.
FT DISULFID 1124 1138 By similarity.
FT DISULFID 1140 1153 By similarity.
FT DISULFID 1159 1171 By similarity.
FT DISULFID 1166 1180 By similarity.
FT DISULFID 1182 1195 By similarity.
FT DISULFID 1201 1212 By similarity.
FT DISULFID 1208 1221 By similarity.
FT DISULFID 1223 1236 By similarity.
FT DISULFID 1242 1254 By similarity.
FT DISULFID 1249 1263 By similarity.
FT DISULFID 1265 1278 By similarity.
FT DISULFID 1284 1296 By similarity.
FT DISULFID 1291 1305 By similarity.
FT DISULFID 1307 1320 By similarity.
FT DISULFID 1326 1339 By similarity.
FT DISULFID 1333 1348 By similarity.
FT DISULFID 1350 1361 By similarity.
FT DISULFID 1367 1380 By similarity.
FT DISULFID 1374 1389 By similarity.
FT DISULFID 1391 1402 By similarity.
FT DISULFID 1408 1420 By similarity.
FT DISULFID 1415 1429 By similarity.
FT DISULFID 1431 1444 By similarity.
FT DISULFID 1450 1461 By similarity.
FT DISULFID 1456 1470 By similarity.
FT DISULFID 1472 1485 By similarity.
FT DISULFID 1491 1502 By similarity.
FT DISULFID 1497 1511 By similarity.
FT DISULFID 1513 1526 By similarity.

Query Match 26.9%; Score 349.5; DB 1; Length 2871;
Best Local Similarity 35.9%; Pred. No. 4.7e-20;
Matches 78; Conservative 21; Mismatches 67; Indels 51; Gaps 9;

QY 6 CLNKGPSYTKNSGFATCVQNLPDQCTP-----NPDCKRGTOA-----CQDL 47
Db 1129 CLNTGSS-----YRC-----ECFQHQIAPNISACIDINECELSAHLCPHGRCVNL 1174
QY 48 MGNFFCLCKAGWG---RLCDKDVNCSQENGGLQI CHNKPGRFHCSCGSEFLLSDGR 104
Db 1175 IGKYCACNPGYHSTPDLRFCDVIDECSIMNGCETFTCTNSEGSEYECSCQPGFALMPDQR 1234
QY 105 TCQDDECADS-EAGCEARCKNLPGSYCLDEGFAYSSQEKACRDVDE-----CLOG 156
Db 1235 SCTDIDCEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMMKTCVDVNECDLNPNICLSG 1294
QY 157 RCEQCVNSPGSYTCHCD---GRGLKLSQDMDTCE 189
Db 1295 TCE---NTKGSFICHDMGYSGKKGKTCTDINECE 1327

RESULT 33
Q81W4
ID Q81W4 PRELIMINARY; PRT; 988 AA.
AC Q81W4;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Signal peptide-CUB-EGF-like domain containing protein 1.
GN Name=SCUBE1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23336413; PubMed=12270931; DOI=10.1074/jbc.M207410200;
RA Yang R.B., Ng C.K.D., Wasserman S.M., Colman S.D., Shenoy S.,
RA Mehraban F., Komuves L.G., Tomlinson J.E., Topper J.N.;
RT "Identification of a novel family of cell-surface proteins expressed
in human vascular endothelium."

J. Biol. Chem. 277:46364-46373 (2002).
[2]
RP SEQUENCE FROM N.A.
RA Yang R.-B., Ng C.K.D., Wasserman S.M., Colman S.D., Shenoy S.,
RA Mehraban F., Komuves L., Tomlinson J.E., Topper J.N.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525689; AA071133.1; -.
DR HSSP; P01130; 1428.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0005509; F:calcium ion binding; TAS.
DR GO; GO:0046982; F:protein heterodimerization activity; IDA.
DR GO; GO:0042804; F:protein homooligomerization activity; IPI.
DR GO; GO:0007512; P:adult heart development; NAS.
DR GO; GO:0007596; P:blood coagulation; NAS.
DR GO; GO:0045446; P:endothelial cell differentiation; NAS.
DR GO; GO:0006954; P:inflammatory response; NAS.
DR GO; GO:0009791; P:post-embryonic development; NAS.
DR InterPro; IPR0010152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR001491; Thrombomodulin.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 4.
DR PRINTS; PR00307; THROMBOMODULN.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 988 AA; 107900 MW; 1BF57BEF7780C9C1 CRC64;

Query Match 26.9%; Score 349; DB 2; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.8e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;

QY 14 YTKNSGFATCVQNLPDQCTP---PCDRKGTQACQDLMGNFCLCKAGW---GGRLCDKD 67
Db 232 YAPHSRGRTCIET---CAVNGGCDR---TKDRTATGRCSCPVGFTLPDQKTC-KD 282
QY 68 VNECSQENGGLQI CHNKPGRFHCSCGSEFLLSDGRTCDIDECADSEAGCEARCKNLP 127
Db 283 INECLVNGGCDHFCRNTVGSFECGCRKGYKLLTDRTCQDIDECSEFERTCDHI-CINSP 341
QY 128 GSYSLCLDEGF-AYSQEKACRDVDEC---LQGRCEQCVNSPGSYTCHCDGRGLKLSQD 184
Db 342 GSPQCLCHRGYLYGTTH---CGDVDECSMNGSCDQGVNTKGSYECVCP---PGRRLHN 397
QY 185 MDTCEDILPC-----VPFSVAKSVKSLYL 208
Db 398 KDCVETGKCLSRKTSPTRAQLSCSKAGGVESCF 432

RESULT 34
Q75N8
ID Q75N8 PRELIMINARY; PRT; 1365 AA.
AC Q75N8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Fibrillin 1.
GN Name=FBN1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Kanazaki R., Toki T.,
RA Yonekura S., Ito E.;
RT "Three novel mutations of the fibrillin-1 gene and ten single
RT nucleotide polymorphisms of the fibrillin-3 gene in Marfan syndrome
RT patients.";
RL J. Hum. Genet. 49:404-407(2004).
CC -1- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AB177802; BAD16738.1; -;
DR HSP; P00736; IAPQ.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_1.
DR InterPro; IPR001438; EGF_1.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF07645; EGF_CA; 17.
DR Pfam; PF00683; TB; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 22.
DR SMART; SM00179; EGF_CA; 19.
DR PROSITE; PS00010; ASX_HYDROXYL; 18.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 15.
DR PROSITE; PS00026; EGF_3; 18.
DR PROSITE; PS01187; EGF_CA; 18.
KW EGF-like domain.
SQ SEQUENCE 1365 AA; 147448 MW; ED83FB79C1B2BD48 CRC64;

Query Match 26.9%; Score 348.5; DB 2; Length 1365;
Best Local Similarity 42.9%; Pred. No. 2.8e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLGNFFCLXAGNGG---RLCDKDVNCSQENGGCLQICHNKGSGFCHSCHSGFELS 100
DB 1171 CVNLKGYCACNPGYHSTPDRFLFCVDIDECSTFMNGGCTFTNSGSGYECSCQPGFALM 1230
QY 101 SDGRTQDIDECADS-EAGCEARCKNLPGSYSLCDGEGAYSSQERACRDVDE----- 152
DB 1231 PDGRTCTDIDECEDNPNICDGGCTWPGYRCLCYDGFNASEDMKTCVDVNECDLNPNI 1290
QY 153 CLGRCQCVNPSGYSYTHCD----GRGLKLSQDMDTCE 189
DB 1291 CLSGTCE---NTKSGFICHCDMGYSKKGKTKCTDINECE 1327

RESULT 35
FBN1 HUMAN STANDARD; PRT; 2871 AA.
AC P3555;
DT 01-JUN-1994 (Rel. 29, Created)
DT 21-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor.
GN Name=FBN1; Synonyms=FBN;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=93372850; PubMed=8364578;
RA Ferreira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
RA Pangillan T., Bonadio J.;
RT "Genomic organization of the sequence coding for fibrillin, the
RT defective gene product in Marfan syndrome.";
RL Hum. Mol. Genet. 2:961-968(1993).
RN [2]
RP SEQUENCE OF 1-932 FROM N.A.

RC TISSUE=Fibroblast, and Placenta;
RX MEDLINE=94010947; PubMed=7691719;
RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
RT "Fibrillin binds calcium and is coded by cDNAs that reveal a
RT multidomain structure and alternatively spliced exons at the 5' end.";
RL Genomics 17:476-484(1993).
RN [3]
RP SEQUENCE OF 899-2871 FROM N.A.
RX MEDLINE=91304568; PubMed=1852207; DOI=10.1038/352334a0;
RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
RT "Partial sequence of a candidate gene for the Marfan syndrome.";
RL Nature 352:334-337(1991).
RN [4]
RP SEQUENCE OF 813-1313 FROM N.A.
RX MEDLINE=91304567; PubMed=1852206; DOI=10.1038/352334a0;
RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
RA Tsipouras P., Ramirez F., Hollister D.W.;
RT "Linkage of Marfan syndrome and a phenotypically related disorder to
RT two different fibrillin genes.";
RL Nature 352:330-334(1991).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=91317849; PubMed=1860873;
RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;
RT "Purification and partial characterization of fibrillin, a cysteine-
RT rich structural component of connective tissue microfibrils.";
RL J. Biol. Chem. 266:14763-14770(1991).
RN [6]
RP STRUCTURE BY NMR OF 2054-2125.
RX MEDLINE=98031893; PubMed=9362480; DOI=10.1093/emboj/16.22.6659;
RYuan X., Downing A.K., Knott V., Handford P.A.;
RT "Solution structure of the transforming growth factor beta-binding
RT protein-like module, a domain associated with matrix fibrils.";
RL EMBO J. 16:6659-6666(1997).
RN [7]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=96144829; PubMed=8568869; DOI=10.1006/jmbi.1996.0003;
RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
RT "Calcium binding properties of an epidermal growth factor-like domain
RT pair from human fibrillin-1.";
RL J. Mol. Biol. 255:22-27(1996).
RN [8]
RP STRUCTURE BY NMR OF 2124-2205.
RX MEDLINE=9622301; PubMed=8653794; DOI=10.1016/S0092-8674(00)81259-3;
RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
RA Handford P.A.;
RT "Solution structure of a pair of calcium-binding epidermal growth
RT factor-like domains: implications for the Marfan syndrome and other
RT genetic disorders.";
RL Cell 85:597-605(1996).
RN [9]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=96174615; PubMed=8594563; DOI=10.1093/nar/24.1.137;
RA Colod G., Beroud C., Soussi T., Junien C., Boileau C.;
RT "Software and database for the analysis of mutations in the human FBN1
RT gene.";
RL Nucleic Acids Res. 24:137-141(1996).
RN [10]
RP REVIEW ON MFS VARIANTS.
RX MEDLINE=97169383; PubMed=9016526; DOI=10.1093/nar/25.1.147;
RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
RA Richards R.I., Wang W., Junien C., Boileau C.;
RT "Marfan Database (second edition): software and database for the
RT analysis of mutations in the human FBN1 gene.";
RL Nucleic Acids Res. 25:147-150(1997).
RN [11]
RP REVIEW ON VARIANTS.
RX MEDLINE=98062175; PubMed=9401003;
RX DOI=10.1002/(SICI)1098-1004(1997)10:6<415::AID-HUMU1>3.3.CO;2-2;
RA Hayward C., Brock D.J.H.;
RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
RT fibrillinopathies.";

RL Hum. Mutat. 10:415-423 (1997).
[12]
RP REVIEW ON MFS.
RX PubMed=10633129;
RA Robinson P.N., Godfrey M.;
RT "The molecular genetics of Marfan syndrome and related
microfibrilopathies";
J. Med. Genet. 37:9-25 (2000).
[13]
RP REVIEW ON VARIANTS.
RX PubMed=12203987; DOI=10.1002/humu.10113;
RA Robinson P.N., Booms P., Katzke S., Ladewig M., Neumann L., Palz M.,
Pregla R., Tiecke F., Rosenberg T.;
RT "Mutations of FBNI and genotype-phenotype correlations in Marfan
syndrome and related fibrillinopathies";
Hum. Mutat. 20:153-161 (2002).
[14]
RP VARIANT MFS PRO-1137.
RX MEDLINE=91304569; PubMed=1852208; DOI=10.1038/352337a0;
RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,
Curtis S.M., Stetten G., Meyers D.A., Francomano C.A.;
RT "Marfan syndrome caused by a recurrent de novo missense mutation in
the fibrillin gene";
Nature 352:337-339 (1991).
[15]
RP VARIANTS MFS SER-1249; ARG-1663; SER-2221 AND SER-2307.
RX MEDLINE=93250834; PubMed=1301946;
RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
RT "Clustering of fibrillin (FBNI) missense mutations in Marfan syndrome
patients at cysteine residues in EGF-like domains";
Hum. Mutat. 1:366-374 (1992).
[16]
RP VARIANT MFS SER-2307.
RX MEDLINE=92232590; PubMed=1569206;
RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
RT "Marfan phenotype variability in a family segregating a missense
mutation in the epidermal growth factor-like motif of the fibrillin
gene";
J. Clin. Invest. 89:1674-1680 (1992).
[17]
RP VARIANTS MFS ILE-548 AND ALA-723.
RX MEDLINE=94010946; PubMed=8406497;
RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
Pyeritz R.E., Francomano C.A.;
RT "Four novel FBNI mutations: significance for mutant transcript level
and EGF-like domain calcium binding in the pathogenesis of Marfan
syndrome";
Genomics 17:468-475 (1993).
[18]
RP VARIANT MFS SER-2144.
RX MEDLINE=93278402; PubMed=8504310;
RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
RT "A novel fibrillin mutation in the Marfan syndrome which could disrupt
calcium binding of the epidermal growth factor-like module";
Hum. Mol. Genet. 2:475-477 (1993).
[19]
RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
ALA-1148.
RX MEDLINE=94108431; PubMed=8281141;
RA Tynan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gsanner C.,
Berg M.A., Miller D.C., Francke U.;
RT "Mutation screening of complete fibrillin-1 coding sequence: report of
five new mutations, including two in 8-cysteine domains";
Hum. Mol. Genet. 2:1813-1821 (1993).
[20]
RP VARIANTS MFS GLY-217 AND ARG-2627.
RX MEDLINE=95067970; PubMed=7977366;
RA Karttunen L., Ragnauth M., Lomqvist L., Peltonen L.;
RT "A compound-heterozygous Marfan patient: two defective fibrillin
alleles result in a lethal phenotype";
Am. J. Hum. Genet. 55:1083-1091 (1994).

RN [21]
RP VARIANT EL LYS-2447.
RX MEDLINE=94245249; PubMed=8189302;
RA Lomqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
Peltonen L.;
RT "A novel mutation of the fibrillin gene causing ectopia lentis";
Genomics 19:573-576 (1994).
[22]
RP VARIANT MFS CYS-627.
RX MEDLINE=94272487; PubMed=8004112;
RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
RT "Two novel mutations and a neutral polymorphism in EGF-like domains of
the fibrillin gene (FBNI): SSCP screening of exons 15-21 in Marfan
syndrome patients";
Hum. Mol. Genet. 3:373-375 (1994).
[23]
RP VARIANT MFS CYS-122.
RX MEDLINE=94314977; PubMed=8040326;
RA Stahl-Hallengren C., Ukonen T., Kainulainen K., Kristofersson U.,
Saxne T., Tornqvist K., Peltonen L.;
RT "An extra cysteine in one of the non-calcium-binding epidermal growth
factor-like motifs of the FBNI polypeptide is connected to a novel
variant of Marfan syndrome";
J. Clin. Invest. 94:709-713 (1994).
[24]
RP VARIANT MFS TYR-1223.
RX MEDLINE=94351682; PubMed=8071963;
RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
RT "A new missense mutation of fibrillin in a patient with Marfan
syndrome";
J. Med. Genet. 31:338-339 (1994).
[25]
Query Match 26.9%; Score 348.5; DB 1; Length 2871;
Best Local Similarity 42.9%; Pred. No. 5.7e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;
Qy 44 QQDLGNFFCLCKAGWG---RLCKDVNECSQBNGLQICHKNKPGSFHCSHGPELS 100
Db 1171 CVNIIGKYQACNPGYHSTPDLFCVDIDCSINWGCTFTCTNSEGSYECQPGFALM 1230
Qy 101 SDGRTCDQIDECADS-EACGEARCKNLPGSYSLCDEGFAYSSQEKACRDYDE----- 152
Db 1231 PDQRSDTIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNI 1290
Qy 153 CLQRCQVCVNSPGSYTHCD----GRGLKLSQDMDTCE 189
Db 1291 CLSGTCE----NTKGSFICHDMGYSGKKGKTGCTDINECE 1327
RESULT 36
Q75N87 PRELIMINARY; PRT; 2871 AA.
ID Q75N87
AC Q75N87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fibrillin 1.
GN Name=FBNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Uyeda T., Takahashi T., Eto S., Sato T., Xu G., Kanazaki R., Toki T.,
RT "Three novel mutations of the fibrillin-1 gene and ten single
nucleotide polymorphisms of the fibrillin-3 gene in Marfan syndrome
patients";
J. Hum. Genet. 49:404-407 (2004).
CC -!- SIMILARITY: Contains 2 EGF-like domains.
DR EMBL; AB177803; BAD16739.1; -.

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DR HSP; P35555; 1APU.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR011398; Fibrillin.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF07645; EGF_CA; 42.
DR PIRSF; PIRSF036312; Fibrillin; 1.
DR SMART; SM00179; EGF CA; 44.
DR PROSITE; PS00010; ASX_HYDROXYL; 42.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS00026; EGF_3; 39.
DR PROSITE; PS01187; EGF_CA; 42.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 2871 AA; 312219 MW; C3D044A80321E082 CRC64;

Query Match 26.9%; Score 348.5; DB 2; Length 2871;
Best Local Similarity 42.9%; Pred.No.5.7e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLMGNFFCLCKAGWG---RLCDKDVNECSQENGGLQICHNKPSPHCSHGFELS 100
Db 1171 CVNLICKYQCACNPGYHSTPDLFCVDIDECSTMGCGCTFCTNSGSEYECSCQCPGALM 1230

QY 101 SGRTQCDIDECADS-EAGEARCKNLPGSYCLDEGFAYSSQEKACRDVDE----- 152
Db 1231 PQRSCTDIDECBDNFCIDGGQCTNIPGEYRCLCYDGFMASEDMDKTCVDVNECDLNPNI 1290

QY 153 CLQGRCEQVNSPGSYTCHCD---GRGLKLSQDMDTCE 189
Db 1291 CLSGTCE---NTKGSFICHDMGYSGKKGKTCTDINECE 1327

RESULT 37
Q6ZW11 PRELIMINARY; PRT; 971 AA.
ID Q6ZW11 PRELIMINARY; PRT; 971 AA.
AC Q6ZW11; 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ41044.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kunagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakanatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK123039; BAC85521.1; -.
DR HSP; P00736; 1APU.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 3.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 10.
DR SMART; SM00179; EGF CA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 971 AA; 106744 MW; 6213C2EED74BD428 CRC64;

Query Match 26.6%; Score 345; DB 2; Length 971;
Best Local Similarity 38.1%; Pred.No.3.9e-20;
Matches 75; Conservative 28; Mismatches 74; Indels 20; Gaps 10;

QY 27 LPDQCTPN--PCDRKGTOACQDLMGNFFCLCKAGW---GGRLCDKDVNECSQENGGLQ 80
Db 282 LMETCAVNVNGCDR---TCKDSTSTGVHCSCVPVFTLQLDGTCTC-KDIDECQTRNGGCDH 336

QY 81 ICHNKPSPHCSHGFELS DGRTCQDIDECADSEACGEARCKNLPGSYCLDEGFA- 139
Db 337 FCKNIVGSPFCCKGKGLLTDEKSCQDVDECSLORTCDHS-CINHPGTFFACACNRGYTL 395

QY 140 YSSQKACRDVDECL--QGRCEQVNSPGSYTCHCDGRGLKLSQDMDTCDLILPCVPF 197
Db 396 YGFTH--CGDTNECSINNGCCQVCVNTVSGYECOC--HPGYKLHWNKDKCCEVVKGLPT 451

QY 198 SVAKSVKSLYLGRMPSG 214
Db 452 SVSPRV-SLHCKSGGG 467

RESULT 38
Q9NQ36 PRELIMINARY; PRT; 999 AA.
ID Q9NQ36 PRELIMINARY; PRT; 999 AA.
AC Q9NQ36; 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CEGP1 protein.
GN Name=CEGP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Amid C., Bahr A., Mujica A., Sampson N., Bikar S.E., Winterpacht A.,
RA Zabel B., Hankeln T., Schmidt E.R.;
RT "Comparative genomic sequencing reveals a strikingly similar
RT architecture of a conserved syntenic region on human chromosome
RT 1p15.3 (including gene STS) and mouse chromosome 7.";
RL Cytochrome. Cell Genet. 93:284-290(2001).
DR EMBL; AJ400877; CAB92285.1; -.
DR HSP; P35555; 1EMW.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_CA; 3.
```

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DR SMART; SM00042; CUB; 1.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 6.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 6.
KW EGF-like domain.
SQ SEQUENCE 999 AA; 109956 MW; 61334844A0053095 CRC64;

Query Match      26.6%; Score 345; DB 2; Length 999;
Best Local Similarity 38.1%; Pred. No. 4e-20;
Matches 75; Conservative 28; Mismatches 74; Indels 20; Gaps 10;

QY 27 LPDQCTPN--PDRKGTQACQDLGNFFCLCKAGW----GGRLCDKDVNECSQENGGLQ 80
DB 282 LMETCAVNGGCDR----TCKDSTGVHCSCVPVFTLQDGTGTC-KDIDECQTRNGGCDH 336
QY 81 ICHNKPFGPHCSHGSEFELSSDGRCTQDIDECADSEAGCEARCKNLPGSYSLCDEGFA- 139
DB 337 FCENIVGDFDCGCKGFKLLTDEKSCQDVDECSLDRDCHS-CINHPTGFACNRYTL 395
QY 140 YSSQBKACRDVDECL--QGRCEQVCNPSGSYTCHDGRGGKJUSQDMDTCEDLPCVPFF 197
DB 396 YGFTH--CGDTNECSINNGGCGQVCNTVGSVEQCQ--HPGYKHLWNKKDCVVKGLLPT 451
QY 198 SVAKSVKSLYLGRMPSG 214
DB 452 SVSPRV-SLHCKSGGG 467

RESULT 39
FBN1_MOUSE
ID FBN1_MOUSE STANDARD; PRT; 2871 AA.
AC Q61554; Q60826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Fibrillin 1 precursor.
GN Name=Fbn1; Synonyms=Fbn-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=95130561; PubMed=7829516; DOI=10.1074/jbc.270.4.1798;
RA Yin W., Germiller J., Sanguinetti C., Smiley E., Pangillan T.,
RA Pereira L., Ramirez F., Bonadio J.;
RT "Primary structure and developmental expression of Fbn-1, the mouse
  fibrillin gene.";
RL J. Biol. Chem. 270:1798-1806 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
RL Submitted (APR-1995) to the EMBL/GenBank/DDAJ databases.
CC -!- FUNCTION: Structural component of connective tissue microfibrils
CC that binds calcium. Fibrillin-1-containing microfibrils provide
CC long-term force bearing structural support.
CC -!- PTM: Forms intermolecular disulfide bonds either with other
CC fibrillin-1 molecules or with other components of the microfibrils
CC (By similarity).
CC -!- SIMILARITY: Belongs to the fibrillin family.
CC -!- SIMILARITY: Contains 7 EGF-like domains.
CC -!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
CC
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CC -----
DR EMBL; L29454; AAA56840.1; -.
DR EMBL; U22493; AAA64217.1; -.
DR PIR; A55624; A55624.
DR HSSP; P35555; IAPJ.
DR MGD; MGI:95489; Fbn1.
DR InterPro; IPR000152; Asx_hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 45.
DR Pfam; PF00683; TB; 9.
DR PIRSF; PIRSF016312; Fibrillin; 1.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS00026; EGF_3; 45.
DR PROSITE; PS01187; EGF_CA; 43.
KW Calcium-binding; EGF-like domain; Extracellular matrix; Glycoprotein;
KW Multigene family; Repeat; Signal.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 2871 Fibrillin 1.
FT DOMAIN 81 112 EGF-like 1.
FT DOMAIN 115 146 EGF-like 2.
FT DOMAIN 147 178 EGF-like 3.
FT DOMAIN 246 287 EGF-like 4, calcium-binding.
FT DOMAIN 288 329 EGF-like 5, calcium-binding.
FT DOMAIN 330 401 TGFBP 1.
FT DOMAIN 402 446 Pro-rich.
FT DOMAIN 449 489 EGF-like 6.
FT DOMAIN 490 529 EGF-like 7, calcium-binding.
FT DOMAIN 530 571 EGF-like 8, calcium-binding.
FT DOMAIN 572 612 EGF-like 9, calcium-binding.
FT DOMAIN 613 653 EGF-like 10, calcium-binding.
FT DOMAIN 656 721 TGFBP 2.
FT DOMAIN 723 764 EGF-like 11, calcium-binding.
FT DOMAIN 765 806 EGF-like 12, calcium-binding.
FT DOMAIN 807 846 EGF-like 13, calcium-binding.
FT DOMAIN 910 951 EGF-like 14, calcium-binding.
FT DOMAIN 952 1018 TGFBP 3.
FT DOMAIN 1028 1069 EGF-like 15, calcium-binding.
FT DOMAIN 1070 1112 EGF-like 16, calcium-binding.
FT DOMAIN 1113 1154 EGF-like 17, calcium-binding.
FT DOMAIN 1155 1196 EGF-like 19, calcium-binding.
FT DOMAIN 1197 1237 EGF-like 19, calcium-binding.
FT DOMAIN 1238 1279 EGF-like 20, calcium-binding.
FT DOMAIN 1280 1321 EGF-like 21, calcium-binding.
FT DOMAIN 1322 1362 EGF-like 22, calcium-binding.
FT DOMAIN 1363 1403 EGF-like 23, calcium-binding.
FT DOMAIN 1404 1445 EGF-like 24, calcium-binding.
FT DOMAIN 1446 1486 EGF-like 25, calcium-binding.
FT DOMAIN 1487 1527 EGF-like 26, calcium-binding.
FT DOMAIN 1528 1599 TGFBP 4.
FT DOMAIN 1606 1647 EGF-like 27, calcium-binding.
FT DOMAIN 1648 1688 EGF-like 28, calcium-binding.
FT DOMAIN 1689 1758 TGFBP 5.
FT DOMAIN 1766 1807 EGF-like 29, calcium-binding.
FT DOMAIN 1808 1848 EGF-like 30, calcium-binding.
FT DOMAIN 1849 1890 EGF-like 31, calcium-binding.
FT DOMAIN 1891 1929 EGF-like 32, calcium-binding.
FT DOMAIN 1930 1972 EGF-like 33, calcium-binding.
FT DOMAIN 1973 2012 EGF-like 34, calcium-binding.
FT DOMAIN 2013 2054 EGF-like 35, calcium-binding.
FT DOMAIN 2055 2121 TGFBP 6.
FT DOMAIN 2127 2165 EGF-like 36, calcium-binding.
FT DOMAIN 2166 2205 EGF-like 37, calcium-binding.
FT DOMAIN 2206 2246 EGF-like 38, calcium-binding.
FT DOMAIN 2247 2290 EGF-like 39, calcium-binding.
FT DOMAIN 2291 2332 EGF-like 40, calcium-binding.
FT DOMAIN 2333 2400 TGFBP 7.
```


CC supramolecular organization of ECM architecture, in particular to
 CC those of basement membranes
 CC -!- SUSUNIT: Interacts with itself and with various extracellular
 CC matrix components (By similarity).
 CC -!- SURCELLULAR LOCATION: Secreted; extracellular matrix (By
 CC similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=C;
 CC IsoId=O77469-1; Sequence=Displayed;
 CC Name=a; Synonyms=C;
 CC IsoId=O77469-2; Sequence=VSP_001387, VSP_001388, VSP_001389;
 CC Name=b; Synonyms=D;
 CC IsoId=O77469-3; Sequence=VSP_001387, VSP_001388, VSP_001389,
 CC VSP_001390;
 CC -!- SIMILARITY: Belongs to the fibulin family.
 CC -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
 CC -!- SIMILARITY: Contains 9 EGF-like domains.
 CC -----
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 CC -----
 CC EMBL; AF051403; AAC28323.1; -;
 CC EMBL; AF051403; AAC28324.1; -;
 CC EMBL; AF051401; AAC28321.1; -;
 CC EMBL; AF051402; AAC28322.1; -;
 CC EMBL; AF070477; AAC24035.1; -;
 CC EMBL; Z68219; CAA92483.1; -;
 CC EMBL; Z68749; CAA92483.1; JOINED.
 CC EMBL; Z68219; CAC35826.1; -;
 CC EMBL; Z68749; CAC35826.1; JOINED.
 CC EMBL; Z68219; CAC35827.1; -;
 CC EMBL; Z68749; CAC35827.1; JOINED.
 CC EMBL; Z68219; CAA92962.1; -;
 CC EMBL; Z68219; CAA92962.1; JOINED.
 CC EMBL; Z68749; CAC35817.1; -;
 CC EMBL; Z68219; CAC35817.1; JOINED.
 CC EMBL; Z68749; CAC35818.1; -;
 CC EMBL; Z68219; CAC35818.1; JOINED.
 CC PIR; T22793; T22793.
 CC PIR; T42760; T42760.
 CC PIR; T42990; T42990.
 CC HSP; P16109; 1FSB.
 CC IntAct; O77469; -;
 CC WormBase; WBGene0001403; fbl-1.
 CC WormPep; F56H11.1a; CE26701.
 CC WormPep; F56H11.1b; CE26702.
 CC WormPep; F56H11.1c; CE16142.
 CC InterPro; IPR000020; Anaphylatoxin.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR009030; Grow_fac_recept.
 CC Pfam; PF01821; ANATO; 2.
 CC Pfam; PF00008; EGF; 5.
 CC SMART; SM00179; EGF_CA; 4.
 CC PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 4.
 CC PROSITE; PS01186; EGF_2; 5.
 CC PROSITE; PS50026; EGF_3; 4.
 CC PROSITE; PS01187; EGF_CA; 8.
 CC Alternative splicing; Calcium-binding; EGF-like domain;
 CC Extracellular matrix; Glycoprotein; Repeat; Signal.
 CC SIGNAL 1 17 Potential.
 CC CHAIN 18 798 Fibulin-1.

FT	DOMAIN	23	64	Anaphylatoxin-like 1.
FT	DOMAIN	65	96	Anaphylatoxin-like 2.
FT	DOMAIN	97	129	Anaphylatoxin-like 3.
FT	DOMAIN	155	194	EGF-like 1.
FT	DOMAIN	195	280	EGF-like 2, calcium-binding (Potential).
FT	DOMAIN	281	345	EGF-like 3, calcium-binding (Potential).
FT	DOMAIN	346	436	EGF-like 4, calcium-binding (Potential).
FT	DOMAIN	437	476	EGF-like 5, calcium-binding (Potential).
FT	DOMAIN	477	520	EGF-like 6, calcium-binding (Potential).
FT	DOMAIN	521	561	EGF-like 7, calcium-binding (Potential).
FT	DOMAIN	562	606	EGF-like 8, calcium-binding (Potential).
FT	DOMAIN	607	652	EGF-like 9, calcium-binding (Potential).
FT	DISULFID	23	49	By similarity.
FT	DISULFID	24	56	By similarity.
FT	DISULFID	37	57	By similarity.
FT	DISULFID	66	94	By similarity.
FT	DISULFID	79	95	By similarity.
FT	DISULFID	97	121	By similarity.
FT	DISULFID	98	128	By similarity.
FT	DISULFID	111	129	By similarity.
FT	DISULFID	159	168	By similarity.
FT	DISULFID	164	178	By similarity.
FT	DISULFID	180	279	By similarity.
FT	DISULFID	285	298	By similarity.
FT	DISULFID	292	307	By similarity.
FT	DISULFID	313	339	By similarity.
FT	DISULFID	350	363	By similarity.
FT	DISULFID	357	372	By similarity.
FT	DISULFID	394	406	By similarity.
FT	DISULFID	400	415	By similarity.
FT	DISULFID	422	435	By similarity.
FT	DISULFID	441	451	By similarity.
FT	DISULFID	446	460	By similarity.
FT	DISULFID	462	475	By similarity.
FT	DISULFID	481	495	By similarity.
FT	DISULFID	489	504	By similarity.
FT	DISULFID	506	519	By similarity.
FT	DISULFID	525	536	By similarity.
FT	DISULFID	532	545	By similarity.
FT	DISULFID	547	560	By similarity.
FT	DISULFID	566	581	By similarity.
FT	DISULFID	577	590	By similarity.
FT	DISULFID	592	605	By similarity.
FT	DISULFID	611	623	By similarity.
FT	DISULFID	616	632	By similarity.
FT	DISULFID	637	651	By similarity.
FT	VARSPPLIC	193	278	Missing (in isoform a and isoform b). /FTid=VSP_001387.
FT	VARSPPLIC	326	345	NNCP111NNTFNCYFFVE -> CR (in isoform a and isoform b). /FTid=VSP_001388.
FT	VARSPPLIC	390	390	Y -> CTSITCPNGYYPKNGMCND (in isoform a and isoform b). /FTid=VSP_001389.
FT	VARSPPLIC	650	798	RCNQPSACGLPEECVKVPLEFTYQFISLARAVPISSHRPA ITLRFQSAFNHADTEVNFPELQLTQIVGAPNVLPAIRANFL LOKGEKNSAVVTLRDSLDGPTVKLQLLLRMSKKGNFT YAANLIVDAARKSHNTVHPFLMKIR -> QIADGYSCKIV CSTEDTECLGNHTREVLVQFRAVPSLTKITISPIEVSRIVTH MGVPFSDYNDLDYVGQRHFRIVQERNIGIVQLVKPISGPTV ETIKVNIHTKSRGTGVILAFNEAIIIEISVSKYPP (in isoform b). /FTid=VSP_001390.
SQ	SEQUENCE	798 AA; 87205 MW; 38F1EE9ED54DBF9	CRC64;	
	Query Match	26.6%;	Score 344.5; DB 1; Length 798;	
	Best Local Similarity	34.2%;	Pred. No. 3.5e-20;	
	Matches	77; Conservative	26; Mismatches 89; Indels 33; Gaps 8;	
QY	5 DCINKYGS-----	-----PYTKNSGFATCVQNL	PDQCTPNPCDRKCTQACQDLMGNFF 52	
DB	405 ECVNTPGSRFCQKGNLCAHGYEVNGATGFCED--	VNECQGVVC---GSMCEINLPGYK 459		

FT	DOMAIN	2024	2067	TGFBP 8.	
FT	DOMAIN	2084	2125	EGF-like 33, calcium-binding.	
FT	DOMAIN	2126	2165	EGF-like 34, calcium-binding.	
FT	DOMAIN	2166	2206	EGF-like 35, calcium-binding.	
FT	DOMAIN	2207	2251	EGF-like 36, calcium-binding.	
FT	DOMAIN	2252	2293	EGF-like 37, calcium-binding.	
FT	DOMAIN	2307	2350	TGFBP 9.	
FT	DOMAIN	2363	2404	EGF-like 38, calcium-binding.	
FT	DOMAIN	2405	2445	EGF-like 39, calcium-binding.	
FT	DOMAIN	2446	2484	EGF-like 40, calcium-binding.	
FT	DOMAIN	2485	2527	EGF-like 41, calcium-binding.	
FT	DOMAIN	2528	2567	EGF-like 42, calcium-binding.	
FT	DOMAIN	2568	2609	EGF-like 43, calcium-binding.	
FT	DOMAIN	2610	2649	EGF-like 44, calcium-binding.	
FT	DISULFID	151	161	By similarity.	
FT	DISULFID	155	167	By similarity.	
FT	DISULFID	169	178	By similarity.	
FT	DISULFID	251	263	By similarity.	
FT	DISULFID	258	272	By similarity.	
FT	DISULFID	274	287	By similarity.	
FT	DISULFID	412	424	By similarity.	
FT	DISULFID	419	433	By similarity.	
FT	DISULFID	435	447	By similarity.	
FT	DISULFID	453	463	By similarity.	
FT	DISULFID	458	472	By similarity.	
FT	DISULFID	474	487	By similarity.	
FT	DISULFID	493	505	By similarity.	
FT	DISULFID	500	514	By similarity.	
FT	DISULFID	516	529	By similarity.	
FT	DISULFID	535	546	By similarity.	
FT	DISULFID	541	555	By similarity.	
FT	DISULFID	557	570	By similarity.	
FT	DISULFID	576	587	By similarity.	
FT	DISULFID	582	596	By similarity.	
FT	DISULFID	598	611	By similarity.	
FT	DISULFID	666	698	By similarity.	
FT	DISULFID	693	707	By similarity.	
FT	DISULFID	709	722	By similarity.	
FT	DISULFID	728	740	By similarity.	
FT	DISULFID	735	749	By similarity.	
FT	DISULFID	751	764	By similarity.	
FT	DISULFID	770	780	By similarity.	
FT	DISULFID	775	789	By similarity.	
FT	DISULFID	791	804	By similarity.	
FT	DISULFID	873	885	By similarity.	
FT	DISULFID	880	894	By similarity.	
FT	DISULFID	896	909	By similarity.	
FT	DISULFID	990	1002	By similarity.	
FT	DISULFID	997	1011	By similarity.	
FT	DISULFID	1013	1026	By similarity.	
FT	DISULFID	1032	1044	By similarity.	
FT	DISULFID	1039	1053	By similarity.	
FT	DISULFID	1055	1069	By similarity.	
FT	DISULFID	1075	1087	By similarity.	
FT	DISULFID	1082	1096	By similarity.	
FT	DISULFID	1098	1111	By similarity.	
FT	DISULFID	1117	1129	By similarity.	
FT	DISULFID	1124	1138	By similarity.	
FT	DISULFID	1140	1153	By similarity.	
FT	DISULFID	1159	1170	By similarity.	
FT	DISULFID	1166	1179	By similarity.	
FT	DISULFID	1181	1194	By similarity.	
FT	DISULFID	1200	1212	By similarity.	
FT	DISULFID	1207	1221	By similarity.	
FT	DISULFID	1223	1236	By similarity.	
FT	DISULFID	1242	1254	By similarity.	
FT	DISULFID	1249	1263	By similarity.	
FT	DISULFID	1265	1278	By similarity.	
FT	DISULFID	1284	1297	By similarity.	
Query Match 26.4%; Score 342.5; DB 1; Length 2809;					
Best Local Similarity 36.2%; Pred. No. 1.8e-19;					
Matches 77; Conservative . 21; Mismatches 70; Indels 45; Gaps 9;					
QY	11	GSPYTKNSGFATCQVNLPLDQCTP-NPCDRKGTQACODL-----MGNF 51			
Db	1084	GGTCTNTDGSYKC-----QCPGHETAKGT-ACEDIDECSLSDGLCPHQCVNVIGAF 1136			
QY	52	FCLCKAGMGG---RLCDKDVNECSQENGGLQICHNKPFGSHCSGFSLSDSGRTCOD 108			
Db	1137	QCSCHAGFQSTPDRQGVGDINECRVQNGGCDVHCINTEGSRVCSGGQSYSLMPDGRACAD 1196			
QY	109	IDECADS-EACGEARCKNLPGSYSLCDEGFAYSSQEKACDVDE-----CLQGRCEQ 160			
Db	1197	VDECEENPRVCDQGHCTNMPGGHRCCLCYDVGPMATPDMRTCDVDVDECDLNPHCILHGDC- 1255			
QY	161	VCVNSPGSYTCHCD---GRGLKLSODMDTCE 189			
Db	1256	---NKGSFVCHCQGLGYWRKGTGCSDDVDECE 1285			
RESULT 42					
FBL1_CHICK					
ID	FBL1_CHICK	STANDARD;	PRT;	704 AA.	
AC	O73775;	O73774;			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	10-OCT-2003	(Rel. 42, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Fibulin-1	precursor.			
CN	Name=FBLN1;				
OS	Gallus gallus	(Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;				
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORMS C AND D).				
RC	TISSUE=Embryo;				
RA	MEDLINE=99120531; PubMed=9923656; DOI=10.1016/S0945-053X(98)90114-7;				
RX	Barth J.L., Argreaves K.M., Roark E.F., Little C.D., Argreaves W.S.;				
RT	"Identification of chicken and C. elegans fibulin-1 homologs and				
RL	characterization of the C. elegans fibulin-1 gene."				
CC	Matrix Biol. 17:635-646(1998).				
CC	-!- FUNCTION: Incorporated into fibronectin-containing matrix fibers.				
CC	May play a role in cell adhesion and migration along protein				
CC	fibers within the extracellular matrix (ECM). Could be important				
CC	for certain developmental processes and contribute to the				
CC	supramolecular organization of ECM architecture, in particular to				
CC	those of basement membranes.				
CC	-!- SUBUNIT: Interacts with itself and with various extracellular				
CC	matrix components (By similarity).				
CC	-!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.				
CC	-!- ALTERNATIVE PRODUCTS:				
CC	Event=Alternative splicing; Named isoforms=2;				
CC	Name=D;				
CC	Isoid=O73775-2; Sequence=Displayed;				
CC	Name=C;				
CC	Isoid=O73775-1; Sequence=VSP_007378;				
CC	-!- SIMILARITY: Belongs to the fibulin family.				
CC	-!- SIMILARITY: Contains 3 anaphylatoxin-like domains.				
CC	-!- SIMILARITY: Contains 9 EGF-like domains.				
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or send an email to license@isb-sib.ch).					
DR	EMBL; AF051399; AAC05387.1; -				
DR	EMBL; AF051400; AAC05388.1; -				
DR	HSP; P01130; 1H28.				
DR	InterPro; IPR000020; Anaphylatoxin.				
DR	InterPro; IPR000152; Asx_hydroxyl_S.				
DR	InterPro; IPR000742; EGF_2.				


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DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF00008; EGF; 6.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 5.
DR PROSITE; PS01187; EGF_CA; 8.
DR PROSITE; PS01187; EGF_CA; 8.
KW Alternative splicing; Calcium-binding; EGF-like domain;
KW Extracellular matrix; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 25 Potential.
FT CHAIN 25 704 Fibrulin-1.
FT DOMAIN 33 74 Anaphylatoxin-like 1.
FT DOMAIN 75 109 Anaphylatoxin-like 2.
FT DOMAIN 110 142 Anaphylatoxin-like 3.
FT DOMAIN 177 216 EGF-like 1.
FT DOMAIN 217 262 EGF-like 2, calcium-binding (Potential).
FT DOMAIN 263 308 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 309 356 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 357 399 EGF-like 5, calcium-binding (Potential).
FT DOMAIN 400 441 EGF-like 6, calcium-binding (Potential).
FT DOMAIN 442 481 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 482 525 EGF-like 8, calcium-binding (Potential).
FT DOMAIN 526 579 EGF-like 9, calcium-binding (Potential).
FT DOMAIN 357 441 Self-association and FNI-binding (By similarity).
FT DISULFID 33 59 By similarity.
FT DISULFID 34 66 By similarity.
FT DISULFID 47 67 By similarity.
FT DISULFID 76 107 By similarity.
FT DISULFID 89 108 By similarity.
FT DISULFID 110 134 By similarity.
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FT DISULFID 181 191 By similarity.
FT DISULFID 187 200 By similarity.
FT DISULFID 202 215 By similarity.
FT DISULFID 221 234 By similarity.
FT DISULFID 228 243 By similarity.
FT DISULFID 249 261 By similarity.
FT DISULFID 267 280 By similarity.
FT DISULFID 274 289 By similarity.
FT DISULFID 295 307 By similarity.
FT DISULFID 313 326 By similarity.
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FT DISULFID 385 398 By similarity.
FT DISULFID 404 416 By similarity.
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FT DISULFID 466 480 By similarity.
FT DISULFID 486 499 By similarity.
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FT DISULFID 510 524 By similarity.
FT DISULFID 530 543 By similarity.
FT DISULFID 537 552 By similarity.
FT DISULFID 557 578 By similarity.
FT CARBOHYD 96 96 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 536 536 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 540 540 N-linked (GlcNAc...) (Potential).
FT VARSPIC 568 704 VLEKTDTRICKSCRPDNCVLPDPVHTVISHVLSLPTFR
EFTRPETILFLKRIPTYTPANQADIFDITEGNLRESFDII
KRYMDGMTGVVVRQVRPIVGPFFHILKLEMMNVVGGVWSHR
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FT NIVNVHIFVSEWTF -> RCERLPCNENKECOSLRLITYY
FT HLSFTNIQVPTDIFRMGPSNAVPGDKILLSIISGNQEGFF
FT TTKVNNHSGIVVMQRIETPRDLLITIQMLTRHGTVNTF
FT IAKLFVVFVSAQL (in isoform C).
FT /FTID=VSP 007378.
SQ SEQUENCE 704 AA; 78137 MW; D47D5A30D5E42932 CRC64;
Query Match 26.4%; Score 342; DB 1; Length 704;
Best Local Similarity 36.9%; Pred. No. 5e-20;
Matches 79; Conservative 29; Mismatches 74; Indels 32; Gaps 12;
QY 6 CINKYGS-----PYTKNSGFATCVQLNPDQCTPN--PCDRKGTQACQDLMGNF 51
DB 326 CLINTDGSYTCORISPSGCGHYLHNEGTRCVD--VDECSSSDQPCGE--GHVCINGPGNY 381
QY 52 FCLCKAGMG---GRLCDKDVNECSQENG--CLQICHNKPGRSFGHSGFELSDGRTC 106
DB 382 RCCEKSGVSVFVIVSRTC-IDINECRYPGRLCNHCENTPGSYCTCTGCTGFKLSDGRSC 440
QY 107 QDIDECADSEACGEARCKNLPGSYCLCDEGFAYSSQEK-ACRDVDECLQGR----CEQV 161
DB 441 EDLNEC-ESSPCSQ-ECANVYGSQYCYCRGFQSLSDIDGISCEDIDECALPTGHCISFR 498
QY 162 CVNSGSGSYTCHCDGRGGLKLSQDMTCEIDILPCV 195
DB 499 CINIFGSPQCTCPST-GYRLAPNARNQCQIDECV 531
RESULT 43
Q8NBH6 PRELIMINARY; PRT; 638 AA.
AC Q8NBH6;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein PSEC0266.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isoqai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075566; BAC11705.1; -
DR HSSP; P01330; 1HJ7.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01821; ANATO; 1.
DR Pfam; PF07645; EGF_CA; 8.
DR SMART; SM00179; EGF_CA; 7.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 8.
KW EGF-like domain.
SQ SEQUENCE 638 AA; 70577 MW; EBCODE3147A7621F CRC64;
Query Match 26.1%; Score 339; DB 2; Length 638;
Best Local Similarity 37.3%; Pred. No. 8.1e-20;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;
QY 6 CINKYGSPTKNSGFATCVQLNPDQCTPN--PCDRKGTQACQ 45
DB 260 CINTEGS-----YTCQKNVPCGRGYHLNEGTRCVDVDECAPPAEPCG-KG-HRCV 309
```


QY	6	CINKYGSPTKNSGFATCVQNI.P	-----DOCTP--NPCDRKGTQACQ 45
Db	325	CINTEGS	-----YTCQKVPNCGRGPHLNEEGTRCVDVDECAPPAFCG-KG-HRCV 374
QY	46	DLMGVFFCLCKAGWG	-----GRLCDKDVNECSOENG-CLQICHNKPGSPHCSCHSGFELS 100
Db	375	NSPGFRCBCECKGYFDGISRMC-VDVNECQRYPRGLCGHKHCENTLGSYLCSVGFRLS 433	
QY	101	SDGRTCQDIDECADSEACGEARCKNLPGSYSLCDBGFPAYSQGE-KACRDVDECLQGR-- 157	
Db	434	VDGRSCEDINECSSPCSQE--CANVYGSQYCCRGYQLSDVDGVTCTEDIDECALPTGG 491	
QY	158	--CEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCV 195	
Db	492	HICSYRCINIPGSFQSCSPS-SGYRLAPNGRNCQDIDECV 530	
RESULT 45			
Q99K58			
ID	Q99K58	PRELIMINARY;	PRT; 1174 AA.
AC	Q99K58;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Fbln2 protein.		
GN	Name=Fbln2;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_Taxid=10090;			
OX	[1]		
SEQUENCE FROM N.A.			
RC	STRAIN=mix FVB/N;		
RC	TISSUE=Mammary tumor;		
RY	MEDLINE=2288257; PubMed=1247732; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RP	[2]		
SEQUENCE FROM N.A.			
RC	STRAIN=mix FVB/N;		
RC	TISSUE=Mammary tumor;		
RL	Strausberg R.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC005443; AAH05443.1; -.		
DR	HSSP; P00736; 1APO.		
DR	MGI; 95488; Fbln2.		
DR	GO; GO:0005515; F.protein binding; IPI.		
DR	InterPro; IPR000020; Anaphylatoxin.		
DR	InterPro; IPR000152; Asx_hydroxyl_S.		
DR	InterPro; IPR000742; EGF 2.		
DR	InterPro; IPR001881; EGF Ca.		
DR	InterPro; IPR006209; EGF_like.		
DR	InterPro; IPR009030; Grow_fac_recept.		
DR	Pfam; PF01821; ANATO; 2.		
DR	Pfam; PF07645; EGF CA; 9.		
DR	SMART; SM00104; ANATO; 3.		

Query Match 26.1%; Score 339; DB 1; Length 703;
Best Local Similarity 37.3%; Pred. No. 8.9e-20;
Matches 82; Conservative 23; Mismatches 71; Indels

```
DR SMART: SM00179; EGF_CA; 9.
DR PROSITE, PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE, PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE, PS00010; ASX HYDROXYL; 5.
DR PROSITE, PS01186; EGF_2; 5.
DR PROSITE, PS00026; EGF_3; 3.
DR PROSITE, PS01187; EGF_CA; 9.
KW EGF-like domain.
SQ SEQUENCE 1174 AA; 126460 MW; 8D628AC710FBA6B8 CRC64;

Query Match      26.1%; Score 339; DB 2; Length 1174;
Best Local Similarity 36.6%; Pred. No. 1.5e-19;
Matches 78; Conservative 27; Mismatches 68; Indels 40; Gaps 11;

QY 6 CLNKYS-----PYTNSGFATCVQLPDQCTPNPCD-----RKGT-QACQDLIM 48
DB 817 CINTVGSYTCQRNPLVCGRGYHANESECVN-----VNECETGVHRCGEGQLCYNLP 869

QY 49 GNFFCLCKAGWG----GRLCDKDVNCEQENG--CLQICHNKPGSFHSCSGFELSSDG 103
DB 870 GSYRCDCKPGFDFAFGTIC-IDVNECWVSPGLCHQHTCENTPGSYRSCAGFLLAADG 928

QY 104 RTCQIDECADSEACGEARCKNLPGSYCLCDGFPAYSSQEKACRDVDECIQGR---CEQ 160
DB 929 KHCEDVNEC-ETRRCSQ-ECANIYGSQCYCRQGYQLAEDGHTCTDIDECAGGAGILCTF 986

QY 161 VCVNSPFGSYTCHDCRGGGLKLS-----QDMDC 188
DB 987 RCNVNPGSYQACPEQGYTMANGRSCKDLDEC 1019

RESULT 46
FBL2_MOUSE
ID FBL2_MOUSE STANDARD; PRT; 1221 AA.
AC P37889; Q9WUI2;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibulin-2 precursor.
GN Name=Fbln2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-35.
RC TISSUE=Fibroblast;
RX MEDLINE=94064787; PubMed=82451330; DOI=10.1083/jcb.123.5.1269;
RA Pan T.-C., Sasaki T., Zhang R.-Z., Faessler R., Timpl R., Chu M.-L.;
RT "Structure and expression of fibulin-2, a novel extracellular matrix
RT protein with multiple EGF-like repeats and consensus motifs for
RT calcium binding.";
RL J. Cell Biol. 123:1269-1277(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99337686; PubMed=10406956;
RA Graessel S., Sicot F.-X., Gotta S., Chu M.-L.;
RT "Mouse fibulin-2 gene. Complete exon-intron organization and promoter
RT characterization.";
RL Eur. J. Biochem. 263:471-477(1999).
RN [3]
RP DEVELOPMENTAL STAGE.
RX MEDLINE=97003230; PubMed=8850569;
RX DOI=10.1002/(SICI)1097-0177(199603)205:3<348::AID-AJAL3>3.0.CO;2-0;
RA Zhang H.-Y., Timpl R., Sasaki T., Chu M.-L., Ekblom P.;
RT "Fibulin-1 and fibulin-2 expression during organogenesis in the
RT developing mouse embryo.";
RL Dev. Dyn. 205:348-364(1996).
RN [4]
RP BINDING TO LAMA2.
RX MEDLINE=99146904; PubMed=10022829; DOI=10.1093/emboj/18.4.863;
RA Talts J.F., Andac Z., Goehring W., Brancaccio A., Timpl R.;
RT "Binding of the G domains of laminin alpha1 and alpha2 chains and
perlecan to heparin, sulfatides, alpha-dystroglycan and several
extracellular matrix proteins.";
EMBO J. 18:863-870(1999).
[5]
DOWN-REGULATION BY GLUCOCORTICOIDS.
MEDLINE=21600963; PubMed=11737251;
Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
"Glucocorticoids down-regulate the extracellular matrix proteins
fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
Eur. J. Haematol. 67:176-184(2001).
CC FUNCTION: Its binding to fibronectin and some other ligands is
calcium dependent.
CC SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2.
CC SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
Name=1;
IsoId=P37889-1; Sequence=Displayed;
Name=2; Synonyms=EGF3-less;
IsoId=P37889-2; Sequence=VSP_001391;
TISSUE SPECIFICITY: Component of both basement membranes and other
connective tissues.
DEVELOPMENTAL STAGE: The differential expression of the fibulin
family contributes to the formation of molecularly distinct
extracellular matrices already during early developmental stages
of a large number of tissues.
INDUCTION: Glucocorticoids suppressed mRNA expression and protein
synthesis.
SIMILARITY: Belongs to the fibulin family.
SIMILARITY: Contains 3 anaphylatoxin-like domains.
SIMILARITY: Contains 11 EGF-like domains.
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or send an email to license@isb-sib.ch).
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EMBL; X75285; CAA53040.1; -.
EMBL; AF135253; AAD34456.1; JOINED.
EMBL; AF135239; AAD34456.1; JOINED.
EMBL; AF135240; AAD34456.1; JOINED.
EMBL; AF135241; AAD34456.1; JOINED.
EMBL; AF135242; AAD34456.1; JOINED.
EMBL; AF135243; AAD34456.1; JOINED.
EMBL; AF135244; AAD34456.1; JOINED.
EMBL; AF135245; AAD34456.1; JOINED.
EMBL; AF135246; AAD34456.1; JOINED.
EMBL; AF135247; AAD34456.1; JOINED.
EMBL; AF135248; AAD34456.1; JOINED.
EMBL; AF135249; AAD34456.1; JOINED.
EMBL; AF135250; AAD34456.1; JOINED.
EMBL; AF135251; AAD34456.1; JOINED.
EMBL; AF135252; AAD34456.1; JOINED.
PIR; A49457; A49457.
HSSP; P00736; 1APQ.
MGD; MGI:95488; Fbln2.
GO; GO:0005515; F:protein binding; IPI.
InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR009030; Grow_fac_recept.
Pfam; PF01821; ANATO; 2.
Pfam; PF00008; EGF; 5.
SMART; SM00104; ANATO; 3.
SMART; SM00179; EGF_CA; 9.
PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
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DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 5.
DR PROSITE; PS01187; EGF_CA; 10.
KW Alternative splicing; Calcium-binding; Direct protein sequencing;
KW EGF-like domain; Extracellular matrix; Glycoprotein; Plasma; Repeat;
KW Signal.
FT SIGNAL 1 26
FT CHAIN 27 1221 Fibulin-2.
FT DOMAIN 27 434 N.
FT DOMAIN 27 176 Subdomain NA (Cys-rich).
FT DOMAIN 177 434 Subdomain NB (Cys-free).
FT DOMAIN 435 477 Anaphylatoxin-like 1.
FT DOMAIN 478 510 Anaphylatoxin-like 2.
FT DOMAIN 511 543 Anaphylatoxin-like 3.
FT DOMAIN 594 635 EGF-like 1, calcium-binding (Potential).
FT DOMAIN 669 708 EGF-like 2.
FT DOMAIN 709 755 EGF-like 3, calcium-binding (Potential).
FT DOMAIN 756 800 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 801 846 EGF-like 5, calcium-binding (Potential).
FT DOMAIN 847 894 EGF-like 6, calcium-binding (Potential).
FT DOMAIN 895 937 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 938 979 EGF-like 8, calcium-binding (Potential).
FT DOMAIN 980 1018 EGF-like 9, calcium-binding (Potential).
FT DOMAIN 1019 1061 EGF-like 10, calcium-binding (Potential).
FT DOMAIN 1062 1106 EGF-like 11, calcium-binding (Potential).
FT DOMAIN 1111 1221 Domain III.
FT SITE 421 423 Cell attachment site (Potential).
FT DISULFID 435 462 By similarity.
FT DISULFID 436 469 By similarity.
FT DISULFID 449 470 By similarity.
FT DISULFID 479 508 By similarity.
FT DISULFID 492 509 By similarity.
FT DISULFID 511 535 By similarity.
FT DISULFID 512 542 By similarity.
FT DISULFID 525 543 By similarity.
FT DISULFID 598 610 By similarity.
FT DISULFID 606 619 By similarity.
FT DISULFID 621 634 By similarity.
FT DISULFID 673 683 By similarity.
FT DISULFID 679 692 By similarity.
FT DISULFID 694 707 By similarity.
FT DISULFID 713 726 By similarity.
FT DISULFID 720 735 By similarity.
FT DISULFID 742 754 By similarity.
FT DISULFID 805 818 By similarity.
FT DISULFID 812 827 By similarity.
FT DISULFID 833 845 By similarity.
FT DISULFID 899 912 By similarity.
FT DISULFID 906 921 By similarity.
FT DISULFID 923 936 By similarity.
FT DISULFID 942 954 By similarity.
FT DISULFID 950 963 By similarity.
FT DISULFID 965 978 By similarity.
FT DISULFID 984 993 By similarity.
FT DISULFID 989 1007 By similarity.
FT DISULFID 1004 1017 By similarity.
FT DISULFID 1023 1035 By similarity.
FT DISULFID 1031 1044 By similarity.
FT DISULFID 1046 1060 By similarity.
FT DISULFID 1066 1079 By similarity.
FT DISULFID 1073 1088 By similarity.
FT DISULFID 1093 1105 By similarity.
FT CARBOHYD 179 179 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 497 497 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 737 737 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1072 1072 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 709 755 Missing (in isoform 2).
FT /FTID=VSP_001391.
FT HSRKYAAGHTVHLSSCRAC -> TVAVSICWYRPLLP
FT 140 159 GF (in Ref. 2).
FT 348 348 S -> L (in Ref. 2).
FT 348 348

FT CONFLICT 507 507 Q -> QQ (in Ref. 2).
FT CONFLICT 1102 1102 Q -> E (in Ref. 2).
SQ SEQUENCE 1221 AA; 131818 MW; 87DB2A10A8FDC45F CRC64;

Query Match 26.1%; Score 339; DB 1; Length 1221;
Best Local Similarity 36.6%; Pred. No. 1.5e-19;
Matches 78; Conservative 27; Mismatches 68; Indels 40; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCD-----RKGT-QACQDLM 48
    |||||
Db 864 CINTVGSYTCQRNPLVCGRGYHANEESGCVD-----VNECETGVHRCGEGQLCYNLP 916

QY 49 GNFFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNVPGSFHCSHSGFELSSDG 103
    ||:|||||
Db 917 GSYRCDCRKFQORDAFGRTC-IDVNECWVSPGRLCQHTCENTFGSYRCSCAAGFLLAADG 975

QY 104 RYCQDIDECADSEAGEARCKNLPGSYCLCDGEPAYSQEKACRDVDVDCLOGR---CRQ 160
    ||:|||||
Db 976 KCEVDNEC-ETRRCSQ-ECANIYGSYQCYKQGLAEHGHTCTDIDECAGQAGILCTF 1033

QY 161 VCVNPSGYSYTHCDGRGGLKLS-----QDMDTTC 188
    |||||
Db 1034 RCVNVPGSYQCACPRQGYTMANGRSCKDLDEC 1066

RESULT 47
QY9Y3V7 PRELIMINARY; PRT; 576 AA.
ID QY9Y3V7
AC QY9Y3V7
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp586A1519 (Fragment).
GN Name=DKFZp586A1519;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050095; CAB43267.1;
DR HSSP; P00736; 1APO.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF07645; EGF_CA; 9.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 9.
KW EGF-like domain; Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 576 AA; 63274 MW; FF2F0E9B185D8AC3 CRC64;

Query Match 26.1%; Score 338; DB 2; Length 576;
Best Local Similarity 38.0%; Pred. No. 8.8e-20;
Matches 79; Conservative 31; Mismatches 74; Indels 24; Gaps 12;

QY 6 CINKYGSPTKNSGFATCVQ--NLFPDQCTP----NPCD-----RKGT-QACQDLMGNFFCL 54
    |||||
Db 219 CINTVGS-YTCQRNPLICARGVHASDDGTCKVDVNECETGVHRCGEGQVCHNLPGSYRCD 277

QY 55 CKAGWG-----GRLCDKDVNECSQENG-CLQICHNVPGSFHCSHSGFELSSDGTQDII 109
    |||||
Db 55 CKAGWG-----GRLCDKDVNECSQENG-CLQICHNVPGSFHCSHSGFELSSDGTQDII 109
    |||||
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Db      278 CKAGQRFDAFRGC-IDVNECWASPERLCQHTCENTILSYRCSCASGFLAAGDKRCBDV 336
Qy      110 DECADESAGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLOGR---CEQVCVNSP 166
Db      337 NEC-EAQRCSQ-ECANIYGSYQCYCRQSGYQAEDGHTCTDIDECAQAGAILCTFFRCLNVP 394
Qy      167 GSYTCHCDGRGGLKLSQMDTCEIDLPC 194
Db      395 GSYQCACPEQ-GYTTWANGRSCKVDDEC 421

RESULT 48
FBL2_HUMAN
ID   FBL2_HUMAN          STANDARD;          PRT;   1184 AA.
AC   P98035;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Fibulin-2 precursor.
GN   Name=FBLN2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95104855; PubMed=7806230;
RA   Zhang R.-Z., Pan T.-C., Zhang Z.-Y., Mattei M.-G., Timpl R.,
RA   Chu M.-L.;
RT   "Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping
RT   of the gene on human and mouse chromosomes.";
RL   Genomics 22:425-430(1994).
RN   [2]
RP   DEVELOPMENTAL STAGE.
RX   MEDLINE=96301678; PubMed=8737292;
RA   Miose N., Gotz W., Sasaki T., Chu M.-L., Timpl R., Herken R.;
RT   "The extracellular matrix proteins fibulin-1 and fibulin-2 in the
RT   early human embryo.";
RL   Histochem. J. 28:109-116(1996).
CC   -!- FUNCTION: Its binding to fibronectin and some other ligands is
CC   calcium dependent.
CC   -!- SUBUNIT: Homotrimer; disulfide-linked. Interacts with LAMA2 (By
CC   similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC   -!- TISSUE SPECIFICITY: Component of both basement membranes and other
CC   connective tissues. Expressed in heart, placenta and ovary.
CC   -!- DEVELOPMENTAL STAGE: Widely expressed during embryonic
CC   development. Primarily detected within the neuroepithelium, spinal
CC   ganglia and peripheral nerves.
CC   -!- SIMILARITY: Belongs to the fibulin family.
CC   -!- SIMILARITY: Contains 3 anaphylatoxin-like domains.
CC   -!- SIMILARITY: Contains 11 EGF-like domains.
-----
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DR   EMBL; X82494; CAA57876.1; -.
DR   FIR; A55184; A55184.
DR   HSSP; P00736; LAPO.
DR   Genew; HGNC:3601; FBLN2.
DR   MIM; 135821; -.
DR   GO; GO:0005578; C:extracellular matrix; TAS.
DR   GO; GO:0005509; F:calcium ion binding; TAS.
DR   GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
DR   InterPro; IPR000020; F:extracellular matrix structural constituent; TAS.
DR   InterPro; IPR000152; Asx hydroxyl_s.
DR   InterPro; IPR000742; EGF_2.

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DR   InterPro; IPR001881; EGF Ca.
DR   InterPro; IPR006209; EGF_like.
DR   InterPro; IPR009030; Grow_fac_recept.
DR   Pfam; PF01821; ANATO; 2.
DR   Pfam; PF00008; EGF; 5.
DR   SMART; SMO0104; ANATO; 3.
DR   SMART; SMO0179; EGF CA; 9.
DR   PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR   PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR   PROSITE; PS00010; ASX_HYDROXYL; 5.
DR   PROSITE; PS00022; EGF_1; FALSE_NEG.
DR   PROSITE; PS01186; EGF_2; 5.
DR   PROSITE; PS00026; EGF_3; 4.
DR   PROSITE; PS01187; EGF_CA; 9.
KW   Calcium-binding; EGF-like domain; Extracellular matrix; Glycoprotein;
KW   Plasma; Repeat; Signal.
FT   SIGNAL      1..27   Potential.
FT   CHAIN       28..1184 Fibulin-2.
FT   DOMAIN      28..444 N.
FT   DOMAIN      28..444 Subdomain NA (Cys-rich).
FT   DOMAIN      178..444 Subdomain NB (Cys-free).
FT   DOMAIN      445..480 Anaphylatoxin-like 1.
FT   DOMAIN      488..519 Anaphylatoxin-like 2.
FT   DOMAIN      521..553 Anaphylatoxin-like 3.
FT   DOMAIN      604..645 EGF-like 1, calcium-binding.
FT   DOMAIN      679..718 EGF-like 2.
FT   DOMAIN      719..763 EGF-like 3, calcium-binding.
FT   DOMAIN      764..809 EGF-like 4, calcium-binding.
FT   DOMAIN      810..857 EGF-like 5, calcium-binding.
FT   DOMAIN      858..900 EGF-like 6, calcium-binding.
FT   DOMAIN      901..942 EGF-like 7, calcium-binding.
FT   DOMAIN      943..981 EGF-like 8, calcium-binding.
FT   DOMAIN      982..1024 EGF-like 9, calcium-binding.
FT   DOMAIN      1025..1069 EGF-like 10, calcium-binding.
FT   DOMAIN      1070..1184 Domain III.
FT   DISULFID    445..472 By similarity.
FT   DISULFID    446..479 By similarity.
FT   DISULFID    459..480 By similarity.
FT   DISULFID    489..518 By similarity.
FT   DISULFID    502..519 By similarity.
FT   DISULFID    521..545 By similarity.
FT   DISULFID    522..552 By similarity.
FT   DISULFID    535..553 By similarity.
FT   DISULFID    608..620 By similarity.
FT   DISULFID    616..629 By similarity.
FT   DISULFID    631..644 By similarity.
FT   DISULFID    689..702 By similarity.
FT   DISULFID    704..717 By similarity.
FT   DISULFID    723..736 By similarity.
FT   DISULFID    730..745 By similarity.
FT   DISULFID    751..762 By similarity.
FT   DISULFID    768..781 By similarity.
FT   DISULFID    775..790 By similarity.
FT   DISULFID    796..808 By similarity.
FT   DISULFID    814..827 By similarity.
FT   DISULFID    821..836 By similarity.
FT   DISULFID    843..856 By similarity.
FT   DISULFID    862..875 By similarity.
FT   DISULFID    884..889 By similarity.
FT   DISULFID    886..899 By similarity.
FT   DISULFID    905..917 By similarity.
FT   DISULFID    913..926 By similarity.
FT   DISULFID    928..941 By similarity.
FT   DISULFID    947..956 By similarity.
FT   DISULFID    952..965 By similarity.
FT   DISULFID    967..980 By similarity.
FT   DISULFID    986..998 By similarity.
FT   DISULFID    994..1007 By similarity.
FT   DISULFID    1009..1023 By similarity.
FT   DISULFID    1029..1042 By similarity.
FT   DISULFID    1036..1051 By similarity.
FT   DISULFID    1056..1068 By similarity.

```

FT CARBOHYD 180 180 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1184 AA; 126543 MW; CA48490A55F9EC5D CRC64;
Query Match 26.0%; Score 337; DB 1; Length 1184;
Best Local Similarity 36.4%; Pred. No. 2.2e-19;
Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;
QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCD-----RKGT-QACQDILM 48
Db 827 CINTVGSYTCQRPNICARGYHASDDGAKCVD-----VNECEGVHRCGEGQVCHNLP 879
QY 49 GNFFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPFSCHSGFELSSDG 103
Db 880 GSYRCDCKAGFQDAFGRGC-IDVNECWASPGRLCQHTCENTLGSYRCSASCAGFLAADG 938
QY 104 RTCODIDECADSEACGEARKNLPSYCLDEGFAYSSQKACRDVDECLOGR---CEQ 160
Db 939 KRCEVDNEC-EAQRCSQ-ECANIYGSQYCRQGYQLAEDGHTCTDIDECAGAGILCTF 996
QY 161 VCVNSPGSYTCHDGRGGLKLSQDMDCEDILPC 194
Db 997 RCLNVPSGYQCACPEQ-GYTMANGRSCKDVDEC 1029
RESULT 49
Q86V58 PRELIMINARY; PRT; 1184 AA.
AC Q86V58;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibulin 2.
GN Name=FBLN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguillano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gichwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051690; AAH51690.1; --
DR HSSP; P00736; IAPQ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR00152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF07645; EGF_CA; 9.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 9.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 9.
KW EGF-like domain.
SQ SEQUENCE 1184 AA; 126507 MW; 4240CD6ADBB9EC5D CRC64;
Query Match 26.0%; Score 337; DB 2; Length 1184;
Best Local Similarity 36.4%; Pred. No. 2.2e-19;
Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;
QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDQCTPNPCD-----RKGT-QACQDILM 48
Db 827 CINTVGSYTCQRPNICARGYHASDDGAKCVD-----VNECEGVHRCGEGQVCHNLP 879
QY 49 GNFFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPFSCHSGFELSSDG 103
Db 880 GSYRCDCKAGFQDAFGRGC-IDVNECWASPGRLCQHTCENTLGSYRCSASCAGFLAADG 938
QY 104 RTCODIDECADSEACGEARKNLPSYCLDEGFAYSSQKACRDVDECLOGR---CEQ 160
Db 939 KRCEVDNEC-EAQRCSQ-ECANIYGSQYCRQGYQLAEDGHTCTDIDECAGAGILCTF 996
QY 161 VCVNSPGSYTCHDGRGGLKLSQDMDCEDILPC 194
Db 997 RCLNVPSGYQCACPEQ-GYTMANGRSCKDVDEC 1029
RESULT 50
Q8UIU0 PRELIMINARY; PRT; 1231 AA.
ID Q8UIU0;
AC Q8UIU0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fibulin 2.
GN Name=FBLN2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Li D., Marian A.J., Roberts R.;
RT "Identification of a novel alternatively spliced isoform of human
fibulin-2 gene abundantly expressed in heart and genetic evaluation in
patients with ARVD.";
RT (In) Unknown A. (eds.);
RL ABSTRACTS OF THE 52ND ANNUAL MEETING OF THE AMERICAN SOCIETY OF HUMAN
GENETICS., pp.323-0, Unknown Publisher (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Li D., Roberts R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY130459; AAN05436.1; --
DR HSSP; P00736; IAPQ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000020; Anaphylatoxin.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.

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DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF01821; ANATO; 2.
DR Pfam; PF07645; EGF_CA; 10.
DR SMART; SM00104; ANATO; 3.
DR SMART; SM00179; EGF_CA; 8.
DR PROSITE; PS01177; ANAPHYLATOXIN_1; 3.
DR PROSITE; PS01178; ANAPHYLATOXIN_2; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 9.
KW EGF-like domain.
SQ SEQUENCE 1231 AA; 131789 MW; 95D69EB2082952A7 CRC64;

Query Match 26.0%; Score 337; DB 2; Length 1231;
Best Local Similarity 36.4%; Pred. No. 2.2e-19;
Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCYQNLPDQCTPNPCD----RKGT-QACQDLM 48
DB 874 CINTVGSYTCORNPLICARGYHASDDGAKVD-----VNECETGVHRCGEGQVCHNLP 926

QY 49 GNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPSSFHCSHSGFELSDDG 103
DB 927 GSYRCDCKAGFORDAFGRCC-IDVNECWASPGRLCQHTCENTLGSYRCSGFLAARDG 985

QY 104 RTCQDIDECADSEACGEARCKNLPGSYCLDEGFAYSQEKACRDVDECIQGR---CEQ 160
DB 986 KRCEQVNEC-EAQRCSQ-ECANIYGSYQCYCRQYQLAEDGHTCTDIDECAGAGILCTF 1043

QY 161 VCVNSPGSYTCHCDGRGGGLKLSQDMDTCEDILPC 194
DB 1044 RCLNVPGSYQCACPEQ-GYTMANGRSCKDVDEC 1076
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Search completed: July 7, 2005, 09:39:25
Job time : 322.706 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2005, 08:53:50 ; Search time 61.1154 Seconds
(without alignments)
357.377 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PRVLDCKNGSPYTKNSGF.....LGRMFGTPIRLRFKRLQP 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1297	100.0	678	2	B48089	growth arrest-spec
2	1117	86.1	674	2	I55476	growth potentiatin
3	1113	85.8	673	2	A48089	growth arrest-spec
4	609.5	47.0	642	2	S53434	plasma protein S p
5	601.5	46.4	676	1	KXHU5	plasma protein S p
6	596.5	46.0	675	1	KXBOS	plasma protein S p
7	593.5	45.8	642	2	S53433	plasma protein S p
8	591.5	45.6	675	1	KXMS5	plasma protein S -
9	586.5	45.2	645	2	S38819	plasma protein S -
10	585.5	45.1	675	1	KXRTS	plasma protein S p
11	362	27.9	685	2	S78040	fibulin, splice fo
12	362	27.9	705	2	S34968	fibulin, splice fo
13	349.5	26.9	2871	2	A55567	fibillin I - bovi
14	348.5	26.9	3002	2	A47221	fibillin-1 precu
15	345	26.6	2871	2	A55624	fibillin-1 precu
16	344.5	26.6	589	2	T43210	fibulin-1D precu
17	344.5	26.6	689	2	T42760	fibulin, splice fo
18	344.5	26.6	712	2	T42990	fibulin 1, splice
19	344.5	26.6	798	2	T22793	hypothetical prote
20	339	26.1	601	2	B36346	fibulin 1 precu
21	339	26.1	683	2	C36346	fibulin 1 precu
22	339	26.1	1221	2	A49457	fibulin-2 precu
23	337	26.0	1184	2	A55184	fibulin-2 precu
24	331.5	25.6	2918	2	A54105	transforming growt
25	330.5	25.5	1394	2	A35626	fibillin-2 precu
26	326.5	25.2	2907	2	A57278	fibillin-2 precu
27	321	24.7	387	2	I38449	extracellular prot
28	320.5	24.7	1820	2	A55494	latent transformin
29	320	24.7	493	2	JC5621	epidermal growth f

30	319.5	24.6	1251	2	A57293	latent transformin
31	319.5	24.6	1620	2	T27283	hypothetical prote
32	319.5	24.6	1712	2	A38261	masking protein pr
33	315.5	24.3	741	2	T46488	hypothetical prote
34	312	24.1	886	2	A57172	probable hormone r
35	310.5	23.9	1574	2	T13954	MEGF6 protein - ra
36	299.5	23.1	2321	2	S78549	notch3 protein - h
37	291.5	22.5	2318	2	S45306	notch3 protein - h
38	278	21.4	3507	2	T34513	hypothetical prote
39	275.5	21.2	1408	2	S16148	gene serrate prote
40	274	21.1	2555	2	A40043	notch protein homo
41	272	21.0	2703	1	A24420	notch protein - fr
42	271.5	20.9	1220	2	A56136	jagged protein pre
43	270.5	20.9	1203	2	A49175	Notch B protein -
44	270.5	20.9	2352	2	T30201	Notch homolog prot
45	270	20.8	2437	2	S42612	transmembrane prot
46	266	20.5	1964	2	T09059	notch4 - mouse
47	265.5	20.5	2471	2	A49128	cell-fate determin
48	264	20.4	2139	2	A35672	crumbs protein - f
49	264	20.4	2531	2	T31070	notch homolog - se
50	263.5	20.3	3623	2	T08618	intrinsic factor-B
51	262.5	20.2	1081	2	T31329	receptor tyrosine
52	262.5	20.2	2524	2	A35844	Xotch protein - Af
53	262.5	20.2	2531	2	A46019	notch-1 protein -
54	259.5	20.0	1084	2	A40136	fibropellin Ia - s
55	259.5	20.0	2531	2	S18188	notch protein homo
56	257	19.8	577	2	A60501	thrombomodulin pre
57	251.5	19.4	1106	2	T18739	hypothetical prote
58	251	19.4	1247	1	MMHND	nidogen precursor
59	251	19.4	1376	2	G00043	osteonidogen - hum
60	249.5	19.2	1245	1	MMMSND	nidogen precursor
61	249	19.2	575	1	THHUB	thrombomodulin pre
62	248.5	19.2	511	2	T17298	hypothetical prote
63	246	19.0	3871	2	T22812	hypothetical prote
64	244.5	18.9	722	2	I48324	DELTA-like 1 - mou
65	244	18.8	851	2	A48825	Notch homolog Motc
66	237	18.3	3623	2	T09456	intrinsic factor-B
67	234	18.0	570	2	A48836	fibropellin C prec
68	232	17.9	1372	2	T25933	hypothetical prote
69	231	17.8	387	2	B49175	Notch A protein -
70	227.5	17.5	860	1	QRHULD	LDL receptor precu
71	227.5	17.5	1687	2	T30176	EGF repeat transme
72	225.5	17.4	1531	2	T42218	slit-1 protein hom
73	224	17.3	869	1	JC4858	LDL receptor prec
74	224	17.3	1295	2	A32901	glp1 protein precu
75	224	17.3	1847	2	T18308	probable vitellog
76	222	17.1	473	2	A56175	adhesive plaque pr
77	222	17.1	728	2	I50719	C-Delta-1 - chicke
78	221.5	17.1	558	2	T17324	hypothetical prote
79	220.5	17.0	356	2	A25918	thrombomodulin - b
80	220	17.0	1217	1	EGMSMG	epidermal growth f
81	219.5	16.9	996	2	JE0237	apolipoprotein B r
82	218.5	16.8	1207	1	EGHU	epidermal growth f
83	216.5	16.7	1429	2	S06434	homeotic protein l
84	215.5	16.6	1025	2	T42626	secreted leucine-r
85	214	16.5	833	2	S19087	gene Delta protein
86	211	16.3	742	2	I37225	leucocyte antigen
87	211	16.3	832	2	A31246	neurogenic protein
88	211	16.3	880	2	S00670	neurogenic repetit
89	211	16.3	1133	1	EGRT	epidermal growth f
90	209.5	16.2	879	1	QRRTLD	LDL receptor precu
91	209	16.1	854	1	QRHYLD	LDL receptor precu
92	208.5	16.1	810	2	T10756	Nel-homolog protei
93	208	16.0	1984	2	T13171	probable vitellog
94	205	15.8	1069	2	T42681	hypothetical prote
95	205	15.8	1523	2	T13953	MEGF5 protein - ra
96	204.5	15.8	642	1	S52111	uromodulin precu
97	204	15.7	1722	2	S89753	protein F11C7.4 [1
98	203.5	15.7	640	1	A30452	uromodulin precu
99	201.5	15.5	862	1	QRMSLD	LDL receptor precu
100	201	15.5	4544	1	S02392	alpha-2-macroglobu
101	200	15.4	835	2	JP0076	nel protein - chic
102	200	15.4	909	1	QRXLL2	LDL receptor 2 pre

103	199.5	15.4	3051	2	S42373	hypothetical prote	176	157	12.1	1170	1	TSHUP1	thrombospondin 1 p
104	199	15.3	4753	1	A47437	LDL receptor-relat	177	157	12.1	1584	2	T22674	hypothetical prote
105	198	15.3	293	2	B26637	neurogenic repetit	178	156.5	12.1	1357	2	T16860	hypothetical prote
106	197.5	15.2	644	1	A40212	uromodulin precurs	179	155.5	12.0	915	2	T21773	hypothetical prote
107	197.5	15.2	644	2	I84634	Tamm-Horsfall prot	180	155.5	12.0	927	2	T21772	hypothetical prote
108	197.5	15.2	4543	1	A53102	alpha-2-macroglobu	181	155.5	12.0	3672	2	T23433	hypothetical prote
109	197	15.2	863	1	S51789	VLDL receptor prec	182	155.5	12.0	3704	2	T37316	probable laminin a
110	197	15.2	873	1	I48952	VLDL receptor prec	183	155.5	12.0	5147	1	IJFFTM	cadherin-related t
111	196	15.1	4545	1	S25111	alpha-2-macroglobu	184	155	12.0	1353	1	JH0675	restrictin precurs
112	195	15.0	909	1	QRXL11	LDL receptor 1 pre	185	154.5	11.9	618	2	T00476	probable vacuolar
113	194.5	15.0	837	1	A29512	LDL receptor precu	186	153	11.8	416	1	KFBO	coagulation factor
114	193.5	14.9	308	2	JC7125	epidermal growth f	187	153	11.8	502	2	T20130	hypothetical prote
115	193	14.9	873	1	QRREVD	VLDL receptor prec	188	153	11.8	647	2	A43902	tenascin - eastern
116	191.5	14.8	601	2	T22025	hypothetical prote	189	153	11.8	925	2	T37475	lipoprotein recept
117	191.5	14.8	601	2	D89711	protein F40E10.4 (190	152.5	11.8	661	2	T42754	hypothetical prote
118	190	14.6	873	1	A49729	VLDL receptor prec	191	152	11.7	3635	2	T10053	laminin alpha 5 ch
119	186.5	14.4	4660	2	T42737	gp330 protein prec	192	150	11.6	461	1	KFHU	coagulation factor
120	185.5	14.3	383	2	S53716	delta-like homeoti	193	150	11.6	1107	2	T15884	hypothetical prote
121	185.5	14.3	686	2	JC7569	Delta-4 protein -	194	149.5	11.5	293	2	T09065	hypothetical prote
122	185	14.3	5175	2	T20992	hypothetical prote	195	149	11.5	396	1	KXBOZ	plasma protein 2 -
123	185	14.3	5198	2	T43290	hemocentin precurs	196	149	11.5	956	2	A57121	thrombospondin 3 p
124	184	14.2	475	1	EXCH	coagulation factor	197	148.5	11.4	4135	2	T42629	tenascin-X - bovin
125	182.5	14.1	685	2	JC7570	Delta-4 protein -	198	148	11.4	626	2	T04895	vacuolar sorting r
126	182	14.0	686	2	S43562	KO8E5.3 protein -	199	147	11.3	956	1	A46016	thrombospondin 3 -
127	181.5	14.0	443	2	I46932	coagulation factor	200	146	11.3	1356	2	A45445	janusin precursor,
128	181	14.0	623	2	T06794	vacuolar sorting r	201	145.5	11.2	2406	2	A54148	odz protein - frui
129	180	13.9	907	2	T27317	hypothetical prote	202	145.5	11.2	2515	2	S47008	tenascin-like prot
130	179.5	13.8	385	2	S53718	homeotic protein d	203	145	11.2	1036	2	T17405	scavenger receptor
131	179.5	13.8	488	1	KFHU	coagulation factor	204	145	11.2	1136	1	S57845	protein-tyrosine k
132	179	13.8	407	1	EXBO7	coagulation factor	205	144.5	11.1	640	2	T19346	hypothetical prote
133	179	13.8	456	1	KXBO	protein C (activat	206	144.5	11.1	2643	2	T29149	hypothetical prote
134	178	13.7	1650	2	S53457	dominant autoantig	207	143.5	11.1	650	2	A34498	glycoprotein antig
135	175.5	13.5	482	1	EXET	coagulation factor	208	143	11.0	491	2	S52920	disintegrin (BC 3.
136	175	13.5	991	2	I49540	procollagen C-endo	209	142.5	11.0	806	2	A46271	integrin beta-7 ch
137	174.5	13.5	986	1	B58788	procollagen C-endo	210	141	10.9	808	2	T23129	hypothetical prote
138	174.5	13.5	1469	2	B36665	slit protein 2 pre	211	141	10.9	972	2	A30363	glycoprotein Gp330
139	174.5	13.5	1480	2	A36665	slit protein 1 pre	212	140	10.8	625	2	F84706	probable vacuolar
140	171.5	13.2	385	2	A54785	preadipocyte facto	213	139	10.7	544	2	S52477	disintegrin (BC 3.
141	169.5	13.1	417	2	T08724	hypothetical prote	214	139	10.7	1125	1	S57846	protein-tyrosine k
142	169.5	13.1	1057	1	A39288	dorsal-ventral pat	215	138	10.6	2195	2	T34264	hypothetical prote
143	169	13.0	1070	2	T31069	colloid-BMP-1 like	216	138	10.6	3566	1	A40701	tenascin-X precurs
144	168.5	13.0	492	1	EXBO	coagulation factor	217	138	10.6	4006	2	T09070	probable tenascin
145	168	13.0	452	1	A30351	hypothetical prote	218	137.5	10.6	955	2	A45441	thrombospondin 4 -
146	168	13.0	1965	2	T33216	hypothetical prote	219	137	10.6	1737	2	T00209	MEGF8 protein - hu
147	167.5	12.9	616	2	T29234	hypothetical prote	220	137	10.6	1808	2	T15099	hypothetical prote
148	167	12.9	459	2	JQ0419	coagulation factor	221	137	10.6	2825	2	T14271	Doc4 protein, stre
149	167	12.9	461	1	JX0210	protein C (activat	222	136.5	10.5	915	2	B48225	probable propotei
150	167	12.9	623	2	T47542	Spot 3 protein and	223	136.5	10.5	2824	2	T22759	hypothetical prote
151	166	12.8	356	2	T20656	hypothetical prote	224	136	10.5	1798	2	S53869	laminin beta-2 cha
152	165	12.7	466	1	KFHU7	coagulation factor	225	134.5	10.4	2180	2	T29764	hypothetical prote
153	165	12.7	624	2	T00044	vacuolar sorting r	226	134.5	10.4	5376	2	T42215	zonadhesin - mouse
154	164	12.6	461	1	KXHU	protein C (activat	227	134	10.3	680	2	PN0510	integrin beta-3 ch
155	163.5	12.6	1827	2	T34288	hypothetical prote	228	134	10.3	3106	1	S53868	laminin alpha-2 ch
156	163	12.6	628	2	T02604	probable vacuolar	229	133.5	10.3	723	2	PN0509	integrin beta-3 ch
157	163	12.6	1170	2	A40558	thrombospondin 1 p	230	133.5	10.3	1023	2	T30257	IGF Fc binding pro
158	162.5	12.5	372	2	T29359	hypothetical prote	231	133.5	10.3	1168	2	I56985	kalinin B1 - mouse
159	162	12.5	628	2	T02602	vacuolar sorting r	232	133	10.2	748	2	S66129	disintegrin (BC 3.
160	162	12.5	2019	1	JQ1322	tenascin precursor	233	132.5	10.2	429	2	T21113	hypothetical prote
161	161.5	12.5	752	2	T20871	hypothetical prote	234	132.5	10.2	1639	1	MMFFB2	laminin gamma-1 ch
162	161	12.4	461	1	S18994	protein C (activat	235	132	10.2	527	2	JE0373	low density lipopr
163	160.5	12.4	1464	2	S58984	development protei	236	132	10.2	755	2	A44315	cartilage oligomer
164	160	12.3	2201	2	A32160	tenascin-C - human	237	132	10.2	1138	1	S24066	protein-tyrosine k
165	159.5	12.3	422	1	KXHUZ	plasma protein 2 p	238	131.5	10.1	1046	2	A26838	prestalk protein p
166	159.5	12.3	961	1	TSHUP4	thrombospondin 4 p	239	131.5	10.1	1807	2	JC6319	integrin beta-4 ch
167	159	12.2	1746	1	S19694	tenascin precursor	240	131	10.1	753	2	B56268	platelet glycoprot
168	158.5	12.2	767	2	T30018	hypothetical prote	241	131	10.1	778	2	A60798	platelet glycoprot
169	158.5	12.2	838	2	T20125	hypothetical prote	242	131	10.1	788	2	I77349	platelet glycoprot
170	158.5	12.2	3712	2	S18253	laminin alpha-1 ch	243	131	10.1	788	2	I51530	integrin beta-3 su
171	158	12.2	252	2	T46247	hypothetical prote	244	131	10.1	788	2	A26547	platelet glycoprot
172	158	12.2	1111	2	T26972	hypothetical prote	245	131	10.1	1124	1	I58388	protein-tyrosine k
173	157.5	12.1	1810	1	A32230	tenascin precursor	246	131	10.1	1615	2	JE0372	low density lipopr
174	157	12.1	621	1	I38467	low density lipopr	247	131	10.1	1748	1	JN0786	integrin beta-4 ch
175	157	12.1	768	2	A42755	P-selectin precurs	248	131	10.1	1797	2	A55677	laminin beta-2 cha

249	130.5	10.1	3191	2	T22945	hypothetical prote	322	119	9.2	1274	2	T42017	cysteine rich prot
250	130	10.0	782	2	A61625	tenascin-like prot	323	119	9.2	1875	2	A36429	integrin beta-4 ch
251	129.5	10.0	799	2	A38308	integrin beta-5 ch	324	119	9.2	2910	2	T42214	otogelin - mouse
252	129	9.9	1178	1	A39804	thrombospondin pre	325	118.5	9.1	769	2	A41029	integrin beta-8 ch
253	129	9.9	1786	1	MMMSB1	laminin beta-1 cha	326	118.5	9.1	1172	1	TSHP2	thrombospondin 2 p
254	128.5	9.9	915	1	A48225	subtilisin-like pr	327	118.5	9.1	1607	1	MMMSB2	laminin gamma-1 ch
255	128.5	9.9	1134	1	JN0711	protein-tyrosine k	328	118.5	9.1	4391	2	A38096	perlecan precursor
256	128.5	9.9	1548	2	S34583	serine proteinase	329	118	9.1	500	2	S66522	cartilage matrix p
257	128.5	9.9	1790	1	MMFFB1	laminin beta-1 cha	330	118	9.1	577	2	B37057	integrin beta-6 ch
258	128	9.9	699	1	154763	Ra-reactive factor	331	118	9.1	1257	2	S28764	neurocan precursor
259	128	9.9	730	1	BMHUI	procollagen C-endo	332	117.5	9.1	781	2	S43534	integrin beta3 - c
260	128	9.9	823	1	A58788	procollagen C-endo	333	117	9.0	883	2	S57653	brevican precursor
261	128	9.9	862	2	S43922	versican - pig-tai	334	117	9.0	933	1	OPHUIT	iodide peroxidase
262	128	9.9	1474	2	D88550	protein ZC84.6 [lim	335	117	9.0	1364	2	T00250	MEGF2 protein - hu
263	128	9.9	2844	2	S28291	hypothetical prote	336	117	9.0	1613	2	JE0272	low density lipopr
264	127.5	9.8	798	2	A40526	integrin beta-7 ch	337	116.5	9.0	152	2	T04140	vacuolar sorting r
265	127.5	9.8	1609	1	MMHUB2	laminin gamma-1 ch	338	116.5	9.0	738	2	D86345	hypothetical prote
266	127.5	9.8	1661	2	T31330	head-activator bin	339	116	8.9	259	2	T21011	hypothetical prote
267	127.5	9.8	1801	1	MWRTS	laminin beta-2 cha	340	116	8.9	883	2	S49126	brevican precursor
268	127.5	9.8	13055	2	T16590	hypothetical prote	341	116	8.9	1122	2	S54237	protein-tyrosine k
269	127	9.8	548	2	T16642	hypothetical prote	342	116	8.9	1123	1	JN0712	protein-tyrosine k
270	127	9.8	2823	2	F87908	protein T22A3.8 [i	343	116	8.9	1328	2	T43060	agrin - electric r
271	127	9.8	2823	2	T23064	hypothetical prote	344	116	8.9	1487	2	G96827	protein F20B17.10
272	127	9.8	3102	2	T43291	laminin alpha chai	345	115.5	8.9	3097	2	T00021	DN-cadherin - frui
273	126.5	9.8	610	2	A35046	E-selectin precurs	346	115	8.9	325	2	S68985	exogastula-induci
274	126.5	9.8	656	2	JC2005	integrin beta-5 ch	347	115	8.9	485	2	S36772	E-selectin - bovin
275	126.5	9.8	3034	2	T14119	seven-pass transme	348	115	8.9	830	2	A30359	P-selectin precurs
276	126	9.7	707	2	JC2218	procollagen C-endo	349	114	8.8	213	2	S25647	ookinete surface p
277	125.5	9.7	211	2	T23590	hypothetical prote	350	114	8.8	253	2	T25768	hypothetical prote
278	125.5	9.7	1643	2	T14274	versican precursor	351	114	8.8	626	2	T27319	hypothetical prote
279	125.5	9.7	2409	1	A60979	versican precursor	352	114	8.8	646	2	JN0473	P-selectin precurs
280	125.5	9.7	3381	2	T42389	versican precursor	353	114	8.8	788	2	A37057	integrin beta-6 ch
281	125	9.6	1786	1	MMHUB1	laminin beta-1 cha	354	114	8.8	2476	2	T34022	zonadhesin - pig
282	124.5	9.6	313	2	S44208	extracellular matr	355	113.5	8.8	603	2	S28941	coagulation factor
283	124.5	9.6	513	2	D88991	protein apx-1 [imp	356	113.5	8.8	1955	1	AGCH	agrin precursor -
284	124.5	9.6	612	2	B42755	E-selectin precurs	357	113	8.7	220	2	S29195	antistasin - Hydra
285	124.5	9.6	2397	1	A55535	versican precursor	358	113	8.7	798	2	B27079	fibronectin recept
286	124	9.6	1302	2	T00038	hypothetical prote	359	113	8.7	1125	1	JH0771	protein-tyrosine k
287	123.5	9.5	720	2	E86297	F309.6 protein - A	360	113	8.7	1268	2	S52781	neurocan - mouse
288	123	9.5	643	2	T25473	hypothetical prote	361	113	8.7	1299	2	T43251	furin (EC 3.4.21.7
289	123	9.5	733	2	E86345	hypothetical prote	362	113	8.7	1353	2	T19157	probable metal bin
290	122.5	9.4	560	1	JC4795	plasma hyaluronan-	363	113	8.7	1424	2	T19156	probable metal bin
291	122.5	9.4	574	2	B88465	protein B0244.8 [i	364	113	8.7	1613	2	JE0273	low density lipopr
292	122.5	9.4	1297	2	T30274	proteoliasin - se	365	112.5	8.7	769	1	JC1121	leukocyte adhesion
293	122.5	9.4	2531	1	C1HURB	hypothetical prote	366	112.5	8.7	899	2	G02428	subtilisin-like pr
294	122	9.4	705	1	C1HURB	complement subcomp	367	112.5	8.7	915	2	JC6148	subtilisin-like pr
295	122	9.4	3562	2	A47171	chondroitin sulfat	368	112.5	8.7	1187	2	T18355	hypothetical prote
296	121.5	9.4	102	2	B55885	chondroitin sulfat	369	112.5	8.7	1506	2	T30886	hypothetical prote
297	121.5	9.4	251	2	A55035	cysteine-rich prot	370	112.5	8.7	2215	2	T00348	integrin beta chai
298	121.5	9.4	551	2	I46709	endothelial leukoc	371	112.5	8.7	2718	2	A23475	LR11 protein - mou
299	121.5	9.4	914	1	S07047	iodide peroxidase	372	112	8.6	677	2	C42125	G surface protein
300	121	9.3	565	2	T16408	hypothetical prote	373	112	8.6	794	2	F88508	trophozoite cystei
301	121	9.3	3707	2	S18252	heparan sulfat pr	374	112	8.6	1192	2	S69000	laminin gamma 2 ch
302	120.5	9.3	1104	2	T38869	transcription fact	375	111.5	8.6	933	2	A31930	cytotactin - chick
303	120.5	9.3	1172	2	A42587	thrombospondin 2 p	376	111.5	8.6	1766	2	A42125	trophozoite cystei
304	120	9.3	591	2	I48141	acroganin - guine	377	111	8.6	294	2	T23682	hypothetical prote
305	120	9.3	732	2	T52588	wall-associated se	378	111	8.6	557	2	A48434	variant-specific s
306	120	9.3	768	2	B41029	integrin beta-8 ch	379	111	8.6	809	2	A57283	integrin beta chai
307	120	9.3	855	2	JC7731	membrane-bound arg	380	111	8.6	846	2	A30889	integrin beta chai
308	120	9.3	1193	2	A44018	laminin B2t chain	381	111	8.6	1160	2	F88369	protein unc-52 [lim
309	120	9.3	1391	2	T20406	hypothetical prote	382	111	8.6	1444	2	T18856	angiogenesis inhib
310	120	9.3	3084	1	MMMSA	laminin alpha-1 ch	383	111	8.6	2295	2	C88369	hypothetical prote
311	119.5	9.2	768	2	I53821	P-selectin - rat	384	111	8.6	3375	2	T19821	protein unc-52 [lim
312	119.5	9.2	914	1	JN0550	iodide peroxidase	385	110.5	8.5	379	2	A59180	hypothetical prote
313	119.5	9.2	1113	2	JE0315	low-density lipopr	386	110.5	8.5	690	2	B86296	hypothetical prote
314	119.5	9.2	1115	2	S40241	G protein-coupled	387	110	8.5	354	2	T22274	hypothetical prote
315	119.5	9.2	1895	2	T15881	hypothetical prote	388	110	8.5	589	2	B38128	epithelin/granulin
316	119.5	9.2	13288	2	T03039	mucin, submaxillar	389	110	8.5	596	2	A45664	variant-specific s
317	119	9.2	378	2	B59180	Wnt inhibitory fac	390	110	8.5	686	1	A59271	Ra-reactive factor
318	119	9.2	496	2	A37979	cartilage matrix p	391	110	8.5	799	2	JC4126	integrin beta olig
319	119	9.2	798	2	S01659	integrin beta-1 ch	392	109.5	8.4	482	2	JC5092	E-selectin - pig
320	119	9.2	799	1	IJMSFB	fibronectin recept	393	109.5	8.4	1188	2	D86236	protein F14N23.5 [
321	119	9.2	964	2	JC5545	integrin beta-4 pr	394	109.5	8.4	1280	2	A39117	170K lectin precur

395	109.5	8.4	1292	2	T09229	galactose binding	468	99	7.6	343	2	S45321	foliostatin - mous
396	109	8.4	434	1	A35005	u-plasminogen acti	469	99	7.6	937	2	I53282	gene PACE4 protein
397	109	8.4	493	2	A33809	cartilage matrix p	470	99	7.6	1049	1	I19421	ATP-dependent pept
398	109	8.4	558	2	JCS878	plasma hyaluronan-	471	99	7.6	3133	2	S52093	hemocytin - silko
399	108.5	8.4	169	1	S18946	ultra high-sulfur	472	98.5	7.6	601	2	T34396	hypothetical prote
400	108.5	8.4	325	2	A40084	exogastrula-induci	473	98.5	7.6	922	2	T37256	metalloproteinase
401	108.5	8.4	589	2	C38128	epithelin/granulin	474	98	7.6	530	2	G02091	pancreatic zymogen
402	108.5	8.4	1170	2	A53612	laminin B1k chain	475	98	7.6	952	2	T18900	disintegrin and me
403	108.5	8.4	3020	2	A43932	mucin 2 precursor,	476	98	7.6	1283	2	T13799	neurexin IV - frui
404	108	8.3	561	2	T27318	hypothetical prote	477	98	7.6	2109	1	I50421	aggreccan precursor
405	108	8.3	601	2	A27020	DiF-induced presen	478	97.5	7.5	344	1	A27701	foliostatin precu
406	108	8.3	770	2	S04847	leukocyte adhesion	479	97.5	7.5	344	2	A32141	foliostatin 1 prec
407	108	8.3	771	2	A45839	leukocyte adhesion	480	97.5	7.5	926	1	OPFGIT	iodide peroxidase
408	108	8.3	2704	2	S09118	G surface protein	481	97.5	7.5	1816	1	S68960	laminin alpha-4 ch
409	108	8.3	2809	2	T30213	G-cadherin - sea u	482	97	7.5	264	2	T16271	hypothetical prote
410	107.5	8.3	2822	2	T20391	hypothetical prote	483	97	7.5	615	1	KFHU12	coagulation factor
411	107.5	8.3	733	1	A46373	probable serine/th	484	97	7.5	1599	2	T16210	hypothetical prote
412	107.5	8.3	1101	2	T16840	hypothetical prote	485	97	7.5	1713	2	A55347	adhesive ligand ep
413	107	8.2	217	2	S00769	25K coo kinase surfa	486	96.5	7.4	330	2	T46256	brevican - human (
414	107	8.2	217	2	A44966	25K coo kinase surfa	487	96.5	7.4	756	2	S47656	tMDC II protein -
415	107	8.2	769	1	IJHULM	leukocyte adhesion	488	96.5	7.4	1077	2	T41146	probable cysteine-
416	107	8.2	1557	2	T28811	hypothetical prote	489	96.5	7.4	1416	2	E88550	protein ZC84.1 [im
417	107	8.2	1959	1	AGRT	agrin - rat	490	96.5	7.4	2101	2	S57245	insulin receptor (
418	106.5	8.2	667	2	A48579	trophozoite surfac	491	96.5	7.4	2148	1	A56081	insulin receptor ty
419	106.5	8.2	3075	2	S14458	laminin alpha-1 ch	492	96.5	7.4	2395	1	S50820	surface protein ty
420	106	8.2	379	2	T16213	APX-1 protein homo	493	96	7.4	527	2	A42032	epidermal growth f
421	106	8.2	402	2	S42367	lag-2 protein - Ca	494	96	7.4	1034	2	JCS598	mucin - rat
422	106	8.2	424	2	S11676	spore coat protein	495	96	7.4	1223	1	TVCHLV	epidermal growth f
423	105.5	8.1	772	2	S32659	integrin beta 2 ch	496	96	7.4	1308	2	A47253	epidermal growth f
424	105.5	8.1	4307	2	T20721	hypothetical prote	497	96	7.4	2233	2	T28669	surface protein 51
425	105	8.1	803	1	IJCH3	integrin, band 3 p	498	95.5	7.4	198	2	T24476	hypothetical prote
426	104.5	8.1	512	2	T37819	probable zinc meta	499	95.5	7.4	212	2	T05936	agglutinin isolect
427	104.5	8.1	1019	2	A38738	coagulation factor	500	95.5	7.4	719	2	T02066	hypothetical prote
428	104.5	8.1	1106	2	T44598	hypothetical prote	501	95	7.3	546	2	T49931	hypothetical prote
429	104.5	8.1	1513	2	A54895	hypothetical prote	502	95	7.3	655	1	A46688	hepatocyte growth
430	104	8.0	295	2	JCS5502	mucin 2, intestina	503	95	7.3	670	2	I65967	disintegrin-like m
431	104	8.0	713	2	A35502	lectin-B - Virgini	504	95	7.3	695	1	S05008	complement subcomp
432	104	8.0	932	2	I52527	PACB4A - mouse (fr	505	95	7.3	812	2	T34212	hypothetical prote
433	104	8.0	1142	2	T30272	hypothetical prote	506	94.5	7.3	205	2	S09623	agglutinin isolect
434	104	8.0	1680	2	A43434	furin (EC 3.4.21.7	507	94.5	7.3	293	2	T22919	hypothetical prote
435	104	8.0	2610	2	T20968	hypothetical prote	508	94.5	7.3	370	2	S22124	L-selectin precurs
436	104	8.0	2946	2	T15840	hypothetical prote	509	94	7.2	243	2	T28802	L-selectin precurs
437	103.5	8.0	583	2	A29154	complement factor	510	94	7.2	372	1	A32375	L-selectin precurs
438	103.5	8.0	773	2	I46059	beta-1 integrin su	511	94	7.2	372	2	S23936	L-selectin-like m
439	103.5	8.0	1106	2	T13938	gene shuttle craft	512	94	7.2	524	2	S38539	disintegrin-like m
440	103.5	8.0	1700	2	S08167	Balbani ring 3 pr	513	94	7.2	798	2	A28193	integrin beta-1 ch
441	103.5	8.0	1895	2	T06609	disease resistance	514	94	7.2	798	2	B28193	integrin beta-1* C
442	103.5	8.0	2813	1	VWU	von Willebrand fac	515	94	7.2	823	2	S18968	cyritestatin precurs
443	103	7.9	606	2	A54665	netrin-1 precursor	516	93.5	7.2	273	2	T16246	hypothetical prote
444	103	7.9	969	1	A39490	subtilisin-like pr	517	93.5	7.2	429	2	T16656	hypothetical prote
445	103	7.9	1373	2	JE0095	gastric mucin MUC5	518	93.5	7.2	2153	2	T30074	hypothetical prote
446	102.5	7.9	1119	2	A88481	protein C16A3.6 [i	519	93.5	7.2	2533	2	T28675	hypothetical prote
447	102.5	7.9	1296	2	T16859	hypothetical prote	520	93.5	7.2	2533	2	T28674	alpha-51D immobili
448	102.5	7.9	1321	2	JE0352	mucin MUC5B, trach	521	93	7.2	714	2	F86345	alpha-51D-immobili
449	102	7.9	389	2	T32167	hypothetical prote	522	93	7.2	736	2	S47645	Fl6f4.8 protein - c
450	102	7.9	419	2	S69207	vascular endotheli	523	93	7.2	903	2	S60257	tMDC I protein - c
451	101.5	7.8	237	2	S08073	cyclic nucleotide	524	93	7.2	2155	2	T30197	alpha tectorin - m
452	101.5	7.8	344	2	I57698	foliostatin - rat	525	93	7.2	2229	2	T16199	hypothetical prote
453	101	7.8	573	2	A33533	cell surface glyco	526	93	7.2	2543	2	T31687	surface antigen - P
454	101	7.8	593	2	S45281	coagulation factor	527	92.5	7.1	337	2	I47079	foliostatin - shee
455	101	7.8	884	2	T18649	hypothetical prote	528	92.5	7.1	397	2	JQ2153	proteinase inhibit
456	101	7.8	1321	2	T00382	hypothetical prote	529	91.5	7.1	409	2	T11743	pp47 protein - pig
457	100.5	7.7	581	2	B54665	netrin-2 precursor	530	91.5	7.1	223	2	B38346	ultra-high-sulfur
458	100.5	7.7	593	1	GYHU	granulin precursor	531	91.5	7.1	470	2	A40697	63K sperm flagella
459	100.5	7.7	1193	2	T21133	hypothetical prote	532	91.5	7.1	588	2	T33815	hypothetical prote
460	100	7.7	646	2	H96665	protein F22C12.10	533	91.5	7.1	686	2	T25987	hypothetical prote
461	100	7.7	649	2	G86434	protein F17F8.23 [534	91.5	7.1	2090	2	T30075	hypothetical prote
462	100	7.7	770	2	T00204	LDL receptor relat	535	91	7.0	323	1	S09702	L-selectin precurs
463	100	7.7	1016	2	G86295	hypothetical prote	536	91	7.0	711	2	D86296	hypothetical prote
464	99.5	7.7	600	2	S07638	spore coat protein	537	91	7.0	792	2	C96719	hypothetical prote
465	99.5	7.7	816	2	C69493	hypothetical prote	538	90.5	7.0	344	2	I45894	foliostatin - bovi
466	99.5	7.7	837	2	A42112	mucin-like peptide	539	90.5	7.0	427	2	S74211	FAS-6/7 protein pr
467	99.5	7.7	912	2	A54423	brevican precursor	540	90.5	7.0	711	2	T27358	hypothetical prote

541	90.5	7.0	770	2	T00203	LDL receptor-relat	614	84.5	6.5	789	2	S28259	androgen-regulated
542	90	6.9	291	2	I38098	t-selectinogen acti	615	84.5	6.5	804	2	A86327	protein F18014.11
543	90	6.9	372	2	JC5377	L-selectin precurs	616	84.5	6.5	825	2	S55060	fertilin alpha-11
544	90	6.9	419	2	A59414	metalloproteinase	617	84.5	6.5	833	2	S51603	receptor-like tyro
545	90	6.9	562	1	UKHUT	t-plasminogen acti	618	84.5	6.5	898	2	S47489	receptor tyrosine
546	90	6.9	572	2	T29880	hypothetical prote	619	84.5	6.5	919	2	T29581	hypothetical prote
547	90	6.9	694	2	JC6554	complement subcomp	620	84.5	6.5	1122	2	T42400	Eph receptor tyros
548	90	6.9	843	1	A27340	complement C7 prec	621	84.5	6.5	1210	1	GQH05	epidermal growth f
549	90	6.9	985	2	I51549	receptor tyrosine	622	84	6.5	71	2	S39422	metallothionein 20
550	90	6.9	1268	2	B36502	insulin receptor-r	623	84	6.5	92	2	D37057	epithelial cell g1
551	90	6.9	1291	2	T21694	hypothetical prote	624	84	6.5	497	2	T27827	hypothetical prote
552	89.5	6.9	178	2	I49259	cellular nucleic a	625	84	6.5	585	2	I46586	complement compone
553	89.5	6.9	186	2	A28401	agglutinin isolect	626	84	6.5	612	2	JH0799	laminin-related pr
554	89.5	6.9	191	2	I46412	keratin KAP5.4 - s	627	84	6.5	613	2	A88448	protein C4509.6 [1
555	89.5	6.9	320	2	A53119	cell adhesion glyco	628	84	6.5	735	2	I48101	ADAM 6 protein pre
556	89.5	6.9	1607	2	T43212	insulin-like growt	629	84	6.5	918	2	JC4361	scavenger receptor
557	89	6.9	197	2	I46413	keratin KAP5.5 - s	630	84	6.5	981	2	S51604	receptor-like tyro
558	89	6.9	376	2	JC4892	L-selectin precurs	631	84	6.5	1005	2	S49015	receptor tyrosine
559	89	6.9	385	1	A34015	L-selectin precurs	632	84	6.5	1260	1	S05479	neural cell adhesi
560	89	6.9	1323	2	E88257	protein let-23 [im	633	83.5	6.4	117	2	A32416	phospholipase A2 (
561	89	6.9	1374	2	S70712	protein-tyrosine k	634	83.5	6.4	329	2	A48805	insulin-like growt
562	89	6.9	4351	2	T00252	MEGF1 protein - ra	635	83.5	6.4	537	2	B33485	spore coat protein
563	88.5	6.8	230	2	A38346	ultra-high-sulfur	636	83.5	6.4	540	2	B47417	insulin receptor-r
564	88.5	6.8	343	2	S55369	folliculin - chic	637	83.5	6.4	868	2	T20239	hypothetical prote
565	88.5	6.8	712	2	A45638	immunodominant mic	638	83.5	6.4	965	2	S62935	hypothetical prote
566	88.5	6.8	803	2	A47723	P-spondin precurs	639	83.5	6.4	1376	1	JQ1534	E2 glycoprotein pr
567	88.5	6.8	1043	2	T19734	hypothetical prote	640	83	6.4	61	1	SMXK1	metallothionein 1
568	88.5	6.8	1252	2	S36016	oocyst wall protei	641	83	6.4	349	2	D36858	gene G4R protein -
569	88	6.8	826	2	A60385	monocyte surface a	642	83	6.4	360	2	B36470	Wnt-2 protein - mo
570	88	6.8	850	2	S56015	gastric mucin MUC5	643	83	6.4	425	2	T38548	hypothetical zinc-
571	88	6.8	975	2	JC5570	subtilisin-like pr	644	83	6.4	429	2	A42572	coagulation factor
572	88	6.8	1522	2	H88360	protein T22P7.3 [1	645	83	6.4	513	2	S28358	prespore vesicle p
573	87.5	6.7	213	1	ABWT2	agglutinin isolect	646	83	6.4	520	2	K88846	protein T12A7.2 [1
574	87.5	6.7	335	2	T32657	hypothetical prote	647	83	6.4	625	1	GFRU1	coagulation factor
575	87.5	6.7	509	1	A37259	membrane glycoprot	648	83	6.4	655	2	JC7850	disintegrin and me
576	87.5	6.7	509	2	T22238	hypothetical prote	649	83	6.4	925	1	A39216	nucleotide diphosp
577	87.5	6.7	713	1	UMMS	period clock prote	650	83	6.4	1369	2	S70713	protein-tyrosine k
578	87.5	6.7	764	2	C86314	hypothetical prote	651	83	6.4	1450	2	T30273	hypothetical prote
579	87.5	6.7	2120	2	T30243	alpha tectorin - c	652	83	6.4	4550	2	T18440	hypothetical prote
580	87.5	6.7	2150	2	T32497	hypothetical prote	653	82.5	6.4	250	2	T30124	hypothetical prote
581	87.5	6.7	2616	2	A57096	nudel protein prec	654	82.5	6.4	310	2	T32006	hypothetical prote
582	87	6.7	71	2	S47577	metallothionein 20	655	82.5	6.4	531	2	T18741	hypothetical prote
583	87	6.7	425	2	T18592	hypothetical prote	656	82.5	6.4	777	2	I48100	ADAM 5 protein pre
584	87	6.7	570	2	T37314	probable kexin (EC	657	82.5	6.4	942	2	D87803	protein b11-4D [im
585	87	6.7	600	2	T18593	hypothetical prote	658	82.5	6.4	1161	1	S31213	neurexin precursor
586	87	6.7	1371	2	A33837	insulin-like growt	659	82.5	6.4	1385	2	T14158	neurexin IV - mous
587	86.5	6.7	318	2	B87929	protein T22H2.6 [1	660	82	6.3	71	2	S39421	metallothionein 20
588	86.5	6.7	549	2	S48169	metalloproteinase	661	82	6.3	170	2	T06056	hypothetical prote
589	86.5	6.7	609	2	S55270	catrocollastatin p	662	82	6.3	178	2	A23219	high-cysteine chor
590	86.5	6.7	1558	2	C89114	protein C37C3.6a [663	82	6.3	258	2	S23106	priA protein - shi
591	86.5	6.7	2167	2	T34395	hypothetical prote	664	82	6.3	281	2	D88637	protein W09G12.1 [
592	86	6.6	182	2	A36686	ultra-high-sulfur	665	82	6.3	360	1	WMBE2E	membrane-bound com
593	86	6.6	348	2	T28623	hypothetical prote	666	82	6.3	660	2	S71949	metalloproteinase
594	86	6.6	491	2	T21421	hypothetical prote	667	82	6.3	661	2	B96596	hypothetical prote
595	86	6.6	738	2	S40992	hypothetical prote	668	82	6.3	704	2	T31227	tran protein homol
596	86	6.6	739	2	B88553	protein K04H4.2b [669	82	6.3	1019	2	T13039	tyrosine kinase re
597	86	6.6	962	2	JC5571	subtilisin-like pr	670	82	6.3	1162	2	T21557	hypothetical prote
598	86	6.6	1091	1	PL0009	complement C3d/Eps	671	82	6.3	1642	2	T19130	hypothetical prote
599	85.5	6.6	206	2	T24484	hypothetical prote	672	82	6.3	2014	2	I36936	complement recepto
600	85.5	6.6	248	2	T19913	hypothetical prote	673	81.5	6.3	186	2	G89614	protein F15G9.5 [1
601	85.5	6.6	255	2	I38426	lymphocyte activat	674	81.5	6.3	195	2	T04161	trypsin inhibitor
602	85.5	6.6	319	2	A53502	folliculin - Afri	675	81.5	6.3	257	2	T18969	hypothetical prote
603	85.5	6.6	571	2	S24789	Jararagin C precu	676	81.5	6.3	345	2	T25138	hypothetical prote
604	85.5	6.6	813	2	T21192	hypothetical prote	677	81.5	6.3	358	2	T25137	hypothetical prote
605	85	6.6	176	2	T31796	hypothetical prote	678	81.5	6.3	437	2	S05478	properdin - mouse
606	85	6.6	349	2	D72175	G2R protein - vari	679	81.5	6.3	552	2	JC7666	serine-type carbox
607	85	6.6	689	4	S30392	hypothetical RrvL-	680	81.5	6.3	776	2	S28258	androgen-regulated
608	85	6.6	905	2	S55059	fertilin alpha-I -	681	81.5	6.3	957	2	T15976	hypothetical prote
609	85	6.6	1627	2	S65464	pregnancy-associat	682	81.5	6.3	1231	1	NBHUH	hypothetical prote
610	84.5	6.5	265	2	H96785	protein F10A5.22 [683	81.5	6.3	1239	2	T13809	compleable disintegr
611	84.5	6.5	302	1	WMBE1E	secretory compleme	684	81.5	6.3	1751	1	MWHUMH	laminin alpha-2 ch
612	84.5	6.5	463	2	T26555	hypothetical prote	685	81.5	6.3	1846	2	T42047	insulin receptor h
613	84.5	6.5	744	2	A43353	ascites sialoglyco	686	81	6.2	400	2	T46383	hypothetical prote

687	6.2	483	2	T24856	hypothetical prote	760	78	6.0	379	2	A35669	gene CYR61 protein
688	81	1260	1	TVRTNU	protein-tyrosine k	761	78	6.0	446	2	T31644	hypothetical prote
689	81	1300	2	A36502	insulin receptor-r	762	78	6.0	550	2	T47158	hypothetical prote
690	80.5	375	2	A41428	CEP-10 protein pre	763	78	6.0	725	2	E96596	hypothetical prote
691	80.5	387	2	G88124	protein nhr-16 [lm	764	78	6.0	757	2	T34362	hypothetical prote
692	80.5	401	2	S65138	glycoprotein antig	765	78	6.0	795	2	T34468	hypothetical prote
693	80.5	478	2	J47040	gene Tt52 protein	766	78	6.0	922	2	T23573	hypothetical prote
694	80.5	734	2	JC4861	fertilin beta cha	767	78	6.0	1028	2	A96719	hypothetical prote
695	80.5	780	2	A34102	von Willebrand fac	768	78	6.0	1042	2	A57534	mucin 5AC (clone L
696	80.5	788	2	T25061	hypothetical prote	769	78	6.0	1166	1	S06142	protein-tyrosine k
697	80.5	987	2	I48652	mouse developmenta	770	78	6.0	1438	2	A48216	neurexin iii-alpha
698	80.5	987	2	I48953	eph-related recept	771	78	6.0	1471	2	B48218	neurexin iii-alpha
699	80.5	1013	2	I50615	receptor-type prot	772	78	6.0	1578	2	I48216	neurexin iii-alpha
700	80.5	1092	2	H96509	protein F27F5.23 l	773	78	6.0	1647	2	T32934	hypothetical prote
701	80.5	1131	2	T15787	hypothetical prote	774	78	6.0	2014	2	T21560	hypothetical prote
702	80.5	2214	2	T16305	hypothetical prote	775	78	6.0	2043	2	T18524	hypothetical prote
703	80.5	2415	1	A39086	aggreccan precursor	776	78	6.0	2489	2	I73012	scavenger receptor
704	80	6.2	117	A34860	phospholipase A2 (777	78	6.0	3968	2	A44265	complement C3b/Cab
705	80	6.2	137	T15609	hypothetical prote	778	78	6.0	83	2	S07405	trithorax homolog
706	80	6.2	148	S06019	isotocin 2 / neuro	779	77.5	6.0	94	2	JC2225	proteinase inhibit
707	80	6.2	177	A32760	cellular nucleic a	780	77.5	6.0	103	1	TISYC2	Bowman-Birk protei
708	80	6.2	177	JC3512	cellular nucleic a	781	77.5	6.0	133	1	PSOXG	proteinase inhibit
709	80	6.2	227	1 LNRZ	lectin precursor -	782	77.5	6.0	141	2	FC1294	phospholipase A2 (
710	80	6.2	266	S65778	chitinase class IV	783	77.5	6.0	459	2	A34791	trophozoite surfac
711	80	6.2	266	A44776	transforming prote	784	77.5	6.0	644	2	T33132	interleukin-7 rece
712	80	6.2	535	T19706	hypothetical prote	785	77.5	6.0	692	2	T32980	hypothetical prote
713	80	6.2	951	T00017	gene ADAMTS-1 prot	786	77.5	6.0	828	2	T23367	hypothetical prote
714	80	6.2	991	T178843	receptor protein t	787	77.5	6.0	1074	2	JC5928	senaphorin F precu
715	80	6.2	1259	S36126	neural cell adhesi	788	77.5	6.0	1360	2	T33922	hypothetical prote
716	80	6.2	1353	JQ2168	E2 glycoprotein pr	789	77.5	6.0	2924	2	T18378	variant-specific s
717	80	6.2	1363	T43220	insulin-like growt	790	77.5	6.0	3343	2	S44887	hypothetical prote
718	80	6.2	1428	T08852	lustrin A - Califo	791	77	5.9	60	1	SMHOLA	ZK112.7 protein -
719	80	6.2	1594	T30549	hensin - rabbit	792	77	5.9	71	2	S39420	metallothionein 1A
720	80	6.2	1715	C40228	neurexin II-alpha	793	77	5.9	118	1	PSNKK3	metallothionein 20
721	80	6.2	1743	T26859	hypothetical prote	794	77	5.9	118	1	C34860	phospholipase A2 (
722	80	6.2	2219	T27684	hypothetical prote	795	77	5.9	153	2	A34132	phospholipase A2 (
723	79.5	6.1	72	1 TIMB	trypsin inhibitor	796	77	5.9	155	2	A45293	vasotocin / neurop
724	79.5	6.1	118	1 PSNKK1	phospholipase A2 (797	77	5.9	160	2	T25185	conopressin precu
725	79.5	6.1	330	T28169	hypothetical prote	798	77	5.9	188	2	T25185	hypothetical prote
726	79.5	6.1	362	I64128	2-dehydro-3-deoxy-	799	77	5.9	264	1	QRBOLD	high sulfur protei
727	79.5	6.1	461	JC4302	tumor necrosis fac	800	77	5.9	375	2	T16248	LDL receptor - bov
728	79.5	6.1	559	1 A29941	t-plasminogen acti	801	77	5.9	454	1	NMIV	hypothetical prote
729	79.5	6.1	559	1 A29941	t-plasminogen acti	802	77	5.9	480	1	A30065	exo-alpha-sialidas
730	79.5	6.1	1603	T24098	hypothetical prote	803	77	5.9	676	1	VCWVPV	trigramin precuro
731	79	6.1	118	T34860	phospholipase A2 (804	77	5.9	735	2	G02937	env polyprotein pr
732	79	6.1	135	T15610	hypothetical prote	805	77	5.9	814	2	G02390	fertilin beta - cr
733	79	6.1	357	S23403	sperm surface prot	806	77	5.9	905	2	T23229	disintegrin-like m
734	79	6.1	422	D86446	hypothetical prote	807	77	5.9	955	2	T18435	hypothetical prote
735	79	6.1	559	1 A35029	t-plasminogen acti	808	77	5.9	1339	2	JC4387	hypothetical prote
736	79	6.1	713	S06546	finger protein (cl	809	77	5.9	1381	2	T31083	epidermal growth f
737	79	6.1	802	T24293	disintegrin-like t	810	76.5	5.9	124	2	A31761	paranodin - rat
738	79	6.1	949	T24294	hypothetical prote	811	76.5	5.9	171	2	I48298	high-cysteine chor
739	79	6.1	975	T148974	receptor-protein t	812	76.5	5.9	323	2	T24836	cellular nucleic a
740	79	6.1	1053	S46199	probable complemen	813	76.5	5.9	328	2	S72647	hypothetical prote
741	79	6.1	1436	A46496	antigen Wc1.1 prec	814	76.5	5.9	345	2	A05279	hypothetical prote
742	79	6.1	2767	1 UIHU	thyroglobulin prec	815	76.5	5.9	383	2	D88633	surface antigen 51
743	78.5	6.1	72	S39419	metallothionein 10	816	76.5	5.9	530	1	A38690	protein F56B3.2 li
744	78.5	6.1	169	T15611	hypothetical prote	817	76.5	5.9	724	2	T25700	membrane glycoprot
745	78.5	6.1	230	T31722	hypothetical prote	818	76.5	5.9	986	2	S78059	mechanosensory pro
746	78.5	6.1	314	T27686	hypothetical prote	819	76.5	5.9	1051	2	JC4091	protein-tyrosine k
747	78.5	6.1	449	1 NBHUHS	complement factor	820	76.5	5.9	1119	2	T16720	glycoprotein A - P
748	78.5	6.1	616	A55796	ecarin precursor -	821	76.5	5.9	1210	2	A53183	hypothetical prote
749	78.5	6.1	617	S48160	metalloproteinase	822	76.5	5.9	1537	2	JC4172	epidermal growth f
750	78.5	6.1	654	T30136	hypothetical prote	823	76.5	5.9	3869	2	A48205	DNA (cytosine-5')-
751	78.5	6.1	689	E69135	coenzyme F420-redu	824	76	5.9	61	2	S69277	All-1 protein +GTE
752	78.5	6.1	843	A27131	epidermal growth f	825	76	5.9	71	2	S47576	metallothionein 1R
753	78.5	6.1	849	T10617	protein-tyrosine k	826	76	5.9	118	2	B34860	metallothionein 20
754	78.5	6.1	1729	T18396	erythrocyte membra	827	76	5.9	119	1	B34860	phospholipase A2 (
755	78.5	6.1	3078	T28432	variant-specific s	828	76	5.9	121	1	PSNSAM	phospholipase A2 h
756	78	6.0	160	TJ0542	185K secretory pro	829	76	5.9	137	2	S68429	myotoxin precursor
757	78	6.0	179	T25841	hypothetical prote	830	76	5.9	171	2	S57894	laminin - Hydra vu
758	78	6.0	250	T29866	hypothetical prote	831	76	5.9	249	2	T24604	hypothetical prote
759	78	6.0	335	2 T31559	hypothetical prote	832	76	5.9	256	2	B32393	T-cell antigen 4-1

833	76	5.9	335	2	T31561	hypothetical prote	906	74.5	5.7	312	2	T19675	hypothetical prote
834	76	5.9	335	2	T31560	hypothetical prote	907	74.5	5.7	343	2	JC7958	galaxin precursor
835	76	5.9	449	2	T48199	hypothetical prote	908	74.5	5.7	351	2	F83033	vanillate O-demeth
836	76	5.9	600	2	I49281	feritin alpha pre	909	74.5	5.7	416	2	A37877	hemorrhagic protei
837	76	5.9	688	1	C1HUS	complement subcomp	910	74.5	5.7	427	2	JC4915	ags protein precu
838	76	5.9	760	2	A40195	meprin A (EC 3.4.2	911	74.5	5.7	548	2	D82175	probable trypsin V
839	76	5.9	764	1	BBHU	complement factor	912	74.5	5.7	568	2	S42225	major envelope gly
840	76	5.9	767	2	T07693	hypothetical prote	913	74.5	5.7	664	2	T20420	hypothetical prote
841	76	5.9	817	2	T24063	hypothetical prote	914	74.5	5.7	807	2	A38152	F-spondin - rat
842	76	5.9	898	2	T14764	hypothetical prote	915	74.5	5.7	915	1	A55144	autotaxin precursor
843	76	5.9	1003	1	PVZAM	spheroidin precurs	916	74.5	5.7	1526	2	T19473	hypothetical prote
844	76	5.9	1122	2	F71606	probable multiple	917	74.5	5.7	2165	2	T21371	hypothetical prote
845	76	5.9	1172	2	F84572	probable cadmium-t	918	74	5.7	61	1	SMHUIG	metallothionein IG
846	76	5.9	1711	2	C71625	variant-specific s	919	74	5.7	61	1	SMHY2C	metallothionein II
847	76	5.9	1717	1	A45558	epidermal growth f	920	74	5.7	61	1	SMMK2	metallothionein 2
848	76	5.9	2153	2	T14893	scavenger receptor	921	74	5.7	61	1	SMRT1	metallothionein I
849	76	5.9	2588	2	T14342	NSD1 protein - mou	922	74	5.7	61	1	S18403	metallothionein II
850	75.5	5.8	72	2	S39417	metallothionein 10	923	74	5.7	61	2	S00810	metallothionein IC
851	75.5	5.8	246	2	B25528	trypsin (EC 3.4.21	924	74	5.7	61	2	I48116	metallothionein II
852	75.5	5.8	249	2	T32060	hypothetical prote	925	74	5.7	118	2	S01801	phospholipase A2 (
853	75.5	5.8	255	2	A40969	folate-binding pro	926	74	5.7	127	2	S29653	textilotoxin chain
854	75.5	5.8	324	2	JC2395	Fas antigen precu	927	74	5.7	127	2	A49269	phospholipase A2 h
855	75.5	5.8	396	2	T23767	hypothetical prote	928	74	5.7	138	2	F48188	phospholipase A2 (
856	75.5	5.8	409	2	T29517	hypothetical prote	929	74	5.7	140	2	T04904	hypothetical prote
857	75.5	5.8	456	2	T17887	lysine/proline-ric	930	74	5.7	153	2	PN0564	von Willebrand fac
858	75.5	5.8	461	1	GQRTI1	tumor necrosis fac	931	74	5.7	170	2	A55499	zinc finger protei
859	75.5	5.8	464	2	C69356	conserved hypothet	932	74	5.7	170	2	I48297	hypothetical nucleic a
860	75.5	5.8	594	2	T04783	hypothetical prote	933	74	5.7	222	2	T27939	hypothetical prote
861	75.5	5.8	649	2	T18063	DNA binding protei	934	74	5.7	242	2	T29699	hypothetical prote
862	75.5	5.8	986	2	I78844	receptor protein-t	935	74	5.7	346	2	T30069	hypothetical prote
863	75.5	5.8	1042	2	T26644	hypothetical prote	936	74	5.7	448	1	H69032	polyferredoxin 2 -
864	75.5	5.8	1208	2	T27822	hypothetical prote	937	74	5.7	464	2	T32401	hypothetical prote
865	75.5	5.8	1372	2	A4157	insulin receptor p	938	74	5.7	470	2	D41977	retinoid receptor
866	75.5	5.8	1376	1	VGIHJ2	B2 glycoprotein p	939	74	5.7	477	1	J50589	endo-1,4-beta-xyla
867	75.5	5.8	1383	2	A36080	insulin receptor p	940	74	5.7	610	2	JC8056	halyase - Glycidu
868	75.5	5.8	1507	2	A40228	neurexin I-alpha p	941	74	5.7	610	2	T45924	protein kinase-lik
869	75.5	5.8	1530	2	I45944	neurexin I-alpha -	942	74	5.7	661	1	KFH013	coagulation factor
870	75	5.8	61	2	I46602	metallothionein -	943	74	5.7	689	2	T52060	protein MEDEA (imp
871	75	5.8	75	2	S17156	metallothionein -	944	74	5.7	732	2	I52361	testicular metallo
872	75	5.8	118	2	JK0223	phospholipase A2 (945	74	5.7	748	2	S24134	endopeptidase 2 (E
873	75	5.8	118	2	G34860	phospholipase A2 (946	74	5.7	905	1	A27410	nucleotide diphosp
874	75	5.8	122	2	S46979	phospholipase A2 -	947	74	5.7	1014	2	T30545	major surface gly
875	75	5.8	176	2	T22110	hypothetical prote	948	74	5.7	1056	2	A53767	mucin WUCSB, trach
876	75	5.8	186	2	A45910	ultra-high-sulfur	949	74	5.7	1257	1	A41060	neural cell adhesi
877	75	5.8	297	2	S06267	B cell-associated	950	74	5.7	1361	2	S29998	surface protein -
878	75	5.8	305	2	A46476	int-1-like protein	951	74	5.7	2386	1	FNHU	fibronectin precu
879	75	5.8	360	2	S00834	trithorax homolog	952	73.5	5.7	146	2	S09415	proteinase inhibit
880	75	5.8	366	2	I53035	transmembrane prot	953	73.5	5.7	177	2	S37650	high-sulfur kerati
881	75	5.8	380	2	G01639	hypothetical prote	954	73.5	5.7	272	2	I48700	gene ox40 protein
882	75	5.8	383	2	T21946	hypothetical prote	955	73.5	5.7	325	2	B43692	T2 protein - rabbi
883	75	5.8	463	1	A36479	milk fat globule m	956	73.5	5.7	326	1	GOVZML	T2 protein - myxom
884	75	5.8	474	2	S18452	variant surface gl	957	73.5	5.7	385	2	T22822	hypothetical prote
885	75	5.8	549	2	T17525	proline-rich prote	958	73.5	5.7	494	2	S57539	probable membrane
886	75	5.8	575	2	C88346	protein P42G4.3a l	959	73.5	5.7	538	2	E84863	hypothetical prote
887	75	5.8	576	2	T18067	hypothetical prote	960	73.5	5.7	710	2	T21339	hypothetical prote
888	75	5.8	584	1	C8H06	complement C8 alph	961	73.5	5.7	987	2	A54092	protein-tyrosine k
889	75	5.8	585	2	S43572	C05B5.5 [i	962	73.5	5.7	1206	1	GVVURV	M polyprotein - Ri
890	75	5.8	585	2	E88571	protein C05B5.5 [i	963	73.5	5.7	1472	2	A84470	hypothetical prote
891	75	5.8	603	2	T22111	hypothetical prote	964	73.5	5.7	1566	2	T20058	hypothetical prote
892	75	5.8	706	2	S33761	transferrin precu	965	73.5	5.7	1914	2	T42635	tenascin Y precurs
893	75	5.8	976	2	A36355	protein-tyrosine k	966	73	5.6	61	1	SMHUIE	metallothionein IE
894	75	5.8	984	1	A34076	protein-tyrosine k	967	73	5.6	61	1	SMHU2	metallothionein 2
895	75	5.8	1025	1	A43526	complement C3d/Eps	968	73	5.6	119	1	PSNOAT	phospholipase A2 (
896	75	5.8	1362	2	A37474	surface glycoprote	969	73	5.6	122	2	S62780	phospholipase A2 (
897	75	5.8	1490	2	JC5145	DNA (cytosine-5)-	970	73	5.6	133	1	T1E2BR	trypsin inhibitor
898	75	5.8	1737	2	T21889	hypothetical prote	971	73	5.6	180	2	A45810	glycoprotein anti
899	75	5.8	1805	2	T21888	hypothetical prote	972	73	5.6	204	2	T08072	proteinase inhibit
900	75	5.8	2098	2	T18397	protein CTRP - mal	973	73	5.6	242	2	JC4360	riboflavin-binding
901	74.5	5.7	125	2	S65624	phospholipase A(2)	974	73	5.6	252	2	B88637	protein W09G12.4 (
902	74.5	5.7	138	1	PSRSB2	phospholipase A2 (975	73	5.6	310	2	G84809	hypothetical prote
903	74.5	5.7	145	2	T15808	hypothetical prote	976	73	5.6	377	2	T05354	hypothetical prote
904	74.5	5.7	251	2	B40969	folate-binding pro	977	73	5.6	470	2	S04801	exo-alpha-sialidas
905	74.5	5.7	292	2	T23966	hypothetical prote	978	73	5.6	579	2	A56740	sperm-egg recognit

979 73 5.6 597 2 S71352 metalloproteinase
980 73 5.6 669 2 S6551 factor H - bovine
981 73 5.6 687 1 B39045 protein-glutamine
982 73 5.6 730 2 H86295 hypothetical prote
983 73 5.6 885 1 A55453 nucleotide diphosp
984 73 5.6 1348 2 S27812 probable epidermal
985 73 5.6 1348 2 A43917 hypothetical prote
986 73 5.6 2225 2 T26063 fibronectin - bov
987 73 5.6 2265 1 FNBO metallothionein 10
988 72.5 5.6 72 2 S39418 phospholipase A2 (
989 72.5 5.6 119 1 PSB2H anticosgulant prot
990 72.5 5.6 119 2 A34816 alpha-1-thionin -
991 72.5 5.6 136 2 S31695 phospholipase A2 (
992 72.5 5.6 138 1 I51381 phospholipase A2 (
993 72.5 5.6 138 1 PSRSBT vasotocin 1 / neur
994 72.5 5.6 152 2 A32669 endonuclease 1 [lm
995 72.5 5.6 235 2 AE0877 trypsin (EC 3.4.21
996 72.5 5.6 247 1 TRDG complement control
997 72.5 5.6 263 1 C36938 hypothetical prote
998 72.5 5.6 263 2 T28450 hypothetical prote
999 72.5 5.6 264 2 T22380 osteonectin precur
1000 72.5 5.6 302 1 GEMSN

ALIGNMENTS

RESULT 1
B48089 growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
R:Accession: B48089
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: UNIPROT:Q14393; GB:L13720; NID:9401766; PIDN:AAA58494.1; PID:9401767
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:41-92/Domain: Gla domain homology #status atypical <GLA>
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-277/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 3e-88;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKNGKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKNGKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPQSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGCGCLOICHNKPQSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQRCQVQCVNSPGSYTCHCDGRGGLK 180
DB 210 ARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQRCQVQCVNSPGSYTCHCDGRGGLK 269

QY 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPIRLRFRKLQ 227
DB 270 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPIRLRFRKLQ 316

RESULT 2
I55476 growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:Accession: I55476
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.;
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating factor f
A:Reference number: I55476; MUID:95197586; PMID:7890695
A:Accession: I55476
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-674 <RES>
A:Cross-references: UNIPROT:Q63772; GB:D42148; NID:91526567; PIDN:BAA07719.1; PID:9893402
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:129-89/Domain: Gla domain homology <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 86.1%; Score 1117; DB 2; Length 674;
Best Local Similarity 82.8%; Pred. No. 5.1e-75;
Matches 188; Conservative 17; Mismatches 22; Indels 0; Gaps 0;

QY 1 PRYLDCKNGKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYLDCKNGKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPQSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 147 GRLCDKDVNECSQENGCGCLOICHNKPQSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQRCQVQCVNSPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYCLCDGEGFAYSSQEKACRDVDECLQRCQVQCVNSPGSYTCHCDGRGGLK 266

QY 181 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPIRLRFRKLQ 227
DB 267 LSQDMTDCEDILPCVPFSPVAKSVKSLYLGRMFSGTPIRLRFRKLQ 313

RESULT 3
A48089 growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
R:Accession: A48089; S37437
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of t
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: UNIPROT:Q61592; GB:X59846; NID:9407060; PIDN:CAA42507.1; PID:9407061
A:Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:38-89/Domain: Gla domain homology #status atypical <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

C;Complex: in plasma forms a complex with C4b binding protein

C;Function:
A;Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage desb
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>
F;26-85/Domain: Gla domain homology <GLA>
F;42-676/Product: plasma protein S #status predicted <MAT>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-667/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F;111-112/Cleavage site: Arg-Ser (thrombin) #status predicted
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;499,509,530/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 46.4%; Score 601.5; DB 1; Length 676;
Best Local Similarity 43.4%; Pred. No. 4.3e-37;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRYLDCINKYSPYTKNSGFAT-----GVATCVQLPDQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 PKYLGLGSGFRAGLFTAAARLSTNAYPDLRSVCVNAISDQCNPLPCNEDGFMTCCKQATFT 142
QY 53 CLCKAGWGRLLCDKVNESQ-----SOENGGCLQICHNKPFGSHCSHGSFELSDGRTCODI 109
DB 143 CTCKPQWQKCFBDFINECKDPNNGGCSQICDNTPGSYHSCNGFVWLNSKKDKDV 202
QY 110 DECA-DSEACGEARCNLPGSYSCLDEGFAYSQBKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSPKPSICTGAVCKNIPGDFECPGEGYRNKLSKSCDIDECSENNCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMDCITLPCVPFSPVSKVSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLADQKSCVSVCLPLNLDTKYELLYLAQFAGV-VLYLKER 316

RESULT 6
KX80S

plasma protein S precursor - bovine
N;Alternate names: vitamin K-dependent protein S
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Aug-1987 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
C;Accession: A24759; A23888
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
Proc. Natl. Acad. Sci. U.S.A. 83, 4199-4203, 1986
A;Title: Primary structure of bovine vitamin K-dependent protein S.
A;Reference number: A24759; MUID:86233400; PMID:2940598
A;Accession: A24759
A;Molecule type: mRNA
A;Residues: 1-675 <DAH>
A;Cross-references: UNIPROT:P07224; GB:M13044; NID:gl63697; PIDN:AAA30757.1; PID:gl63698
A;Note: parts of this sequence, including the amino end of the mature protein, were dete
R;Dahlback, B.; Lundwall, A.; Stenflo, J.
J. Biol. Chem. 261, 5111-5115, 1986
A;Title: Localization of thrombin cleavage sites in the amino-terminal region of bovine
A;Reference number: A23888; MUID:86158236; PMID:2937785
A;Accession: A23888
A;Molecule type: protein
A;Residues: 42-141 <DA2>
C;Complex: in plasma forms a complex with C4b binding protein

A;Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage desb
C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-41/Domain: propeptide #status predicted <PRO>

F;26-85/Domain: Gla domain homology <GLA>
F;42-675/Product: plasma protein S #status experimental <MAT>
F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG4>
F;315-666/Domain: sex hormone-binding globulin homology <SHB>
F;325-478/Domain: laminin G repeat homology <LGR>
F;47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #statu
F;58-63,88-113,121-134,126-143,145-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F;111-112/Cleavage site: Arg-Ala (thrombin) #status experimental
F;136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental
F;177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status experimental
F;499/Binding site: carboxylate (Asn) (covalent) #status experimental
F;509/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 46.0%; Score 596.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 1e-36;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

QY 1 PRYLDCINKYSPYTKNSGFAT-----CVQNLPDQCTPNPCDRKGTQACQDLMGNFF 52
DB 83 PKYLGLGSGFRAGLFTAAARLSTNAYPDLRSVCVNAISDQCNPLPCNEDGFMTCCKQATFT 142
QY 53 CLCKAGWGRLLCDKVNESQ-----NGGCLQICHNKPFGSHCSHGSFELSDGRTCODI 109
DB 143 CTCKPQWQKCFBDFINECKDPNNGGCSQICENTPGSYHSCNGFVWLNSKKDKDV 202
QY 110 DECA-DSEACGEARCNLPGSYSCLDEGFAYSQBKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECVLKPSICTGAVCKNIPGDFECPGEGYRNKLSKSCDIDECSENNCAQLCVNYPGG 262
QY 169 YTHCDGRGGLKLSQDMDCITLPCVPFSPVSKVSLYLGRMFSGTPIRLRFK 223
DB 263 YTCYCDGKGFKLADQKSCVAVPCLPLDLDKNYELLYLAQFAGV-VLYLKER 316

RESULT 7
S53433

plasma protein S precursor, vitamin K dependent - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Aug-1995 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: S53433
R;Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
Biochem. J. 305, 397-403, 1995
A;Title: Identification of candidate residues for interaction of protein S with C4b bindi
A;Reference number: S53433; MUID:95134217; PMID:7832752
A;Accession: S53433
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-642 <GRE>
A;Cross-references: UNIPROT:Q29094; EMBL:L31379
A;Experimental source: tissue type liver
C;Genetics:
A;Gene: PROS

C;Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F;1-51/Domain: Gla domain homology (fragment) <GLA>
F;1-7/Domain: signal sequence (fragment) #status predicted <SIG>
F;8-642/Product: plasma protein S #status predicted <MAT>
F;87-120/Domain: EGF homology <EG1>
F;127-165/Domain: EGF homology <EG2>
F;171-207/Domain: EGF homology <EG3>
F;213-248/Domain: EGF homology <EG4>
F;281-633/Domain: sex hormone-binding globulin homology <SHB>
F;291-444/Domain: laminin G repeat homology <LGR>

Query Match 45.8%; Score 593.5; DB 2; Length 642;
Best Local Similarity 43.4%; Pred. No. 1.6e-36;
Matches 102; Conservative 40; Mismatches 80; Indels 13; Gaps 4;

QY 1 PRYLDCINKYSPYTKNSGFAT-----CVQNLPDQCTPNPCDRKGTQACQDLMGNFF 52

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Db 49 PAYLACGSGFRAGLFTARLSTNAYPDLRSVCNVAIPDQCNPPLPCNEDGFWTKDQGMFT 108
Qy 53 CLCKAGGRLCDKDVNECSQE---NGGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 109 CICKSGWEGEKELDINECKDPNNGGCSQICDNTFGSHCSKSGFIMLSNKKDKDV 168
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 169 DECVKPSICDTAVCKNIPGDCECEPGYRNPFTLSCEDVDCESENMCALCVNYPGG 228
Qy 169 YTHCHDGRGGLKLSQDMDCEDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 229 YSCYCDGKRGFKLAQDKSCSAVPVCLPLNLDKNYELLYLAEQFVG-VLYLRFK 282

RESULT 8
KXRTS
Plasma protein S precursor - mouse
N/Alternate names: vitamin K-dependent glycoprotein S
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004
A/Accession: S43504; 159616; S35962
R/Chu, M.D.; Sun, J.; Bird, P
Biochim. Biophys. Acta 1217, 325-328, 1994
A/Title: Cloning and sequencing of a cDNA encoding the murine vitamin K-dependent protein S
A/Reference number: S43504; MUID:94198297; PMID:8148380
A/Accession: S43504
A/Molecule type: mRNA
A/Residues: 1-675 <CHU>
A/Cross-references: UNIPROT:Q08761; EMBL:Z25469; NID:G396426; PIDN:CAA80961.1; PID:G3964
R/Lu, D.; Schmidt, D.K.; Long, G.L.
Thromb. Res. 74, 135-142, 1994
A/Title: Structure of mouse protein S as determined by PCR amplification and DNA sequencing
A/Reference number: 159616; MUID:94302659; PMID:8029814
A/Accession: 159616
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 33-492, 'L', 494-675 <RES>
A/Cross-references: GB:127439; NID:G487866; PIDN:AAA40006.1; PID:G487867
C/Complex: in plasma forms a complex with C4b binding protein
C/Function:
A/Description: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest
C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
C/Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; blood coagulation; carbox
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:26-85/Domain: Gla domain homology <GLA>
F:42-675/Product: plasma protein S #status predicted <MAT>
F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-666/Domain: sex hormone-binding globulin homology <SHB>
F:325-478/Domain: laminin G repeat homology <LGR>
F:47,48,55,57,60,61,66,67,70,73,77/Modified site: gamma-carboxyglutamic acid (Glu) #stat
F:58-63,88-113,121-134,126-143,154-154,161-175,171-184,186-199,205-217,212-226,228-241,2
F:111-112/cleavage site: Arg-Ser (thrombin) #status predicted
F:119-121/cleavage site: Arg-Ser (thrombin) #status predicted
F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F:177,219,258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F:499,509/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 45.6%; Score 591.5; DB 1; Length 675;
Best Local Similarity 44.7%; Pred. No. 2.3e-36;
Matches 105; Conservative 35; Mismatches 82; Indels 13; Gaps 5;
KXRTS
Qy 1 PRYLDICNKY--GSPYTNNGS-----FATCVQNLPCQCTPNPCDRKGTOACQDLMGNFF 52
Db 83 KYLGCLGAFVSGFHAARQSANAYPDLRSVCVAISDQCDIPICNEDGYLACDQGAFT 142
Qy 53 CLCKAGGRLCDKDVNECSQE---SQENGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109
Db 143 CFCKPGWQGRQCYDVNECKDPSNVNGGCSQICDNTFGSHCSKRGFAMLPNKKDKDL 202
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Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECALKPSCGTAVCKNIPGDCECEPGYRNPFTLSCEDVDCESENMCALCVNYPGG 262
Qy 169 YTHCHDGRGGLKLSQDMDCEDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRFK 223
Db 263 YSCYCDGKRGFKLAQDKSCSAVPVCLPLNLDKNYELLYLAEQFVG-VLYLRFK 316
```

RESULT 9

S38819

Plasma protein S - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 18-Feb-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

A/Accession: S38819; S37238

R/He, X.; Dahlbaeck, B.

Eur. J. Biochem. 217, 857-865, 1993

A/Title: Molecular cloning, expression and functional characterization of rabbit anticoag

A/Reference number: S38819; MUID:94039141; PMID:8223642

A/Accession: S38819

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-646 <HEX>

A/Cross-references: UNIPROT:P98118; EMBL:Z26485

R/He, X.; Dahlbock, B.

submitted to the EMBL Data Library, September 1993

A/Description: Molecular Cloning and Expression of Rabbit Anticoagulant Vitamin K-depende

A/Reference number: S37238

A/Accession: S37238

A/Molecule type: mRNA

A/Residues: 1-502, 'L', 504-646 <HE2>

A/Cross-references: EMBL:Z26485; NID:G403306; PIDN:CAA81259.1; PID:G403307

C/Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

F:1-56/Domain: Gla domain homology (fragment) <GLA>

F:92-125/Domain: EGF homology <EG1>

F:132-170/Domain: EGF homology <EG2>

F:176-212/Domain: EGF homology <EG3>

F:218-253/Domain: EGF homology <EG4>

F:286-637/Domain: sex hormone-binding globulin homology <SHB>

F:296-449/Domain: laminin G repeat homology <LGR>

Query Match

Best Local Similarity 45.2%; Score 586.5; DB 2; Length 646;

Matches 101; Conservative 39; Mismatches 81; Indels 13; Gaps 5;

Qy 1 PRYLDICNKYGSFY---TKNSG-----FATCVQNLPCQCTPNPCDRKGTOACQDLMGNFF 52

Db 54 KYLGCLGSGFRALKFTATRRSANGYPDLRSVCNVAIPDQCNPPLPCSEEGYLNCKDQATFT 113

Qy 53 CLCKAGGRLCDKDVNECSQE---NGGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDI 109

Db 114 CICKPGWQGRQCYDVNECKDPSNVNGGCSQICDNTAGSYHCSKSGFVLANEKCKDM 173

Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGRCEQVCVNSPGS 168

Db 174 DECVKPSICGTAVCKNIPGDCECEPGYRNPFTLSCEDVDCESENMCALCVNYPGG 233

Qy 169 YTHCHDGRGGLKLSQDMDCEDILPCVPPFSVAKSVKSLYLGRMFSGTPVIRLRF 222

Db 234 YSCYCDGKRGFKLAQDKSCSAVPVCLPLDLDKNYQLLYLAEQFVG-VLYLRF 286

RESULT 10

KXRTS

Plasma protein S precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 04-Oct-1995 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004

A/Accession: JCA4180

R/Vasada, F.; Hayashi, T.; Tanitame, K.; Nishioka, J.; Suzuki, K.

J. Biochem. 117, 374-383, 1995

A/Title: Molecular cloning and functional characterization of rat plasma protein S.

A/Reference number: JCA4180; MUID:95332263; PMID:7608128

A:Accession: J04180
A:Molecule type: mRNA
A:Residues: 1-675 <YAS>
C:Cross-references: UNIPROT:P53813; GB:S78744; NID:G1041903; PIDN:AAC60704.1; PID:gl0419
C:Comment: This protein is a vitamin K-dependent plasma glycoprotein that has an anticoagulation of coagulation factors Va and VIIa. This protein also binds to factor Va and C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat homology; beta-hydroxyaspartic acid; beta-hydroxyaspartic acid; blood coagulation; carboxyl; 1-24/Domain: signal sequence #status predicted <SIG>
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-41/Domain: propeptide #status predicted <PRO>
F:42-675/Domain: Gla domain homology <GLA>
F:88-116/Domain: thrombin-sensitive #status predicted <THS>
F:121-154/Domain: EGF homology <EG1>
F:161-199/Domain: EGF homology <EG2>
F:205-241/Domain: EGF homology <EG3>
F:247-282/Domain: EGF homology <EG4>
F:315-478/Domain: sex hormone-binding globulin homology <SHB>
F:325-478/Domain: laminin G repeat homology <LGR>
F:47, 48, 55, 57, 60, 61, 66, 67, 70, 73, 77/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted <G>
F:58-63, 88-113, 121-134, 126-143, 145-154, 161-175, 171-184, 186-199, 205-217, 212-226, 228-241, 247-258/Modified site: Arg-Ser (thrombin) #status predicted <S>
F:111-112/Cleavage site: Arg-Ser (thrombin) #status predicted <S>
F:136/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted <ASP>
F:177, 219, 258/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted <ASP>
F:499, 509/Binding site: carboxylate (Asn) (covalent) #status predicted <ASP>

Query Match 45.1%; Score 585.5; DB 1; Length 675;
Best Local Similarity 43.0%; Pred. No. 6.5e-36;
Matches 101; Conservative 41; Mismatches 80; Indels 13; Gaps 5;

QY 1 PRLYDCINRY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLGLGAFRCVAFSAQAQANAYPDLRSCVNAIFDQDPFPCNEDGYLSCDKGGQAT 142

QY 53 CLKAGGRLCDKDVNEC---SQENGGLQICHNKPFGSHCHSGFELSSDGRTCQDI 109
Db 143 CIKCPGWQDKQCFDINECKDPNENGGCSQTCNDTPGSHVCSCKIGFAMLTNKKCKDV 202

QY 110 DECA-DSEACGEARCNLPQSVCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECLSPKSPGCTAVCKNIPGDFECPNGYDPSKSKVDCESENTCAQLCVNYPGG 262

QY 169 YTHCHDGRGLKLSQDMDCITLPCVPFSPVSAKSVKSLYLGRMFGTTPVIRLRFK 223
Db 263 YSYCDGKKGFKLAQQRCEGIPVCLSLDLNKNVYLLAEQFAGV-VLYLKER 316

RESULT 11
S78040
fibulin, splice form C precursor - mouse
N:Alternate names: basement-membrane protein BM-90
C:Species: Mus musculus (house mouse)
C:Date: 24-Jul-1998 #sequence revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S78040; S78560; S36440
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A:Reference number: S34968; MUID:93358897; PMID:8354280
A:Accession: S78040
A:Molecule type: mRNA
A:Residues: 1-685 <PAN>
A:Cross-references: UNIPROT:Q08879; EMBL:X70854
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-depe
A:Reference number: S36440
A:Accession: S78560
A:Molecule type: mRNA
A:Residues: 1-39, 'P', 41-685 <CHU>
A:Cross-references: EMBL:X70854
C:Genetics: 568/3
C:Superfamily: fibulin-1; EGF homology

C:Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-685/Product: fibulin, splice form C #status predicted <MAT>
F:98,537,541/Binding site: carboxylate (Asn) (covalent) #status predicted <MAT>

Query Match 27.9%; Score 362; DB 2; Length 685;
Best Local Similarity 38.2%; Pred. No. 1.8e-19;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 6 CINKYGSPTKNSGFATCVQNLDP-----DQCTP--NPCDRKGTQACQ 45
Db 327 CINTEGS-----YTCQKNVPCNGRGYHLNEEGTRCVDVDECAPPAEPCG-KG-HHCL 376

QY 46 DLMGNFFCLCKAGWG----GRLCDKDVNECSQENG-CLQICHNKPFGSHCHSGFELS 100
Db 377 NSPGSFRCCKAGFYFDIGISRTC-VDINECQYPRGLGHKCENTPGFSGHSCSAGFRLS 435

QY 101 SDGRTCDIDECADSEACGEARCNLPQSVCLDEGFAYSSQEKACRDVDECLQGR-- 157
Db 436 VDRSCEDVNECLNPFCSQEQ--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 493

QY 158 --CEQVCVNSPGSYTCHDGRGLKLSQDMDCITLPCV 195
Db 494 HTCSYRCINIPGSGFQSCPS-SGYRLAPNGRNCQDIDECV 532

RESULT 12
S34968
fibulin, splice form D precursor - mouse
N:Alternate names: basement-membrane protein BM-90; calcium-binding protein BM-90
C:Species: Mus musculus (house mouse)
C:Date: 10-Dec-1993 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S34968; S36441; S13814
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
Eur. J. Biochem. 215, 733-740, 1993
A:Title: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-dependent
A:Reference number: S34968; MUID:93358897; PMID:8354280
A:Accession: S34968
A:Molecule type: mRNA
A:Residues: 1-705 <PAN>
A:Cross-references: UNIPROT:Q08879
R:Pan, T.C.; Kluge, M.; Zhang, R.Z.; Mayer, U.; Timpl, R.; Chu, M.L.
submitted to the EMBL Data Library, January 1993
A:Description: Sequence of extracellular mouse protein BM-90/fibulin and its calcium-depe
A:Reference number: S36440
A:Accession: S36441
A:Molecule type: mRNA
A:Residues: 1-39, 'P', 41-705 <PAN>
A:Cross-references: EMBL:X70854; NID:G396820; PIDN:CAA50207.1; PID:G396821
A:Experimental source: cell-line F9 teratocarcinoma
R:Kluge, M.; Mann, K.; Dziadek, M.; Timpl, R.
Eur. J. Biochem. 193, 651-659, 1990
A:Title: Characterization of a novel calcium-binding 90-kDa glycoprotein (BM-90) shared
A:Reference number: S13814; MUID:91065369; PMID:2249686
A:Accession: S13814
A:Molecule type: protein
A:Residues: 28:31-49, 'X', 51-53, 'XX', 110-117, 231-240, 'X', 242-243, 339-362, 'S', 364-387, 434-4
C:Superfamily: fibulin-1; EGF homology
C:Keywords: alternative splicing; basement membrane; calcium binding; extracellular matrix
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-705/Product: fibulin, splice form D #status predicted <MAT>
F:98,537,541/Binding site: carboxylate (Asn) (covalent) #status predicted <MAT>

Query Match 27.9%; Score 362; DB 2; Length 705;
Best Local Similarity 38.2%; Pred. No. 1.9e-19;
Matches 84; Conservative 24; Mismatches 68; Indels 44; Gaps 12;

QY 6 CINKYGSPTKNSGFATCVQNLDP-----DQCTP--NPCDRKGTQACQ 45
Db 327 CINTEGS-----YTCQKNVPCNGRGYHLNEEGTRCVDVDECAPPAEPCG-KG-HHCL 376

QY 46 DLMGNFFCLCKAGWG----GRLCDKDVNECSQENG-CLQICHNKPFGSHCHSGFELS 100

Db 325 CINTGSG-----YTCQKNVPCGRGYHLNEEGTRCVDVDECAPPEPCG-KG-HRCV 374

QY 46 DLGMNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 100

Db 375 NSPGSFCECKTGYFDGIRMC-VDVNECORYPGLCHGKCENTUGSLYSCSVGFRUS 433

QY 101 SDGRTQDIDECADSEACGEARCKNLPFGSYCLCDGFAFVSSQE-KACRDVDECLQGR-- 157

Db 434 VDGSRCEIDNECSSPCSQE--CANVYGSYQCYCRGYQLSDVDGVTCEIDECALPTGG 491

QY 158 --CEQVNVSPGTYTCHDGRGGLKLSQDMTCEIDLPCV 195

Db 492 HICSYRCINIFGSCFQSCPS-SGYRLAPNRCNQDIDECV 530

RESULT 22

A49457

fibulin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C:Accession: A49457; S74095

R:Pan, T.C.; Sasaki, T.; Zhang, R.Z.; Paessler, R.; Timpl, R.; Chu, M.L.

J. Cell Biol. 123, 1269-1277, 1993

A:Title: Structure and expression of fibulin-2, a novel extracellular matrix protein with a calcium binding site

A:Reference number: A49457; MUID:94064787; PMID:8245130

A:Accession: A49457

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1221 <PAN>

A:Cross-references: UNIPROT:P37889; GB:X75285; NID:9437046; PIDN:CAA53040.1; PID:9437047

R:Sasaki, T.; Mann, K.; Murphy, G.; Chu, M.L.; Timpl, R.

Eur. J. Biochem. 240, 427-434, 1996

A:Title: Different susceptibilities of fibulin-1 and fibulin-2 to cleavage by matrix metalloproteinases

A:Reference number: S74094; MUID:96439073; PMID:8841408

A:Accession: S74095

A:Molecule type: protein

A:Residues: 236-238, 'X', 346-361, 'L', 346-361, 405-426, 566-568, 'EM', 569-589

C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C:Keywords: calcium binding; duplication; extracellular matrix; glycoprotein; homotrimer

F;942-978/Domain: EGF homology <EGF>

Query Match 26.1%; Score 339; DB 2; Length 1221;

Best Local Similarity 36.6%; Pred. No. 1.4e-17;

Matches 78; Conservative 27; Mismatches 68; Indels 40; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCD-----RKGT-QACQDLM 48

Db 864 CINTVGSYTCQRNPLVCGRGYHANESEGCVD-----VNECETGVHRCGEGQLCYNLP 916

QY 49 GNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 103

Db 917 GSYRCCKPGFQDAFGRTC-IDVNECWSPGLCQHTCENTPGSYRCSNAGFLLAADG 975

QY 104 RTCODIDECADSBACGEARCKNLPFGSYCLCDGFAFVSSQEKACRDVDECLQGR---CEQ 160

Db 976 KHCEDVNEC-ETRRCSQ-ECANIYGSYQCYCRGYQLAEDGHTCTDIDECACGAGILCTF 1033

QY 161 VCVNSPGSYTCHDGRGGLKLS-----QMDTC 188

Db 1034 RCNVNFGSYQACPEQGYTMANGRSCKDLDEC 1066

RESULT 23

A55184

fibulin-2 precursor - human

N:Alternate names: protein DKFPz586A1519.1

C:Species: Homo sapiens (man)

C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 09-Jul-2004

R:Zhang, R.Z.; Pan, T.C.; Zhang, Z.Y.; Mattei, M.G.; Timpl, R.; Chu, M.L.

Genomics 22, 425-430, 1994

A:Title: Fibulin-2 (FBLN2): human cDNA sequence, mRNA expression, and mapping of the gene

A:Reference number: A55184; MUID:95104855; PMID:7806230

A:Accession: A55184

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1184 <ZHA>

A:Cross-references: UNIPROT:P98095; GB:X82494; NID:9575232; PIDN:CAA57876.1; PID:9575233

R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z16471

A:Accession: T08744

A:Molecule type: mRNA

A:Residues: 656-719, 'QDECLMGADCSRQFCVNTLGSFVCVNHVLCADGYILNAHRKCDV', 720-853, 'T', 855-111

A:Cross-references: EMBL:AL050095

A:Experimental source: adult uterus; clone DKFPz586A1519

C:Genetics:

A:Gene: GDB:FBLN2

A:Cross-references: GDB:293037; OMIM:135821

A:Map position: 3p25-3p24

A>Note: DKFPz586A1519.1

C:Superfamily: fibulin-2; EGF homology; von Willebrand factor type C repeat homology

C:Keywords: alternative splicing; extracellular matrix

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-1184/Product: fibulin-2 protein #status predicted <MAT>

F:905-941/Domain: EGF homology <EGF>

Query Match 26.0%; Score 337; DB 2; Length 1184;

Best Local Similarity 36.4%; Pred. No. 1.9e-17;

Matches 78; Conservative 30; Mismatches 70; Indels 36; Gaps 11;

QY 6 CINKYGS-----PYTKNSGFATCVQNLPDQCTPNPCD-----RKGT-QACQDLM 48

Db 827 CINTVGSYTCQRNPLICARGYHASDDGAKCDV-----VNECETGVHRCGEGQVCHNLP 879

QY 49 GNFFCLCKAGWG---GRLCDKDVNECSQENG-CLQICHNKPGSPHCSCHGSFELS 103

Db 880 GSYRCCKAGFQDAFGRC-IDVNECWSPGLCQHTCENTPGSYRCSNAGFLLAADG 938

QY 104 RTCODIDECADSEACGEARCKNLPFGSYCLCDGFAFVSSQEKACRDVDECLQGR---CEQ 160

Db 939 KHCEDVNEC-EAQRCSQ-ECANIYGSYQCYCRGYQLAEDGHTCTDIDECACGAGILCTF 996

QY 161 VCVNSPGSYTCHDGRGGLKLSQDMTCEIDLPC 194

Db 997 RCLNVFGSYQACPEQ-GYTMANGRSCKDVDEC 1029

RESULT 24

A54105

fibillin-2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004

C:Accession: A54105; S17063; S31101

R:Zhang, H.; Apfelroth, S.D.; Hu, W.; Davis, B.C.; Sanguinetti, C.; Bonadio, J.; Mecham, F.

J. Cell Biol. 124, 855-863, 1994

A:Title: Structure and expression of fibillin-2, a novel microfibrillar component preferentially expressed in bone

A:Reference number: A54105; MUID:94165150; PMID:8120105

A:Accession: A54105

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-2918 <ZHA>

A:Cross-references: UNIPROT:P35556; GB:U03272

R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.; Nature 352, 330-334, 1991

A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different genes on chromosome 15

A:Reference number: S17062; MUID:91304567; PMID:1852206

A:Accession: S17063

A:Molecule type: mRNA

A:Residues: 752-1489, 1791, 'GS', 1794-1796, 'QLI', 1922-1923, 'LD', 1926, 'P', 1928 <LEE>

A:Cross-references: EMBL:X62009

R:Milewicz, D.M.

submitted to the EMBL Data Library, December 1992

A:Reference number: S31101

A:Accession: S31101

A:Molecule type: mRNA

A;Residues: 752-1407,'R',1409-1489,1791,'GS',1794-1796,'QLI',1922-1923,'LD',1926,'P',1928
A;Cross-references: EMBL:X62009
C;Genetics:
A;Gene: GDB:FBN2
A;Cross-references: GDB:128122; OMIM:121050
A;Map position: 5q23-5q31
C;Superfamily: fibrillin; EGF homology
C;Keywords: extracellular protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-2918/Product: fibrillin-2 #status predicted <MAT>
F;1245-1280/Domain: EGF homology <EGF1>
F;1970-2013/Domain: EGF homology <EGF>

Query Match 25.6%; Score 331.5; DB 2; Length 2918;
Best Local Similarity 35.4%; Pred. No. 1e-16;
Matches 75; Conservative 32; Mismatches 76; Indels 29; Gaps 12;

QY 5 DCINKYGS-----PYTKNSGFATCVQNLDPDOCT--PNPCDRKGTQACQDLGMNFFCLC 55
Db 1339 ECENTKGSFICHQGLSVKVGKGTGCTD--VDECEGAHNCMDHA--SCNIFGSKCSC 1394

QY 56 KAGW-GGRLCDKDVNECSQENGGCL--QICHNKPFGSCHSGFELSSDGRTCQDIDEC 112
Db 1395 REGWIGNGIKIDLDSCSNTHQCSINAQCVNTPGSRACSGEP--TGDGFTCSVDDEC 1452

QY 113 ADS-EACGEARCKNLPGSYCLDDEGFAYSSQKACRDVDEC-LQGRG-EQVCVNPSGYS 169
Db 1453 AENINLCNGQCLNVPAYRCEEMGFTPASDSRSCQDIDECFQNICVSGTCNNLPGMF 1512

QY 170 TCHCDGRGGLKLSQ-----DMDTCEDILPCV 195
Db 1513 HCICD--DGYELDRTGNCCTDIDECADPINC 1542

RESULT 25
A35626
transforming growth factor beta-1-binding protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35626
R;Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claess
Cell 61, 1051-1061, 1990
A;Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1
A;Reference number: A35626; MUID:90275601; PMID:2350783
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1394
A;Cross-references: UNIPROT:P22064; GB:M34057; NID:g339547; PIDN:AAA61160.1; PID:g339548
C;Keywords: alternative splicing
F;750-791/Domain: EGF homology <EGF>

Query Match 25.5%; Score 330.5; DB 2; Length 1394;
Best Local Similarity 31.3%; Pred. No. 6.6e-17;
Matches 79; Conservative 33; Mismatches 77; Indels 63; Gaps 11;

QY 6 CINKYGS-----PYTKNSGF----ATCVQNLDPQC--TPNPCDRKGTQACQDLGMNFFCLCK 56
Db 686 CVNPSGYSQYQVPCTE--GFRGWNQGCLD--VDECLEPNCV---ANGDCSNLEGSYMCSC 738

QY 57 AGNGRGLCD-----KDVNECSQENGGCLQICHNKPFGSCHSGFELSSDGRTCQDIDEC 112
Db 739 KGY-TRTPDHKCRDIDECQOQNLVNGQCNTGSGFRCTCGQGYQLSAKQOCEIDEC 797

QY 113 ADSEAGEARCKNLPGSYCLDDEGFAYSSQKACRDVDECLOGR--CEQ--VCVNPSGYS 169
Db 798 QHRHLCAHGQCRNTEGFSQCVQDQGYRASGLGDHCEIDNECLBDKSVQCQGDCTINTAGSY 857

QY 170 TC-----HCDGRGGLKLSQDMDTCED 190
Db 858 DCTCPDGFQLDNKTCCODINECEHPGLCGPQGECLNTEGFSFHCVCQGFISADGRCTCED 917

QY 191 ILPCVPFSAKS 202

Db 918 IDECVNNTVCDSS 929

RESULT 26
A57278
fibrillin-2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57278
R;Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995
A;Title: Developmental expression of fibrillin genes suggests heterogeneity of extracellular
A;Reference number: A57278; MUID:95263670; PMID:7744963
A;Accession: A57278
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2907 <ZHA>
A;Cross-references: UNIPROT:Q61555; GB:L39790; NID:g762830; PIDN:AAA74908.1; PID:g762831
C;Superfamily: fibrillin; EGF homology
F;1239-1274/Domain: EGF homology <EGF1>
F;2488-2523/Domain: EGF homology <EGF>

Query Match 25.2%; Score 326.5; DB 2; Length 2907;
Best Local Similarity 31.7%; Pred. No. 2.4e-16;
Matches 80; Conservative 31; Mismatches 90; Indels 51; Gaps 10;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMNFFCLCKAG 58
Db 1167 CVNTEGFSQDCPLGHGELSPSREDCVDINECSLSNLC--RNG--KCVNMGITVQCCSNPG 1223

QY 59 WGG----RLCDKDVNECSQENGGCLQICHNKPFGSCHSGFELSSDGRTCQDIDECADS 115
Db 1224 YQATPDROGCTDIDECIMNNGGCDTQCTINSEGSYECSEGYALMPDGRSCADIDECENN 1283

QY 116 -EACGEARCKNLPGSYCLDDEGFAYSSQKACRDVDE-----CLQGRCEQVCVNPSG 167
Db 1284 PDICDGGQCTNIPGEYRCCLCYDGFMA5MDMKTCTIDVNECDLNPNCMFGECE----NTKG 1339

QY 168 SYTCHCDGRGGLKLSQDMDTCEDILPC-----VPPFS-----VAKSV 203
Db 1340 SFICHG--QLGYSVKVKGTTGCTDDECEIGAHCMDHASCNLPVPSFKSCREGWVGNGI 1397

QY 204 KSLYLGRMFSGT 215
Db 1398 KCIDLDECANGT 1409

RESULT 27
I38449
extracellular protein - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I38449
R;Jeska-Czernik, B.; Lumpkin, C.K.
Mol. Cell. Biol. 15, 120-128, 1995
A;Title: An overexpressed gene transcript in senescent and quiescent human fibroblasts er
A;Reference number: I38449; MUID:95097983; PMID:7799918
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: EMBL:U03877; NID:g458227; PIDN:AAA65590.1; PID:g458228
C;Genetics:
A;Gene: S1-5

Query Match 24.7%; Score 321; DB 2; Length 387;
Best Local Similarity 38.2%; Pred. No. 1.2e-16;
Matches 65; Conservative 30; Mismatches 65; Indels 10; Gaps 7;

QY 29 DQCTPNPCDRKGTQACQDLGMNFFCLCKAGW--GGRLCDKDVNECSQENGGCLQICHNKP 86
Db 69 DECTAGTHNCRADQVCINLRGSAFCQCPGPKRQGC--VDIDECTIP--PYHQRCVNTP 126

T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27283
R;Ainscough, R.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20336
A;Accession: T27283
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1620 <N1>
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CA854471.1; CESP:Y64G10A.f
A;Experimental source: clone Y64G10A
C;Genetics:
A;Gene: CESP:Y64G10A.f
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7
Query Match 24.6%; Score 319.5; DB 2; Length 1620;
Best Local Similarity 37.3%; Pred. No. 4.8e-16;
Matches 66; Conservative 17; Mismatches 87; Indels 7; Gaps 4;
QY 23 CVQNLDPQCTPNPCDRKGTQACQDLGN-FPCLCKAGWGRLCDKDVNCSQENGGGLQI 81
DB 71 CLLRVQANCADLCHNGGTCTVPSEHNDNEQVCECPVGTAKQCYDANECHVANNGGCEHE 130
QY 82 CHNKPFSFCHSGHSGFELSDGRTCDIDECADSEACGEARCKNLPGSYSLCDEGFAYS 141
DB 131 CVNTIGTYRCWPGFELSDGNTCSIDIECAVSNCGSDRCVNSPGFRCDPCSDIYLH 190
QY 142 SOEKACRDVDECL--QRCQGVNCSFGS--YTHCDGRGLKLSQMDTCEDILPC 194
DB 191 ADGRTCGVKTSCTDNGGCGEHCENDSNGEYRCRC--RVGFKLSENKRSCQPVDPDC 245
RESULT 32
A38261
masking protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jun-1991 #sequence_revision 14-Jun-1991 #text_change 09-Jul-2004
C;Accession: A38261
R;Tsuiji, T.; Okada, F.; Yanaguchi, K.; Nakamura, T.
Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990
A;Title: Molecular cloning of the large subunit of transforming growth factor type beta
A;Reference number: A38261; MUID:91062373; PMID:2247454
A;Accession: A38261
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1712 <TSU>
A;Cross-references: UNIPROT:Q00918; GB:M55431; NID:g207285; PIDN:AAA42235.1; PID:g207286
F;911-947/Domain: EGF homology <EGF>
Query Match 24.6%; Score 319.5; DB 2; Length 1712;
Best Local Similarity 31.3%; Pred. No. 5e-16; Mismatches 78; Indels 63; Gaps 12;
Matches 79; Conservative 32; Mismatches 78; Indels 63; Gaps 12;
QY 6 CINKYGS----PYTKNSGF----ATCVQNLDPQC--TPNPCDRKGTQACQDLGNFFCLCK 56
DB 1005 CVNSPGSYQVCPCTE--GFRGNGCQLD--VDECLQPKVCT---NGSCTNLEGSYMSCH 1057
QY 57 AGWG-----GRLCDKDVNCSQENGGGLQICHNKPFSFCHSGHSGFELSDGRTCDIDEC 112
DB 1058 KGYSPTPDHRC-QDIDECQGNLCMNGQCKNTDGSFRCTCGQGYQLSAAKQDCEDIDEC 1116
QY 113 ADSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGR--CE-QVCVNSPGSY 169
DB 1117 EHRHLSHGQCRNTEGFSQCLCNQGYRASVLGDHCEIDNECLSDSSVCGQDCINTAGSY 1176
QY 170 TCHC-----DGRG-----GLKLSQMDTCED 190
DB 1177 DCTCPDGLQNDNKGCCODINECAQPLGCPHGBCLNTQGSFHCVCQGFISADGRTCED 1236
QY 191 ILPCVPFSAKS 202

Db 1237 IDECVANTVCDS 1248
RESULT 33
T46488
hypothetical protein DKFPz434J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23035
A;Accession: T46488
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: UNIPROT:Q8ND56; EMBL:AL137638
A;Experimental source: adult testis; clone DKFPz434J065
C;Genetics:
A;Note: DKFPz434J065.1
Query Match 24.3%; Score 315.5; DB 2; Length 741;
Best Local Similarity 38.4%; Pred. No. 5.1e-16;
Matches 61; Conservative 21; Mismatches 64; Indels 13; Gaps 4;
QY 44 CQDLMGNFCLCKAGWGRLCDKDVNE-----CSQENGGGLQICHNKPFSFCHSGHSGF 97
DB 38 CINIPGSYVCRCKQGY---ILNSDQTTCTRIQDLICAMEDHNCQECQVCVNVPGSFVCQCVSGY 94
QY 98 ELSSDQRTQDIDECADSEACGEARCKNLPGSYSLCDEGFAYSQEKACRDVDECLQGR 157
DB 95 ALAEDGKRCVADVDCASENHGCEHCENADGSLCQCHGEGFALNPDEKCTCTKIDYCASSN 154
QY 158 --CEQVCVNSPGSYTCHCDGRGLKLSQMDTCEDILPC 194
DB 155 HGCQHECVNTDSDSYCHC--LKGFTLNPDKTKTCTRRINYC 191
RESULT 34
A57172
probable hormone receptor EMR1 precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57172
R;Baud, V.; Chissole, S.L.; Viegas-Pequignot, E.; Diriong, S.; N'Guyen, V.C.; Roe, B.A.; I
Genomics 26, 334-344, 1995
A;Title: EMR1, an unusual member in the family of hormone receptors with seven transmembr
A;Reference number: A57172; MUID:95324926; PMID:7601460
A;Accession: A57172
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-886 <BAU>
A;Cross-references: UNIPROT:Q14246; GB:X81479; NID:g784993; PIDN:CAA57232.1; PID:g784994
C;Genetics:
A;Gene: GDB:EMR1
A;Cross-references: GDB:378349; OMIM:600493
A;Map position: 19p13.3-19p13.3
C;Keywords: transmembrane protein
F;136-170/Domain: EGF homology <EGF>
Query Match 24.1%; Score 312; DB 2; Length 886;
Best Local Similarity 30.8%; Pred. No. 1.1e-15;
Matches 82; Conservative 29; Mismatches 81; Indels 74; Gaps 15;
QY 1 PRYLDICNKYGSPTYNKSGFATCVQL-----PDQC--TPNPCDRKG 40
DB 42 PAYATCTN-----TVDSYCTCKQGLSSNGQNHFPDGVRCOKIDECSSQSPQCG--P 93
QY 41 TQACQDLGNFFCLCKAGWG-----GRLCDKDVNEC-----SQENGGGLQICH 83
DB 94 NSCKNLGRYKCSCLDGFSSPTGNDWVPGKPGNFCTDINECLTSRVCPHEHSDCV---- 149

QY 84 NKPSPGSHCSHGFELSSDGTQDIDECADSEACGE-ARCKNLPGSYSLCDEGFAYSS 142
 DB 150 NSNGSYSCSQGVF--ISRNSICEDVNECADPRACPEHATCNTVTGNYSCFCNPFESS 207
 QY 143 -----QEKACRDVDECLQGR--BOVCVNSPGSYTYHC-----DGRGLKLS 182
 DB 208 GHLSCQGLKASCEIDECTE-MCPINSTCTNTPGSYFCTCHPGFADSPSQLNFTDQGVC 266
 QY 183 QDMWTC-EDILPCVPSPVAKSVKSLY 207
 DB 267 RDIDECQDPSTCGPNSICTNALGSY 292

RESULT 35
 T13954
 MEGF6 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13954
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Status: preliminary
 A:Accession: T13954
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1574 <NAK>
 A:Cross-references: UNIPROT:O88281; EMBL:AB011532; NID:G3449293; PIDN:BAAB32462.1; PID:93
 A:Experimental source: strain Sprague-Dawley; brain
 C:Genetics:
 A:Gene: MEGF6

Query Match 23.9%; Score 310.5; DB 2; Length 1574;
 Best Local Similarity 34.5%; Pred. No. 2.2e-15;
 Matches 79; Conservative 23; Mismatches 76; Indels 51; Gaps 13;

QY 19 GFATCVQNLPDQCTPN---PCDRKGTQ-----ACQDLMGNFFCLCKAGW-- 59
 DB 267 GLAHC-----GCHPGYQLAARDKTEDVDICALGALQAQCNLTQGSFKVCVCHAGYEL 320
 QY 60 --GGRLCDK----DVNECSQENGCGLOIC-HNKPSPGSHCSHGFELSSDGTQDIDSC 112
 DB 321 GADGRQCYRIEMIVNCEAGNGSGHGSHTSGPL-CTCPRGYELDEDQKTCIDIDDC 379
 QY 113 ADSEAGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGR--CEQVCVNSPGSYT 170
 DB 380 ANSPCCQQA-CANTPGYECSPAGYRLNTDGCCEVDVDEACSGHGGCEHHCSNLAGSFQ 438
 QY 171 CHCDGRGGLKLSQDMTCDILPCVPSPVAKSVKSLYLGRMFSGTPVIR 219
 DB 439 CFCE--AGYRLDEDRGCT-----SLEESVVLDL-GRL---PFVR 472

RESULT 36
 S78549
 notch3 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S78549; S71825
 R:Youtel, A.; Tournier-Lasserre, E.
 submitted to the EMBL Data Library, April 1997
 A:Reference number: S78549
 A:Accession: S78549
 A:Molecule type: mRNA
 A:Residues: 1-2321 <JOUT>
 A:Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:G2668591; PIDN:AA93171.1; PID:G266
 R:Youtel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitc
 x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserre, E.
 Nature 383, 707-710, 1996
 A:Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
 A:Reference number: S71825; MUID:97032728; PMID:8878478
 A:Accession: S71825
 A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
 A:Residues: 67-113,138-194,268-333,'G',335-346,536-613,716-765,1240-1279,1815-1888 <JOU2>
 A:Cross-references: EMBL:U97669
 C:Genetics:
 A:Gene: notch3
 A:Map position: 19p13.1
 C:Function:
 A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: tandem repeat; transmembrane protein
 C:Key words: EGF homology <EGX1>
 F:123-155/Domain: EGF homology <EGF1>
 F:162-194/Domain: EGF homology <EGX2>
 F:240-271/Domain: EGF homology <EGX2>
 F:318-349/Domain: EGF homology <EGX2>
 F:473-504/Domain: EGF homology <EGX3>
 F:853-884/Domain: EGF homology <EGX3>
 F:928-959/Domain: EGF homology <EGX4>
 F:1838-1870/Domain: ankyrin repeat homology <AN1>
 F:1871-1903/Domain: ankyrin repeat homology <AN2>
 F:1905-1937/Domain: ankyrin repeat homology <AN3>
 F:1938-1970/Domain: ankyrin repeat homology <AN4>
 F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 23.1%; Score 299.5; DB 2; Length 2321;
 Best Local Similarity 33.5%; Pred. No. 1.9e-14;
 Matches 75; Conservative 29; Mismatches 87; Indels 33; Gaps 13;

QY 6 CLNKYGS-----PYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLMGNFFCLCKAG 58
 DB 408 CVNTQGSFLCQCGRGYTG-----PRCETDV-NECLSGPCRNQAT--CLDRIGQFTCLCMAG 460
 QY 59 WGRCLCDKDVNECSQE---NGGCLQICHNKPSPGSHCSHGFELSSDGTQCO-DIDECA 114
 DB 461 FGTGTYCEVDIDECQSSPCVNGG---VCKDRVNGFSCCTPSGF----SGSTCQLDVDECA 513
 QY 115 SPACGEARCKNLPGSYSLCDEGFAYSSQEKAC-RDVDECLQGRCEQ-VCVNSPGSYTCH 172
 DB 514 TPCRNKAKCVDQPDGQYECRCABEGF---EGTLCDRNVDDCSPPDCHGRCVDGDIASFCA 569
 QY 173 C-DGRGGLKLSQDMTCDILPCVPSPVAKSVKSLYLGRMFSGT 215
 DB 570 CAPGYTGRCESQVDECRS-QPCRHGGKCLDLVDKYLRCPSGT 612

RESULT 37
 S45306
 notch3 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C:Accession: S45306
 R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
 Mech. Dev. 46, 123-136, 1994
 A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1
 A:Reference number: S45306; MUID:95001556; PMID:7918097
 A:Accession: S45306
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2318 <LAR>
 A:Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:G483580; PIDN:CAA52776.1; PID:G48358
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 F:163-195/Domain: EGF homology <EGF1>
 F:474-505/Domain: EGF homology <EGF>
 F:854-885/Domain: EGF homology <EGF2>
 F:1839-1871/Domain: ankyrin repeat homology <AN1>
 F:1872-1904/Domain: ankyrin repeat homology <AN2>
 F:1906-1938/Domain: ankyrin repeat homology <AN3>
 F:1939-1971/Domain: ankyrin repeat homology <AN4>
 F:1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 22.5%; Score 291.5; DB 2; Length 2318;
 Best Local Similarity 32.7%; Pred. No. 7.4e-14;
 Matches 73; Conservative 30; Mismatches 89; Indels 31; Gaps 12;

QY 6 CINKYGS-----PYTKNSGFATCVQNLDPQCTPNFCDRKGTQACQDLMGNFCLCKAG 58
Db 409 CVNTQGSFLQCCGGYTG----PRCETDV-NECLSGPCRQAT--CLDRIGQFTCIWAG 461
QY 59 WGGRLCKDVNCSQEQ---NGGCLQIQIHNKPGSFHCSHGFSFELSSDGRTCQ-DIDSCAD 114
Db 462 FTGYCYEVDIDECOSSPCVNGG---VCKDRVNGFSCTCPSPGF-----SGSMCQLDVBECAS 514
QY 115 SEACGEARCKNLPGSYCLCDEGFPAYSQEKACRDVDECIQGRCEQ-VCVNSPGSYTCHC 173
Db 515 TPCRNAGKCVDPQDGYECRAEGFGLTCE---RNVDDCSPDPCHGRCVGDGIASFSCAC 571
QY 174 -DGRGGLKLSQDMTCDLILPCVFPFSVAKSVKSLYLGRMPSGT 215
Db 572 APGYTGIRCSQVDECRS-QPCRYGKCLDLVDKYLRCPPGT 613
RESULT 38
T34513
hypothetical protein ZK783.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T34513
R;Faville, A.; Vaudin, M.
submitted to the EMBL Data Library, August 1994
A;Description: The sequence of C. elegans cosmid ZK783.
A;Reference number: 221536
A;Accession: T34513
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-3507 <FAV>
A;Cross-references: UNIPROT:Q23587; EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783
A;Experimental source: strain Bristol N2; clone ZK783
C;Genetics:
A;Gene: CESP:ZK783.1
A;Map position: 3
A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/2; 3504/1
Query Match 21.4%; Score 278; DB 2; Length 3507;
Best Local Similarity 29.0%; Pred. No. 1e-12;
Matches 79; Conservative 31; Mismatches 58; Indels 104; Gaps 18;
QY 6 CINKYGSPTYK-NSGFATCVQNLDP--QCTP---NPCD----- 37
Db 1510 CVNKPQYSCENGF-----LGDGYCQVPTTKPKCDSTQSSKSHCSNMSCEVDVTD 1563
QY 38 -----RKGTCACQD-----LMGNFFCLCKAGW--GRLC 64
Db 1564 GSVECKECMGYKSGKVCEDINECVAEKAPCSLNANCVNMNGTFSCSKQGYRGDGFMC 1623
QY 65 DKDVNCSQENGGCLQICH-----NKPQSFHCSHGFSFELSSDQ-----RTCODI 109
Db 1624 -TDINECDERHP-----CHPAAECTNLEGSFKCECHSGFE--GDGIYKTNPLERSCEDV 1675
QY 110 DE-C--ADSBACGEARCKNLPGSYCLCDEGFPAYSQEKACRDVDECIQGR--CE---QV 161
Db 1676 EKFCGRVDHVSCLSVRIYNGSLSVCECPGFREKESNCSVDIDEESRNCDPASAV 1735
QY 162 CVNPSPGSYTCHC-----DGRGGLKLSQDMTCE 189
Db 1736 CVNTEGSYRCEAGYEGEGG--VCTDIDEC 1765
RESULT 39
S16148
gene serrate protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1991 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S16148; S16878; A36666
R;Thomas, U.; Speicher, S.A.; Knust, E.
Development 111, 749-761, 1991
A;Title: The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a cd

A;Reference number: S16148; MUID:91347903; PMID:1840519
A;Accession: S16148
A;Molecule type: mRNA
A;Residues: 1-1408 <THO1>
A;Cross-references: UNIPROT:P18168; EMBL:X56811
R;Thomas, U.
submitted to the EMBL Data Library, November 1990
A;Reference number: S16878
A;Accession: S16878
A;Molecule type: mRNA
A;Residues: 1-1351,'T',1353-1408 <THO2>
A;Cross-references: EMBL:X56811; NID:g8563; PID:g8564
R;Fleming, R.J.; Scottgale, T.N.; Diederich, R.J.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2188-2201, 1990
A;Title: The gene Serrate encodes a putative EGF-like transmembrane protein essential for
A;Reference number: A36666; MUID:91099666; PMID:2125287
A;Accession: A36666
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15,20-26,'A',28-1408 <PLE>
A;Cross-references: GB:M35759; NID:g158605; PID:g158606
C;Genetics:
A;Gene: FlyBase:Ser
A;Cross-references: FlyBase:FBgn0004197
C;Keywords: glycoprotein; transmembrane protein
F;1-84/Domain: signal sequence #status predicted <SIG>
F;85-1408/Product: gene serrate protein #status predicted <MAT>
F;85-1221/Domain: extracellular #status predicted <EXT>
F;283-316/Domain: EGF homology <EG01>
F;319-348/Domain: EGF homology <EG02>
F;355-388/Domain: EGF homology <EG03>
F;395-488/Domain: EGF homology #status atypical <EG04>
F;495-526/Domain: EGF homology <EG05>
F;533-608/Domain: EGF homology #status atypical <EG06>
F;615-645/Domain: EGF homology <EG07>
F;652-683/Domain: EGF homology <EG08>
F;690-720/Domain: EGF homology <EG09>
F;727-796/Domain: EGF homology #status atypical <EG10>
F;803-834/Domain: EGF homology <EG11>
F;841-876/Domain: EGF homology <EG12>
F;883-914/Domain: EGF homology <EG13>
F;921-952/Domain: EGF homology <EG14>
F;997-1060/Domain: cysteine-rich
F;1222-1246/Domain: transmembrane #status predicted <TM1>
F;1247-1408/Domain: intracellular #status predicted <INT>
F;152,196,247,331,412,452,558,739,965,977,1004,1030,1150/Binding site: carbohydrate (Asn)
Query Match 21.2%; Score 275.5; DB 2; Length 1408;
Best Local Similarity 27.3%; Pred. No. 7.4e-13;
Matches 74; Conservative 25; Mismatches 75; Indels 97; Gaps 12;
QY 5 DCINKYGSPTYKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLMGNFCLCKAGWGRLC 64
Db 478 DCAAGWTGP-----TCEINI-DECAAGPCEHGT--CIDLIGFRCCEPPEWHGDVC 526
QY 65 DKDVNCSQEN-----ELSSD-----GGCLQI- 81
Db 527 QVDVNECEAPHASAGIAANALLTTTATAIGSNLSSTALLAALTSAAVSTSLAIGPCINAK 586
QY 82 -CHNKFGSFHCSHGFE-----ELSSD-----GRTQC 107
Db 587 ECRNQPQSFACICKEGMGWVTCENLDLDCVQCGRNGATCIDLVNDYRCACASGFTGRDCE 646
QY 108 -DIDECADSEACGEARCKNLPGSYCLCDEGFPAYSQEKACRDV--DECIQGRCEQVCVN 164
Db 647 TDIDECATSPCRNGGECVDMVGKFNICPLGYSGSLCEERAKENCTSPCLGEH----CLN 702
QY 165 SPGSYTCCHC-DGRGGLKLSQDMTCDLILPC 194
Db 703 TPBGYCHCPDPDRAGKHCEQLRPLCSQ-PPC 732
RESULT 40

A40043

notch protein homolog TAN-1 precursor - human

C:Species: Homo sapiens (man)
C:Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004C:Accession: A40043
R:Billiesen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar, R.
Cell 66, 649-661, 1991

A:Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal

A:Reference number: A40043; MUID:91347367; PMID:1931692

A:Accession: A40043

A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A:Molecule type: mRNA

A:Residues: 1-2555 <ELL>

A:Cross-references: GB:M73980

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F:261-292/Domain: EGF homology <EGX1>
F:494-525/Domain: EGF homology <EGF1>
F:987-1018/Domain: EGF homology <EGX2>
F:1149-1180/Domain: EGF homology <EGF>
F:1187-1218/Domain: EGF homology <EGF3>
F:1233-1264/Domain: EGF homology <EGX3>
F:1921-1959/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN2>
F:1994-2026/Domain: ankyrin repeat homology <AN3>
F:2027-2059/Domain: ankyrin repeat homology <AN4>
F:2060-2092/Domain: ankyrin repeat homology <AN5>

Query Match 21.1%; Score 274; DB 2; Length 2555;

Best Local Similarity 30.7%; Pred. No. 1.5e-12;
Matches 69; Conservative 70; Mismatches 90; Indels 36; Gaps 11;

QY 6 CINKYSPYTKNSGF-ATCVQNLP-----DOCTPNPCDRKGTQACODLMGNPFCLCK 56

DB 429 CINTLGS-----FQCQLQGYTGRCEIDVNECVSNPCQNDAT--CLDQIGEPQCMCM 479

QY 57 AGWGRGLCDKDVNECSQ----ENGGCLQICHNKPFGHSCHSFELSDDGRTCQDIDRC 112

DB 480 PGVEGVHCEVNTDECASSPCLHNGRCL----DKINEFQCECTGTF--TGHLCQDVDEC 531

QY 113 ADSEAGEARCKNLPQSYCLDEGFAYSSQAEKACRDVDECTQGRCEQ--VCVNSPGSYTC 171

DB 532 ASTPCNKAGAKLDGPNYTYTCVTEGYTGTHCEV---DIDECDDPDPCHYCKDGVATFTC 588

QY 172 HC-DGRGGLKLSQDMTDCEDILPCVPFVSAKSVKLSYLVGRMFSGT 215

DB 589 LCRPGYTHHCHETNINECSS-QPCRURGTCQDPDNNAYLCFLCKGT 632

RESULT 41

A24420

notch protein - fruit fly (Drosophila melanogaster)

N:Alternate names: neurogenic repetitive locus protein

C:Species: Drosophila melanogaster

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004

C:Accession: A24420; A24768; S09358; A05267

R:Kidd, S.; Kelley, M.R.; Young, M.W.

Mol. Cell. Biol. 6, 3094-3108, 1986

A:Reference number: A24420; MUID:87064624; PMID:3097517

A:Accession: A24420

A:Molecule type: DNA

A:Residues: 1-2703 <KID>

A:Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PID:AAA28725.1; PID:g157993

R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.

Cell 43, 567-581, 1985

A:Reference number: A24768; MUID:86079539; PMID:3935325

A:Accession: A24768

A:Molecule type: mRNA

A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958,

A>Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044

R:Tautz, D.

Nucleic Acids Res. 17, 6463-6471, 1989

A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma

A:Reference number: S09358; MUID:89385974; PMID:2780284

A:Accession: S09358

A:Molecule type: DNA

A:Residues: 2505-2551, 'OOQQ', 2552-2576, 'E', 2578-2604 <TAU>

R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.

Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other c

A:Reference number: A05267; MUID:85099329; PMID:2981631

A:Molecule type: DNA

A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>

C:Genetics:

A:Gene: notch; opa

A:Cross-references: FlyBase:FBgn0004647

A:Map position: 8,96-9,36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C:Keywords: differentiation; tandem repeat; transmembrane protein

F:27-43/Domain: transmembrane #status predicted <TM1>

F:297-328/Domain: EGF homology <EGF1>

F:530-561/Domain: EGF homology <EGF1>

F:568-599/Domain: EGF homology <EGF>

F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGX3>

F:1746-1762/Domain: transmembrane #status predicted <TM2>

F:1950-1982/Domain: ankyrin repeat homology <AN1>

F:1983-2015/Domain: ankyrin repeat homology <AN2>

F:1988-2004/Domain: transmembrane #status predicted <TM3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>

F:2050-2082/Domain: ankyrin repeat homology <AN4>

F:2083-2115/Domain: ankyrin repeat homology <AN5>

F:2538-2568/Region: glutamine-rich

F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 21.0%; Score 272; DB 1; Length 2703;

Best Local Similarity 28.7%; Pred. No. 2.3e-12;

Matches 74; Conservative 25; Mismatches 71; Indels 88; Gaps 14;

QY 19 GFA--TCVQNLPDQCTPNPCDRKGTQACODLMGNPFCLCKAGWGRGLCDKDVNECSQ--- 73

DB 208 GFTGTCTSYDI--EECQSNPKYGGT--CVNTHGYSQCMPCTGTGTGRDCTDKYKPCSPSC 264

QY 74 ENGGCLQICHNKPFGHSCHSFGFE-----LSSDGRTC----- 106

DB 265 QNGG---ICRNSGLSVECKPKGFEKQCEQNYDDCLGHLCONGTCTDIDGIDYTCRCPP 321

QY 107 -----QDIDECA--DSEAC-GEARCKNLPQSYCLDEGFQ---YSSQEKACRDV--- 150

DB 322 NFGTRFCDDVDECAQRDHPVCQNGATCTNTHTGYSYSCICVNWAGLDCSNNTDDCKQAAAC 381

QY 151 -----DECLQGRG---EQVCVNSP--GSYTCG-DCR 176

DB 382 FYGATCIDGVGFYQCTKGTGTLCHLDDACTSNPCHADALCDTSPNGSYACSCATGY 441

QY 177 GGLKLSQDMTDCEDILPC 194

DB 442 KGVDCSEIDEDCDQGSPC 459

RESULT 42

A56136

jagged protein precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003

C:Accession: A56136

R:Rindsell, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.

Cell 80, 909-917, 1995

A:Title: Jagged: a mammalian ligand that activates Notch1.

A:Reference number: A56136; MUID:95211842; PMID:7697721

A:Accession: A56136

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1220 <LIN>

A:Cross-references: GB:L38483
F:379-410/Domain: EGF homology <EGF1>
F:492-523/Domain: EGF homology <EGF>
F:634-665/Domain: EGF homology <EGF2>

Query Match 20.9%; Score 271.5; DB 2; Length 1220;
Best Local Similarity 33.5%; Pred. No. 1.3e-12;
Matches 68; Conservative 25; Mismatches 83; Indels 27; Gaps 11;

Qy 6 CINKYGSPTKNSGF-----ATCVNLPDQCTPNPCDRKGTQACODLGMNFFCLC 55
Db CHNR-GSKETSSGCECESPGWTGPTCTSTNI-DDCSNNCSHGTT--CQDLVNGFKVC 401

Qy 56 KAGHGGRLCKDVNECSQENGGLQICHNPGSFHCSHGFSLSGDRTCQ-DIDECAD 114
Db PPQWTGRTQCLDANECAKPCVNARSCKNLASYCDLFGWM-----GQNCININDCL- 456

Qy 115 SEAGGEARCKNLPGSYCLCDEGFAYSSQSKACRVDDECLQRCQ--VCVNSPGSYTCH 172
Db 457 GQCONDASCRDLVNGYRCICPPGVAGDHCE---RDIDECASNPLCGHGHCQNEINRFQCL 513

Qy 173 C-DGRGGLKLSQMDMTCTEDILPC 194
Db 514 CPTGFSNLCQLDIDYCEP-NPC 535

RESULT 43

A49175
Motch B protein - mouse (fragment)
N:Alternate names: Motch homolog
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Motch A and Motch B--two mouse Notch homologues coexpressed in a wide variety of tissues
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:9287989; PIDN:CAA48340.1; PID:g2879
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision between proliferation and differentiation.
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:143-174/Domain: EGF homology <EGX1>
F:143-174/Domain: EGF homology <EGX1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Query Match 20.9%; Score 270.5; DB 2; Length 1203;
Best Local Similarity 28.9%; Pred. No. 1.5e-12;
Matches 79; Conservative 23; Mismatches 66; Indels 105; Gaps 15;

Qy 4 LDCINKYG---SPYTKNSGFATCVNLP--DQCTPNPCDRKGTQACODLGM----- 49
Db 343 VDGINRYSCVSP-----GFTGQRNCNIDIDECASNPC-RKGTATCINDVNGFRICPEGPH 396

Qy 50 -----NFFCLCKAGMGGRLCKDVNECSQ---ENGGLQ 80
Db 397 HPSCYSQVNECLSNPCIHNGTCTGLSGYKCLCDAGWGVNCEVDKNECLSNPCQNGG--- 453

Qy 81 ICHNPGSFHCSHGFSLSGDRTCQ-DIDECADSEACE----- 120
Db 454 TCNNLVNGYRCTCKGFK-----GYNCQVNTIDECASNPLNQGTCTFDVSGYTCHCMLPYT 509

Qy 121 -----ARCKNLPG--SYSCLCDEGFAYSSQSKACR--DVDECLQRC 158
Db 510 GKNCQTVLAPCSNPNCENAAVCFAPNFESFSLCAPGW-----QGRCTVDVDECISKPC 565

Qy 159 --EQVCVNSPGSYTCHC-DGRGGLKLSQMDTC 188
Db 566 MNGVGVCHTQGSYVCECPGPGFGMGDCEDINDC 598

RESULT 44

T30201
Notch homolog protein - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 08-Sep-2002
C:Accession: T30201
R:Hori, S.; Saichoh, T.; Matsumoto, M.; Makabe, K.W.; Nishida, H.
Dev. Genes Evol. 207, 371-380, 1997
A:Title: Notch homologue from Halocynthia roretzi is preferentially expressed in the central nervous system
A:Reference number: Z20775
A:Accession: T30201
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2352 <HOR>
A:Cross-references: EMBL:AB001327; NID:d1204472; PID:d1026501; PIDN:BAA25571.1
C:Genetics:
A:Gene: Notch
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 20.9%; Score 270.5; DB 2; Length 2352;
Best Local Similarity 29.4%; Pred. No. 2.6e-12;
Matches 67; Conservative 25; Mismatches 69; Indels 67; Gaps 12;

Qy 6 CINKYGSPTKNSGFATCVNLPDQCTPNPCDRKGTQACODLGMNFFCLCKAGMGGRLCD 65
Db 367 CVAGYSGP-----RCETNI-NECEPNCRNDAT--CLDMTGNFNCVCMPTGTGLICD 415

Qy 66 KDVNECSQE---NGGCLQICHNPGSFHCSHGFSLSGDRTC-QIDIDECADSEACEA 121
Db 416 EDIDECESNFCANGG---TCIDENVATYTCALGF---TGDDCSQNIIDECASSTPCWNKA 468

Qy 122 RCNKLPGSYSLCDEGFA-----YSSQEKACR----- 148
Db 469 TCIDKANAYECECAPGYTGVHCEITNIDCVINPHYGS---CRDGVNTFYCDLLGYEG 524

Qy 149 -----DVDECLQRCQ--VCVNSPGSYTCHC-DGRGGLKLSQMDTC 188
Db 525 TKQDTNCEACSPCENGCTCTDEIGYTTCTPTGTSGSSCEINPDCC 572

RESULT 45

S42612
transmembrane protein precursor - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S42612
R:Bierkamp, C.; Campos-Ortega, J.A.
Mech. Dev. 43, 87-100, 1993
A:Title: A zebrafish homologue of the Drosophila neurogenic gene Notch and its pattern of expression
A:Reference number: S42612; MUID:94128602; PMID:8297791
A:Accession: S42612
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2437 <BIE>
A:Cross-references: UNIPROT:P46530; EMBL:X69088; NID:g433866; PIDN:CAA448831.1; PID:g433866
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:755-786/Domain: EGF homology <EGF1>
F:1023-1054/Domain: EGF homology <EGF2>
F:1185-1216/Domain: EGF homology <EGF2>
F:1915-1947/Domain: ankyrin repeat homology <AN1>
F:1948-1980/Domain: ankyrin repeat homology <AN2>
F:1982-2014/Domain: ankyrin repeat homology <AN3>
F:2015-2047/Domain: ankyrin repeat homology <AN4>
F:2048-2080/Domain: ankyrin repeat homology <AN5>

Query Match 20.8%; Score 270; DB 2; Length 2437;
Best Local Similarity 30.4%; Pred. No. 2.9e-12;

QY 23 CVON-----LPDQCTPNPCDRKGTQACODL-MGNFFCLCKAGWGRLCDKDVNECSQ 73
Db 597 CVQOQCLCPENKVCNQATQCQNGG--ECVDLPNGDYECKCTRGWTGRTCGNDVDECTL 654
QY 74 E-----NGGCLQICHNKPFGSHCSGFELSSDGRTC-QDIDECADSEACGEARCKNLP 127
Db 655 HPKICGNG-----ICKNEKGSYKVCYCTPGF-----TGVHCDSDVDECLSPFLNGATCHNKI 706
QY 128 GSYSCLCDEGFAYSSQBKACR-DVDECLQGRCE--QVCVNSPGSYTCHC-DGRGGLKLSQ 183
Db 707 NAYECVCPQGY-----EGENCEVDIDECNSPCNSGSTCIDRINNFTCNCPGMRGRICDI 762
QY 184 DMDTCEIDILPCV 195
Db 763 DIDDCVGD-PCL 773

RESULT 49
T31070
notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
Development 124, 3363-3374, 1997
A;Title: Identification and localization of a sea urchin Notch homologue: insights into
A;Reference number: Z20966; MUID:97454256; PMID:9310331
A;Accession: T31070
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2531 <SHE>
A;Cross-references: EMBL:AF000634; NID:G2570350; PID:G2570351; PIDN:AAB82088.1
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 20.4%; Score 264; DB 2; Length 2531;
Best Local Similarity 29.9%; Pred. No. 8.3e-12;
Matches 64; Conservative 38; Mismatches 78; Indels 34; Gaps 14;

QY 5 DCINKYSPYTKNSGFATCVQNLDPDQCT---PNPCDRKGTQACODLMGNFFCLCKAGWGG 61
Db 421 DCATGY-----QGF-NCSEDI-DECSLMSDSICQSGGT--CQNPFGWMSCLCSSGFTG 469
QY 62 RLCDKDVNECSQE---NGGCLQICHNKPFGSHCSGFELSSDGRTCQ-DIDECADSEA 117
Db 470 SRCETDIDECDDDPYNGG---TCLNKRGGYACICLTGF---TGTLCETDINECSSNPC 522
QY 118 CGEARCKNLPYSCLDEGFAYSSQBKACR-DVDECLQGRCEQ--VCVNSPGSYTCHCD 174
Db 523 LNGASCFDITGRPEACLAGTGTFT---CQVNIIDCQSPCENGSGTCTIDGVNQFTCLCE 578
QY 175 -GRGGLKLSQDMDTCEIDILPCVPFSAKSVKSLY 207
Db 579 TGYEGHRCMDSDCAS-RFCMNGGVCEDLIGFY 611

RESULT 50
T08618
intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08618
R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kayser, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
A;Reference number: Z16459; MUID:98148073; PMID:9478979
A;Accession: T08618
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-3623 <MOE>
A;Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:G3834379; PIDN:AAC71661.1; PID:G3834379
C;Genetics:
A;Gene: CUBILIN
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology

C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: EGF homology <EGF1>
F;436-467/Domain: EGF homology <EGF>

Query Match 20.3%; Score 263.5; DB 2; Length 3623;
Best Local Similarity 31.9%; Pred. No. 1.2e-11;
Matches 82; Conservative 33; Mismatches 79; Indels 63; Gaps 20;

QY 5 DCINKYSPYTKNSGFATCVQNLDPD---QCTP-----NPPCDRKGTQ-----ACQ 45
Db 170 ECVVSGTPFGCQSG-STCVNTVGSFRCDCTPTTYGPOCASKYNDCEQSKQLCKHGICE 228
QY 46 DL-----MGNFFCLCKAGW-----GGRLCDKDVNECSQENGGLQ---ICHNKPSPHFC-S 92
Db 229 DLQRVHHGQPNFHCICDAGWTTTPPNGISCTEDKDECSLQSPSCSEHAQCFNTQGSFYCGA 288
QY 93 CHSGFELSSDGRTCQDIDEC-ADSEACGEA---RCKNLPQSYSC-LCDEGFAYSSQBKAC 147
Db 289 CPKGMQ--GNGYECODINECEINNGGCSQAPLVFCLNTPGFSFCGNCPCAGF--SGDGRVC 344
QY 148 RDVDECL--QGRG--EQVCVNSP--GSY--TCHC-----DGRGGLKLSQDMDTCE 190
Db 345 TPVDICSIHNGGCHPEATCSCSSPVLGSFLPVCTCPPGYTGNGYSGNCGVRLS---NICS 401
QY 191 ILPCVPFSAKSVKSLY 207
Db 402 -HFCVNGQCIETVSSYP 417

Search completed: July 7, 2005, 09:38:46
Job time : 67.1154 secs

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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:06:22 ; Search time 119.736 Seconds
(without alignments)
141.522 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

Sequence: 1 PVLDCINKYSGPTKNSGF.....LGRMFGTPIRLRKLQ 227

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1297	100.0	678	1	US-08-282-141-2
2	1297	100.0	678	1	US-08-435-434-2
3	1297	100.0	678	1	US-08-435-436-2
4	1297	100.0	678	2	US-08-438-863-2
5	1297	100.0	678	2	US-08-438-864-2
6	1297	100.0	678	3	US-08-438-862-2
7	1297	100.0	678	3	US-08-402-253-2
8	1297	100.0	678	3	US-08-443-866B-2
9	1289	99.4	678	3	US-08-628-747-2
10	1113	85.8	673	1	US-08-282-141-3
11	1113	85.8	673	1	US-08-435-434-1
12	1113	85.8	673	1	US-08-435-436-1
13	1113	85.8	673	2	US-08-438-863-1
14	1113	85.8	673	2	US-08-438-864-1
15	1113	85.8	673	3	US-08-438-862-1
16	1113	85.8	673	3	US-08-628-747-1
17	1113	85.8	673	3	US-08-402-253-1
18	1113	85.8	673	3	US-08-443-866B-1
19	601.5	46.4	635	1	US-07-907-190-1
20	601.5	46.4	635	1	US-07-985-691-2
21	601.5	46.4	635	1	US-08-436-804-2
22	601.5	46.4	635	1	US-08-267-387-2
23	601.5	46.4	676	1	US-08-282-141-4
24	601.5	46.4	676	1	US-08-435-434-3
25	601.5	46.4	676	1	US-08-435-436-3
26	601.5	46.4	676	2	US-08-438-863-3
27	601.5	46.4	676	2	US-08-438-864-3

SUMMARIES

28	601.5	46.4	676	3	US-08-438-862-3	Sequence 3, Appli
29	601.5	46.4	676	3	US-08-628-747-3	Sequence 3, Appli
30	601.5	46.4	676	3	US-08-402-253-3	Sequence 3, Appli
31	601.5	46.4	676	3	US-08-443-866B-3	Sequence 3, Appli
32	596.5	46.0	675	6	5258288-1	Patent No. 5258288
33	596.5	46.0	675	6	5258288-1	Patent No. 5258288
34	586.5	45.2	652	6	5258288-4	Patent No. 5258288
35	586.5	45.2	652	6	5258288-4	Patent No. 5258288
36	353.5	27.3	997	4	US-09-747-371-3	Sequence 3, Appli
37	348.5	26.9	1935	4	US-09-949-016-10403	Sequence 10403, A
38	348.5	26.9	2871	4	US-09-538-092-1076	Sequence 1076, Ap
39	345	26.6	999	4	US-09-747-371-2	Sequence 2, Appli
40	339	26.1	575	4	US-09-949-016-11264	Sequence 11264, A
41	339	26.1	575	4	US-09-949-016-11265	Sequence 11265, A
42	339	26.1	575	4	US-09-949-016-11266	Sequence 11266, A
43	339	26.1	575	4	US-09-949-016-11267	Sequence 11267, A
44	339	26.1	575	4	US-09-949-016-11268	Sequence 11268, A
45	339	26.1	575	4	US-09-949-016-11269	Sequence 11269, A
46	339	26.1	575	4	US-09-949-016-11270	Sequence 11270, A
47	339	26.1	575	4	US-09-949-016-11271	Sequence 11271, A
48	339	26.1	575	4	US-09-949-016-11272	Sequence 11272, A
49	339	26.1	575	4	US-09-949-016-11273	Sequence 11273, A
50	339	26.1	575	4	US-09-949-016-11274	Sequence 11274, A
51	339	26.1	575	4	US-09-949-016-11275	Sequence 11275, A
52	330.5	25.5	1394	4	US-09-949-016-8254	Sequence 8254, Ap
53	330.5	25.5	1394	4	US-09-949-016-8255	Sequence 8255, Ap
54	330.5	25.5	1394	6	5177197-30	Patent No. 5177197
55	330.5	25.5	1394	6	5177197-30	Patent No. 5177197
56	328.5	25.3	1253	3	US-08-479-722B-4	Sequence 4, Appli
57	328.5	25.3	1253	4	US-09-592-685-4	Sequence 4, Appli
58	327	25.2	448	4	US-09-409-096-4	Sequence 4, Appli
59	323	24.9	335	4	US-09-312-283C-186	Sequence 186, App
60	323	24.9	448	2	US-08-884-072-1	Sequence 1, Appli
61	323	24.9	448	3	US-09-212-168-1	Sequence 1, Appli
62	323	24.9	504	4	US-09-949-016-7403	Sequence 7403, Ap
63	322	24.8	956	4	US-09-949-016-6215	Sequence 6215, Ap
64	321	24.7	325	4	US-09-949-016-11467	Sequence 11467, A
65	321	24.7	325	4	US-09-949-016-11468	Sequence 11468, A
66	321	24.7	352	4	US-09-949-016-8273	Sequence 8273, Ap
67	321	24.7	352	4	US-09-949-016-8274	Sequence 8274, Ap
68	321	24.7	387	2	US-08-884-072-5	Sequence 5, Appli
69	321	24.7	387	2	US-08-833-963C-9	Sequence 9, Appli
70	321	24.7	387	3	US-08-980-514-3	Sequence 3, Appli
71	321	24.7	387	3	US-09-212-168-5	Sequence 5, Appli
72	321	24.7	387	4	US-09-409-096-2	Sequence 2, Appli
73	321	24.7	493	4	US-09-322-357-1	Sequence 1, Appli
74	319.5	24.6	1251	5	PCT-US95-02251-3	Sequence 3, Appli
75	319.5	24.6	1252	1	US-08-199-780-3	Sequence 3, Appli
76	319.5	24.6	1252	2	US-08-316-650-3	Sequence 3, Appli
77	319.5	24.6	1656	4	US-09-949-016-7247	Sequence 7247, Ap
78	319.5	24.6	1821	4	US-09-949-016-5938	Sequence 5938, Ap
79	318	24.5	337	3	US-09-188-930-186	Sequence 186, App
80	318	24.5	638	2	US-08-897-443-1	Sequence 1, Appli
81	318	24.5	915	4	US-09-907-794A-34	Sequence 34, Appl
82	318	24.5	915	4	US-09-905-175A-34	Sequence 34, Appl
83	318	24.5	915	4	US-09-902-775A-34	Sequence 34, Appl
84	318	24.5	915	4	US-09-906-700-34	Sequence 34, Appl
85	318	24.5	915	4	US-09-903-603A-34	Sequence 34, Appl
86	318	24.5	915	4	US-09-904-920A-34	Sequence 34, Appl
87	318	24.5	915	4	US-09-909-064-34	Sequence 34, Appl
88	318	24.5	915	4	US-09-905-381A-34	Sequence 34, Appl
89	318	24.5	915	4	US-09-906-618-34	Sequence 34, Appl
90	318	24.5	963	4	US-09-949-016-11519	Sequence 11519, A
91	318	24.5	963	4	US-09-949-016-11520	Sequence 11520, A
92	314.5	24.2	443	2	US-08-833-963C-2	Sequence 2, Appli
93	314.5	24.2	443	3	US-08-980-514-1	Sequence 1, Appli
94	314.5	24.2	466	4	US-09-949-016-7792	Sequence 7792, Ap
95	312	24.1	886	3	US-09-110-116-3	Sequence 3, Appli
96	312	24.1	886	3	US-09-631-603-14	Sequence 14, Appl
97	308.5	23.8	1833	3	US-08-479-722B-2	Sequence 2, Appli
98	308.5	23.8	1833	4	US-09-592-685-2	Sequence 2, Appli
99	308.5	23.8	1833	5	PCT-US95-02251-18	Sequence 18, Appl
100	304	23.4	439	4	US-09-409-096-6	Sequence 6, Appli

101	299.5	23.1	2321	4	US-09-230-652-2	Sequence 2, Appli	174	249	19.2	456	1	US-08-307-444A-3	Sequence 3, Appli
102	289	22.3	956	2	US-08-897-443-3	Sequence 3, Appli	175	249	19.2	456	1	US-08-307-444A-4	Sequence 4, Appli
103	279.5	21.5	274	3	US-09-188-930-336	Sequence 336, App	176	249	19.2	456	1	US-08-587-389-3	Sequence 3, Appli
104	279.5	21.5	274	4	US-08-312-283C-336	Sequence 336, App	177	249	19.2	456	1	US-08-587-389-4	Sequence 4, Appli
105	275.5	21.2	1404	2	US-08-400-159-2	Sequence 2, Appli	178	249	19.2	475	1	US-08-307-444A-1	Sequence 1, Appli
106	275.5	21.2	1404	3	US-08-611-729A-2	Sequence 2, Appli	179	249	19.2	475	1	US-08-307-444A-2	Sequence 2, Appli
107	275.5	21.2	1404	4	US-09-195-524-2	Sequence 2, Appli	180	249	19.2	475	1	US-08-587-389-1	Sequence 1, Appli
108	274.5	21.2	481	4	US-09-914-259-36	Sequence 36, Appl	181	249	19.2	475	1	US-08-587-389-2	Sequence 2, Appli
109	273	21.0	1193	2	US-08-400-159-10	Sequence 10, Appl	182	249	19.2	476	1	US-08-014-723-1	Sequence 1, Appli
110	273	21.0	1193	3	US-08-611-729A-10	Sequence 10, Appl	183	249	19.2	476	1	US-08-014-723-2	Sequence 2, Appli
111	273	21.0	1193	4	US-09-195-524-10	Sequence 10, Appl	184	249	19.2	476	1	US-08-014-723-18	Sequence 18, Appl
112	271.5	20.9	1219	3	US-08-882-046-5	Sequence 5, Appli	185	249	19.2	476	1	US-08-110-011A-1	Sequence 1, Appli
113	271.5	20.9	1219	4	US-09-566-047-5	Sequence 5, Appli	186	249	19.2	476	1	US-08-110-011A-2	Sequence 2, Appli
114	269	20.7	652	2	US-08-751-305-2	Sequence 2, Appli	187	249	19.2	476	1	US-08-110-011A-18	Sequence 18, Appl
115	269	20.7	2703	1	US-08-185-432-19	Sequence 19, Appl	188	249	19.2	494	1	US-08-014-723-14	Sequence 14, Appl
116	269	20.7	2703	4	US-08-899-232-4	Sequence 4, Appli	189	249	19.2	494	1	US-08-014-723-16	Sequence 16, Appl
117	269	20.7	2703	4	US-09-121-457-4	Sequence 4, Appli	190	249	19.2	494	1	US-08-110-011A-14	Sequence 14, Appl
118	268	20.7	452	4	US-09-914-259-34	Sequence 34, Appl	191	249	19.2	494	1	US-08-110-011A-16	Sequence 16, Appl
119	267.5	20.6	2556	1	US-08-185-432-17	Sequence 17, Appl	192	249	19.2	497	1	US-08-312-870-3	Sequence 3, Appli
120	267.5	20.6	2556	4	US-08-899-232-2	Sequence 2, Appli	193	249	19.2	497	1	US-09-331-793-4	Sequence 4, Appli
121	267.5	20.6	2556	4	US-09-121-457-2	Sequence 2, Appli	194	249	19.2	498	2	US-08-733-564-2	Sequence 2, Appli
122	266	20.5	1964	3	US-09-467-997-1	Sequence 1, Appli	195	249	19.2	516	4	US-09-509-994-1	Sequence 1, Appli
123	265.5	20.5	1010	3	US-08-882-046-7	Sequence 7, Appli	196	249	19.2	516	4	US-09-509-994-2	Sequence 2, Appli
124	265.5	20.5	1010	4	US-09-566-047-7	Sequence 7, Appli	197	249	19.2	575	1	US-08-261-206A-59	Sequence 59, Appl
125	265.5	20.5	1036	3	US-09-068-740A-6	Sequence 6, Appli	198	249	19.2	575	1	US-08-312-870-1	Sequence 1, Appli
126	265.5	20.5	1067	4	US-09-579-536C-18	Sequence 18, Appl	199	249	19.2	575	4	US-08-170-290A-54	Sequence 54, Appl
127	265.5	20.5	1187	3	US-09-068-740A-7	Sequence 7, Appli	200	249	19.2	575	4	US-09-880-484D-2	Sequence 2, Appli
128	265.5	20.5	1208	4	US-09-199-865-1	Sequence 1, Appli	201	249	19.2	575	6	US-10-438-648-2	Sequence 2, Appli
129	265.5	20.5	1208	4	US-10-213-329-1	Sequence 1, Appli	202	249	19.2	575	6	5466668-6	Patent No. 5466668
130	265.5	20.5	1218	2	US-08-400-159-6	Sequence 6, Appli	203	249	19.2	575	6	5466668-6	Patent No. 5466668
131	265.5	20.5	1218	3	US-08-611-729A-6	Sequence 6, Appli	204	247	19.0	572	6	5256770-7	Patent No. 5256770
132	265.5	20.5	1218	3	US-08-882-046-2	Sequence 2, Appli	205	247	19.0	572	6	5256770-7	Patent No. 5256770
133	265.5	20.5	1218	3	US-09-214-278-7	Sequence 7, Appli	206	244.5	18.9	720	3	US-08-872-855-4	Sequence 4, Appli
134	265.5	20.5	1218	4	US-09-668-740A-11	Sequence 11, Appl	207	243.5	18.8	725	1	US-08-312-870-7	Sequence 7, Appli
135	265.5	20.5	1218	4	US-09-855-722-7	Sequence 7, Appli	208	243.5	18.8	722	3	US-08-981-392-12	Sequence 12, Appl
136	265.5	20.5	1218	4	US-09-566-047-2	Sequence 2, Appli	209	243.5	18.8	722	3	US-09-908-322-12	Sequence 12, Appl
137	265.5	20.5	1218	4	US-09-917-254-85	Sequence 85, Appl	210	242.5	18.7	713	3	US-08-872-855-5	Sequence 5, Appli
138	265.5	20.5	1218	4	US-09-195-524-6	Sequence 6, Appli	211	242	18.7	1055	3	US-09-214-278-2	Sequence 2, Appli
139	265.5	20.5	1218	4	US-09-579-536C-1	Sequence 1, Appli	212	242	18.7	1055	3	US-09-855-722-2	Sequence 2, Appli
140	265.5	20.5	1218	4	US-09-949-016-5902	Sequence 5902, Ap	213	242	18.7	1065	2	US-08-400-159-8	Sequence 8, Appli
141	265.5	20.5	1254	4	US-09-949-016-10297	Sequence 10297, A	214	242	18.7	1212	3	US-09-214-278-3	Sequence 3, Appli
142	263.5	20.3	2523	1	US-08-185-432-18	Sequence 18, Appl	215	242	18.7	1212	3	US-09-855-722-3	Sequence 3, Appli
143	263.5	20.3	2523	4	US-08-899-232-3	Sequence 3, Appli	216	242	18.7	1238	3	US-09-214-278-5	Sequence 5, Appli
144	263.5	20.3	2523	4	US-09-121-457-3	Sequence 3, Appli	217	242	18.7	1238	4	US-09-855-722-5	Sequence 5, Appli
145	263.5	20.3	2556	1	US-08-083-590A-20	Sequence 20, Appl	218	242	18.7	1257	3	US-08-611-729A-8	Sequence 8, Appli
146	263.5	20.3	2556	3	US-08-532-384-20	Sequence 20, Appl	219	242	18.7	1257	4	US-09-195-524-8	Sequence 8, Appli
147	262.5	20.2	575	4	US-09-482-273-159	Sequence 159, App	220	238.5	18.4	172	4	US-09-706-722A-8	Sequence 8, Appli
148	262.5	20.2	638	4	US-09-482-273-245	Sequence 245, App	221	238.5	18.4	835	3	US-09-284-819-6	Sequence 6, Appli
149	262	20.2	3623	4	US-09-341-461-2	Sequence 2, Appli	222	238.5	18.4	835	4	US-09-262-537-12	Sequence 12, Appl
150	261.5	20.2	2471	1	US-08-185-432-16	Sequence 16, Appl	223	238.5	18.4	835	4	US-09-631-603-9	Sequence 9, Appli
151	261.5	20.2	2471	1	US-08-083-590A-19	Sequence 19, Appl	224	238	18.4	1148	3	US-08-883-046-4	Sequence 4, Appli
152	261.5	20.2	2471	3	US-08-532-384-19	Sequence 19, Appl	225	238	18.4	1148	4	US-09-566-047-4	Sequence 4, Appli
153	261.5	20.2	2471	4	US-08-899-232-1	Sequence 1, Appli	226	236.5	18.2	321	4	US-09-270-767-33762	Sequence 33762, A
154	261.5	20.2	2471	4	US-09-121-457-1	Sequence 1, Appli	227	236.5	18.2	321	4	US-09-270-767-48979	Sequence 48979, A
155	261	20.1	486	4	US-09-914-259-35	Sequence 35, Appl	228	234.5	18.1	1139	3	US-08-537-210A-4	Sequence 4, Appli
156	261	20.1	486	4	US-09-976-594-278	Sequence 278, App	229	234.5	18.1	1139	3	US-09-113-825-4	Sequence 4, Appli
157	261	20.1	486	4	US-09-949-016-6216	Sequence 6216, Ap	230	234	18.0	1064	1	US-08-537-210A-3	Sequence 3, Appli
158	261	20.1	507	4	US-09-949-016-9878	Sequence 9878, Ap	231	234	18.0	1064	3	US-09-113-825-3	Sequence 3, Appli
159	255	19.7	509	4	US-09-307-794A-315	Sequence 315, App	232	233.5	18.0	1074	2	US-08-470-058-2	Sequence 2, Appli
160	255	19.7	509	4	US-09-305-125A-315	Sequence 315, App	233	233.5	18.0	1074	3	US-09-037-188-2	Sequence 2, Appli
161	255	19.7	509	4	US-09-302-775A-315	Sequence 315, App	234	233.5	18.0	1074	3	US-09-285-310-2	Sequence 2, Appli
162	255	19.7	509	4	US-09-306-700-315	Sequence 315, App	235	233	17.8	284	4	US-09-312-283C-389	Sequence 389, App
163	255	19.7	509	4	US-09-903-603A-315	Sequence 315, App	236	231.5	17.8	353	4	US-09-482-273-243	Sequence 243, App
164	255	19.7	509	4	US-09-304-920A-315	Sequence 315, App	237	231.5	17.8	823	4	US-09-949-016-6852	Sequence 6852, Ap
165	255	19.7	509	4	US-09-309-064-315	Sequence 315, App	238	231	17.8	1068	1	US-08-537-210A-2	Sequence 2, Appli
166	255	19.7	509	4	US-09-305-381A-315	Sequence 315, App	239	229.5	17.7	1068	3	US-09-113-825-2	Sequence 2, Appli
167	255	19.7	509	4	US-09-306-618-315	Sequence 315, App	240	229.5	17.7	520	3	US-09-068-740A-3	Sequence 3, Appli
168	253.5	19.5	3571	4	US-09-911-842A-2	Sequence 2, Appli	241	229.5	17.7	702	3	US-09-068-740A-4	Sequence 4, Appli
169	253	19.3	3594	4	US-09-911-842A-4	Sequence 4, Appli	242	229.5	17.7	723	3	US-09-068-740A-9	Sequence 9, Appli
170	250	19.3	1246	4	US-08-919-497-85	Sequence 85, Appl	243	229.5	17.7	723	4	US-09-423-753-27	Sequence 27, Appl
171	250	19.3	1247	4	US-09-361-403-14	Sequence 14, Appl	244	229.5	17.7	723	4	US-09-641-612-6	Sequence 6, Appli
172	249	19.2	446	1	US-08-307-444A-5	Sequence 5, Appli	245	229.5	17.7	846	4	US-09-949-016-10381	Sequence 10381, A
173	249	19.2	446	1	US-08-587-389-5	Sequence 5, Appli	246	228.5	17.6	729	3	US-08-872-855-8	Sequence 8, Appli

247	228	17.6	816	2	US-08-820-170A-37	Sequence 37, Appl	320	203.5	15.7	750	4	US-09-270-767-42975	Sequence 42975, A
248	228	17.6	816	3	US-09-055-699-37	Sequence 37, Appl	321	201	15.5	105	4	US-09-621-976-5035	Sequence 5035, Ap
249	228	17.6	816	3	US-09-273-565-37	Sequence 37, Appl	322	201	15.5	4544	1	US-08-469-486-52	Sequence 52, Appl
250	228	17.6	816	3	US-09-565-538-37	Sequence 37, Appl	323	201	15.5	4544	2	US-08-469-486-52	Sequence 52, Appl
251	228	17.6	816	3	US-09-661-468-37	Sequence 37, Appl	324	200	15.4	584	4	US-09-949-016-10340	Sequence 10340, A
252	228	17.6	816	4	US-09-976-165-37	Sequence 37, Appl	325	200	15.4	584	4	US-09-949-016-10341	Sequence 10341, A
253	228	17.6	1248	3	US-08-882-046-6	Sequence 6, Appl	326	199	15.3	1523	3	US-09-182-024A-2	Sequence 2, Appl
254	228	17.6	1248	4	US-09-566-047-6	Sequence 6, Appl	327	198.5	15.3	545	3	US-10-067-422-11	Sequence 11, Appl
255	227.5	17.5	860	1	US-08-032-817-4	Sequence 4, Appl	328	198.5	15.3	737	4	US-09-866-028-15	Sequence 15, Appl
256	227.5	17.5	860	3	US-08-485-128-4	Sequence 4, Appl	329	198.5	15.3	737	4	US-09-944-457-15	Sequence 15, Appl
257	227.5	17.5	860	4	US-09-804-778A-8	Sequence 8, Appl	330	198	15.3	578	3	US-08-981-392-13	Sequence 13, Appl
258	227.5	17.5	860	4	US-09-824-637-4	Sequence 4, Appl	331	198	15.3	578	3	US-09-908-322-13	Sequence 13, Appl
259	227.5	17.5	1410	2	US-08-470-058-4	Sequence 4, Appl	332	195	15.0	846	1	US-08-149-103-4	Sequence 4, Appl
260	227.5	17.5	1410	3	US-09-037-188-4	Sequence 4, Appl	333	195	15.0	846	1	US-08-451-883-4	Sequence 4, Appl
261	227.5	17.5	1410	3	US-09-285-310-4	Sequence 4, Appl	334	195	15.0	4654	3	US-08-476-515A-84	Sequence 84, Appl
262	227	17.5	721	3	US-08-872-855-7	Sequence 7, Appl	335	195	15.0	4655	3	US-08-652-877-84	Sequence 84, Appl
263	227	17.5	721	3	US-08-981-392-5	Sequence 5, Appl	336	195	15.0	4655	3	US-08-652-877-86	Sequence 86, Appl
264	227	17.5	721	4	US-09-908-322-5	Sequence 5, Appl	337	195	15.0	4655	3	US-08-652-877-88	Sequence 88, Appl
265	227	17.5	721	4	US-08-872-855-10	Sequence 10, Appl	338	195	15.0	4655	3	US-08-652-877-90	Sequence 90, Appl
266	222.5	17.2	502	3	US-09-363-316B-18	Sequence 18, Appl	339	191.5	14.8	735	3	US-09-191-647-9	Sequence 9, Appl
267	222.5	17.2	502	4	US-10-136-227A-18	Sequence 18, Appl	340	191.5	14.8	735	3	US-09-540-245A-9	Sequence 9, Appl
268	222.5	17.2	502	4	US-09-981-649A-18	Sequence 18, Appl	341	191.5	14.8	735	3	US-09-540-153-9	Sequence 9, Appl
269	222.5	17.2	537	3	US-09-249-697A-4	Sequence 4, Appl	342	190	14.6	846	1	US-08-149-103-3	Sequence 3, Appl
270	222.5	17.2	537	3	US-09-363-316B-4	Sequence 4, Appl	343	190	14.6	846	1	US-08-451-883-3	Sequence 3, Appl
271	222.5	17.2	537	4	US-10-136-227A-4	Sequence 4, Appl	344	190	14.6	904	4	US-09-949-016-9528	Sequence 9528, Ap
272	222.5	17.2	537	4	US-09-981-649A-4	Sequence 4, Appl	345	189.5	14.6	353	4	US-09-907-794A-2	Sequence 2, Appl
273	222.5	17.2	553	3	US-09-249-697A-6	Sequence 6, Appl	346	189.5	14.6	353	4	US-09-905-125A-2	Sequence 2, Appl
274	222.5	17.2	553	3	US-09-363-316B-6	Sequence 6, Appl	347	189.5	14.6	353	4	US-09-902-775A-2	Sequence 2, Appl
275	222.5	17.2	553	3	US-09-249-697A-19	Sequence 19, Appl	348	189.5	14.6	353	4	US-09-906-700-2	Sequence 2, Appl
276	222.5	17.2	553	3	US-09-363-316B-24	Sequence 24, Appl	349	189.5	14.6	353	4	US-09-903-603A-2	Sequence 2, Appl
277	222.5	17.2	553	4	US-10-136-227A-6	Sequence 6, Appl	350	189.5	14.6	353	4	US-09-904-920A-2	Sequence 2, Appl
278	222.5	17.2	553	4	US-09-981-649A-6	Sequence 24, Appl	351	189.5	14.6	353	4	US-09-909-064-2	Sequence 2, Appl
279	222.5	17.2	553	4	US-09-981-649A-6	Sequence 24, Appl	352	189.5	14.6	353	4	US-09-905-381A-2	Sequence 2, Appl
280	222.5	17.2	554	4	US-10-136-227A-30	Sequence 30, Appl	353	189.5	14.6	353	4	US-09-906-618-2	Sequence 2, Appl
281	222.5	17.2	554	4	US-10-136-227A-32	Sequence 32, Appl	354	186.5	14.4	383	1	US-08-597-545-2	Sequence 2, Appl
282	222.5	17.2	554	4	US-09-981-649A-30	Sequence 30, Appl	355	186.5	14.4	383	1	US-08-457-135-2	Sequence 2, Appl
283	222.5	17.2	554	4	US-09-981-649A-30	Sequence 32, Appl	356	186.5	14.4	726	6	5208144-37	Patent No. 5208144
284	222.5	17.2	554	4	US-09-981-649A-32	Sequence 32, Appl	357	186.5	14.4	726	6	5208144-37	Patent No. 5208144
285	222.5	17.2	559	4	US-10-136-227A-28	Sequence 28, Appl	358	185.5	14.3	383	4	US-09-142-027A-12	Sequence 12, Appl
286	222.5	17.2	559	4	US-09-981-649A-28	Sequence 28, Appl	359	185.5	14.3	585	4	US-09-641-612-5	Sequence 5, Appl
287	222.5	17.2	594	4	US-09-949-016-8175	Sequence 8175, Ap	360	184	14.2	437	1	US-08-487-037-2	Sequence 2, Appl
288	222	17.1	728	3	US-08-981-392-2	Sequence 2, Appl	361	184	14.2	437	1	US-08-487-037-3	Sequence 3, Appl
289	222	17.1	728	3	US-09-908-322-2	Sequence 2, Appl	362	184	14.2	873	1	US-08-393-734-2	Sequence 2, Appl
290	218.5	16.8	1015	1	US-08-537-210A-1	Sequence 1, Appl	363	184	14.2	873	3	US-08-894-489-2	Sequence 2, Appl
291	218.5	16.8	1015	3	US-09-113-825-1	Sequence 1, Appl	364	182.5	14.1	500	4	US-09-423-753-2	Sequence 2, Appl
292	217.5	16.8	148	4	US-09-270-767-31657	Sequence 31657, A	365	182.5	14.1	659	4	US-09-423-753-3	Sequence 3, Appl
293	217	16.7	757	4	US-09-949-016-6963	Sequence 6963, Ap	366	182.5	14.1	685	3	US-08-872-855-2	Sequence 2, Appl
294	217	16.7	758	4	US-09-949-016-8087	Sequence 8087, Ap	367	182.5	14.1	685	4	US-09-423-753-25	Sequence 25, Appl
295	216.5	16.7	717	3	US-08-872-855-9	Sequence 9, Appl	368	182.5	14.1	685	4	US-09-641-612-7	Sequence 7, Appl
296	214.5	16.5	1529	4	US-09-312-283C-396	Sequence 396, App	369	182	14.0	2362	4	US-09-949-016-8985	Sequence 8985, Ap
297	214	16.5	830	3	US-08-872-855-11	Sequence 11, Appl	370	180.5	13.9	583	4	US-09-641-612-2	Sequence 2, Appl
298	214	16.5	833	1	US-08-264-534-6	Sequence 6, Appl	371	179.5	13.8	385	1	US-08-597-545-1	Sequence 1, Appl
299	214	16.5	833	1	US-08-083-590A-2	Sequence 2, Appl	372	179.5	13.8	385	1	US-08-457-135-1	Sequence 1, Appl
300	214	16.5	833	1	US-08-455-500-6	Sequence 6, Appl	373	179.5	13.8	385	4	US-09-142-027A-10	Sequence 10, Appl
301	214	16.5	833	2	US-08-346-126-6	Sequence 6, Appl	374	179.5	13.8	448	5	PCT-US92-10068-1	Sequence 1, Appl
302	214	16.5	833	2	US-08-346-126-6	Sequence 6, Appl	375	179.5	13.8	448	4	US-09-367-777-44	Sequence 44, Appl
303	214	16.5	833	3	US-08-532-384-2	Sequence 2, Appl	376	179.5	13.8	488	4	US-09-367-791A-27	Sequence 27, Appl
304	214	16.5	833	3	US-08-893-828-6	Sequence 6, Appl	377	179.5	13.8	496	4	US-09-949-016-9524	Sequence 9524, Ap
305	212.5	16.4	492	3	US-09-724-864-39	Sequence 39, Appl	378	177.5	13.7	448	1	US-08-295-411-3	Sequence 3, Appl
306	211.5	16.3	810	2	US-08-820-170A-34	Sequence 34, Appl	379	177.5	13.7	448	2	US-08-855-471-3	Sequence 3, Appl
307	211.5	16.3	810	3	US-09-055-699-34	Sequence 34, Appl	380	177.5	13.7	448	5	PCT-US92-10242-3	Sequence 3, Appl
308	211.5	16.3	810	3	US-09-273-565-34	Sequence 34, Appl	381	174.5	13.5	788	1	US-08-572-225-1	Sequence 1, Appl
309	211.5	16.3	810	3	US-09-565-538-34	Sequence 34, Appl	382	174.5	13.5	986	4	US-09-285-385C-19	Sequence 19, Appl
310	211.5	16.3	810	3	US-09-661-468-34	Sequence 34, Appl	383	174.5	13.5	986	4	US-09-949-016-6690	Sequence 6690, Ap
311	211.5	16.3	810	4	US-09-976-165-34	Sequence 34, Appl	384	174.5	13.5	1012	4	US-09-285-385C-4	Sequence 4, Appl
312	211.5	16.3	1525	3	US-09-131-647-2	Sequence 2, Appl	385	174.5	13.5	1480	3	US-09-191-647-7	Sequence 7, Appl
313	211.5	16.3	1525	3	US-09-540-245A-2	Sequence 2, Appl	386	174.5	13.5	1480	3	US-09-540-245A-7	Sequence 7, Appl
314	211.5	16.3	1525	3	US-09-540-153-2	Sequence 2, Appl	387	174.5	13.5	1480	3	US-09-540-153-7	Sequence 7, Appl
315	211	16.3	832	3	US-08-981-392-6	Sequence 6, Appl	388	174.5	13.5	1480	5	PCT-US91-09055-5	Sequence 5, Appl
316	211	16.3	832	4	US-09-908-322-6	Sequence 6, Appl	389	174.5	13.5	1480	5	PCT-US91-09055-5	Sequence 2, Appl
317	210.5	16.2	716	4	US-09-312-283C-183	Sequence 183, App	390	172.5	13.3	488	1	US-08-487-037-1	Sequence 1, Appl
318	210.5	16.2	771	3	US-09-188-330-183	Sequence 183, App	391	172	13.3	164	3	US-09-249-697A-9	Sequence 9, Appl
319	203.5	15.7	614	4	US-09-949-016-8536	Sequence 8536, Ap	392	172	13.3	164	3	US-09-363-316B-9	Sequence 9, Appl

393	172	13.3	164	4	US-10-136-227A-9	Sequence 9, Appli	466	164	12.6	460	6	5270178-15	Patent No. 5270178
394	172	13.3	164	4	US-09-981-649A-9	Sequence 9, Appli	467	164	12.6	460	6	5270178-16	Patent No. 5270178
395	170.5	13.1	139	1	US-08-330-978-2	Sequence 2, Appli	468	164	12.6	461	4	US-10-182-263-2	Sequence 2, Appli
396	170.5	13.1	139	1	US-08-474-042-2	Sequence 2, Appli	469	164	12.6	461	4	US-09-054-272-32	Sequence 32, Appli
397	170.5	13.1	139	1	US-08-484-558-2	Sequence 2, Appli	470	164	12.6	461	4	US-09-949-016-5921	Sequence 5921, Ap
398	170.5	13.1	139	1	US-08-774-592-2	Sequence 2, Appli	471	164	12.6	461	6	5225537-2	Patent No. 5225537
399	169.5	13.1	157	3	US-08-981-392-68	Sequence 68, Appl	472	164	12.6	461	6	5270178-2	Patent No. 5270178
400	169.5	13.1	157	4	US-09-908-322-68	Sequence 68, Appl	473	164	12.6	461	6	5270178-17	Patent No. 5270178
401	169.5	13.1	420	4	US-09-907-794A-109	Sequence 109, App	474	164	12.6	461	6	5270178-18	Patent No. 5270178
402	169.5	13.1	420	4	US-09-905-125A-109	Sequence 109, App	475	164	12.6	461	6	5460953-3	Patent No. 5460953
403	169.5	13.1	420	4	US-09-902-775A-109	Sequence 109, App	476	164	12.6	461	6	5225537-2	Patent No. 5225537
404	169.5	13.1	420	4	US-09-906-700-109	Sequence 109, App	477	164	12.6	461	6	5270178-2	Patent No. 5270178
405	169.5	13.1	420	4	US-09-903-603A-109	Sequence 109, App	478	164	12.6	461	6	5270178-17	Patent No. 5270178
406	169.5	13.1	420	4	US-09-904-920A-109	Sequence 109, App	479	164	12.6	461	6	5270178-18	Patent No. 5270178
407	169.5	13.1	420	4	US-09-909-064-109	Sequence 109, App	480	164	12.6	461	6	5460953-3	Patent No. 5460953
408	169.5	13.1	420	4	US-09-905-381A-109	Sequence 109, App	481	164	12.6	485	4	US-09-949-016-10882	Sequence 10882, A
409	169.5	13.1	420	4	US-09-906-618-109	Sequence 109, App	482	162.5	12.5	591	3	US-08-991-408-4	Sequence 4, Appli
410	168.5	13.0	242	4	US-09-312-283C-393	Sequence 393, App	483	162.5	12.5	591	3	US-09-432-473-4	Sequence 4, Appli
411	168.5	13.0	487	1	US-08-469-486-53	Sequence 53, Appl	484	162.5	12.5	1013	2	US-08-866-650-5	Sequence 5, Appli
412	168.5	13.0	487	2	US-08-469-658-53	Sequence 53, Appl	485	162.5	12.5	1013	2	US-09-021-287-5	Sequence 5, Appli
413	168.5	13.0	482	1	US-08-469-486-2	Sequence 2, Appli	486	162.5	12.5	1013	3	US-08-991-408-2	Sequence 2, Appli
414	168.5	13.0	422	2	US-08-469-658-2	Sequence 2, Appli	487	162.5	12.5	1013	3	US-09-240-473-5	Sequence 5, Appli
415	168.5	13.0	1013	2	US-08-866-650-3	Sequence 3, Appli	488	162.5	12.5	1013	3	US-09-432-473-2	Sequence 2, Appli
416	168.5	13.0	1013	3	US-09-021-287-3	Sequence 3, Appli	489	162.5	12.5	1013	4	US-09-285-385C-20	Sequence 20, Appl
417	168.5	13.0	1013	3	US-09-240-473-3	Sequence 3, Appli	490	160	12.3	884	6	5208144-8	Patent No. 5208144
418	167.5	12.9	157	3	US-08-872-855-6	Sequence 6, Appli	491	160	12.3	884	6	5208144-8	Patent No. 5208144
419	165	12.7	136	3	US-08-981-392-35	Sequence 35, Appl	492	160	12.3	2200	4	US-09-796-575-2	Sequence 2, Appli
420	165	12.7	136	4	US-09-908-322-35	Sequence 35, Appl	493	159.5	12.3	961	4	US-09-657-472-4	Sequence 4, Appli
421	165	12.7	406	1	US-08-295-411-5	Sequence 5, Appli	494	159.5	12.3	961	5	PCT-US93-11725-4	Sequence 4, Appli
422	165	12.7	406	2	US-08-955-471-5	Sequence 5, Appli	495	158.5	12.2	970	4	US-09-949-016-10131	Sequence 10131, A
423	165	12.7	406	4	US-09-782-587B-1	Sequence 1, Appli	496	158	12.2	406	1	US-08-293-778-24	Sequence 24, Appl
424	165	12.7	406	4	US-09-782-587B-3	Sequence 3, Appli	497	157.5	12.1	986	3	US-08-872-757-4	Sequence 4, Appli
425	165	12.7	406	5	PCT-US92-10242-5	Sequence 5, Appli	498	157.5	12.1	986	4	US-09-850-048A-4	Sequence 4, Appli
426	165	12.7	444	1	US-08-475-845-2	Sequence 2, Appli	499	157.5	12.1	1810	4	US-08-793-273C-4	Sequence 4, Appli
427	165	12.7	444	2	US-08-327-690-2	Sequence 2, Appli	500	157.5	12.1	1810	5	PCT-US95-11684-4	Sequence 4, Appli
428	165	12.7	444	2	US-08-660-289-2	Sequence 2, Appli	501	157	12.1	356	4	US-09-054-272-18	Sequence 18, Appl
429	165	12.7	444	2	US-08-537-807-2	Sequence 2, Appli	502	157	12.1	943	3	US-08-476-515A-12	Sequence 12, Appl
430	165	12.7	444	2	US-08-871-003-2	Sequence 2, Appli	503	157	12.1	944	3	US-08-652-877-12	Sequence 12, Appl
431	165	12.7	444	3	US-08-464-233-2	Sequence 2, Appli	504	157	12.1	1170	1	US-08-313-288B-20	Sequence 20, Appl
432	165	12.7	444	3	US-09-189-607-2	Sequence 2, Appli	505	157	12.1	1170	4	US-09-657-472-2	Sequence 2, Appli
433	165	12.7	444	3	US-09-378-907-2	Sequence 2, Appli	506	155.5	12.0	1015	4	US-09-285-385C-2	Sequence 2, Appli
434	165	12.7	444	3	PCT-US94-05779-2	Sequence 2, Appli	507	155.5	12.0	2199	4	US-08-793-273C-2	Sequence 2, Appli
435	165	12.7	461	4	US-09-949-016-8839	Sequence 8839, Ap	508	155.5	12.0	2199	5	PCT-US95-11684-2	Sequence 2, Appli
436	165	12.7	461	4	US-07-982-202A-4	Sequence 4, Appli	509	154.5	11.9	777	4	US-09-270-767-44409	Sequence 44409, A
437	165	12.7	466	1	US-08-021-615A-4	Sequence 4, Appli	510	152	11.7	233	4	US-09-216-393B-110	Sequence 110, App
438	165	12.7	466	1	US-08-321-777-4	Sequence 14, Appl	511	152	11.7	3635	4	US-09-845-583A-2	Sequence 2, Appli
439	165	12.7	466	3	US-09-009-217-14	Sequence 14, Appl	512	150	11.6	415	1	US-08-073-531B-1	Sequence 1, Appli
440	165	12.7	466	3	US-09-009-656-14	Sequence 14, Appl	513	150	11.6	415	1	US-08-295-411-2	Sequence 2, Appli
441	165	12.7	466	5	PCT-US93-04493-4	Sequence 4, Appli	514	150	11.6	415	2	US-08-955-471-2	Sequence 2, Appli
442	165	12.7	483	4	US-09-949-016-9523	Sequence 9523, Ap	515	150	11.6	415	2	US-08-766-288-1	Sequence 1, Appli
443	164.5	12.7	239	4	US-09-270-767-33770	Sequence 33770, A	516	150	11.6	415	4	US-09-118-748-2	Sequence 2, Appli
444	164.5	12.7	239	4	US-09-270-767-48987	Sequence 48987, A	517	150	11.6	415	5	PCT-US92-10242-2	Sequence 2, Appli
445	164	12.6	409	3	US-09-065-872-2	Sequence 2, Appli	518	150	11.6	461	3	US-08-742-877-2	Sequence 2, Appli
446	164	12.6	409	4	US-09-667-570A-2	Sequence 2, Appli	519	150	11.6	461	3	US-09-053-877A-21	Sequence 21, Appl
447	164	12.6	410	3	US-09-065-872-1	Sequence 1, Appli	520	150	11.6	461	4	US-09-053-877A-21	Sequence 5, Appli
448	164	12.6	410	4	US-09-667-570A-1	Sequence 1, Appli	521	150	11.6	461	6	5521070-2	Patent No. 5521070
449	164	12.6	419	1	US-08-295-411-1	Sequence 1, Appli	522	150	11.6	461	6	5521070-2	Patent No. 5521070
450	164	12.6	419	2	US-08-955-471-1	Sequence 1, Appli	523	150	11.6	480	4	US-09-949-016-11123	Sequence 11123, A
451	164	12.6	419	4	US-09-667-570A-3	Sequence 3, Appli	524	149	11.5	956	4	US-09-949-016-11332	Sequence 11332, A
452	164	12.6	419	4	US-10-182-263-1	Sequence 1, Appli	525	146.5	11.3	192	3	US-08-981-392-65	Sequence 65, Appl
453	164	12.6	419	4	US-10-182-263-3	Sequence 3, Appli	526	146.5	11.3	192	4	US-09-908-322-65	Sequence 65, Appl
454	164	12.6	419	4	US-10-182-263-4	Sequence 4, Appli	527	146.5	11.3	276	3	US-08-981-392-43	Sequence 43, Appl
455	164	12.6	419	4	US-10-182-263-5	Sequence 5, Appli	528	146.5	11.3	276	4	US-09-908-322-43	Sequence 43, Appl
456	164	12.6	419	4	US-10-182-263-6	Sequence 6, Appli	529	146.5	11.3	549	1	US-08-325-071-61	Sequence 61, Appl
457	164	12.6	419	5	PCT-US92-10242-1	Sequence 1, Appli	530	146.5	11.3	549	3	US-08-461-004A-61	Sequence 61, Appl
458	164	12.6	460	2	US-08-756-506-2	Sequence 2, Appli	531	146.5	11.3	650	1	US-08-325-071-63	Sequence 63, Appl
459	164	12.6	460	2	US-08-756-506-4	Sequence 4, Appli	532	146.5	11.3	650	3	US-08-461-004A-63	Sequence 63, Appl
460	164	12.6	460	6	5270178-13	Patent No. 5270178	533	145.5	11.2	299	3	US-09-188-930-332	Sequence 332, App
461	164	12.6	460	6	5270178-14	Patent No. 5270178	534	145.5	11.2	299	4	US-09-312-283C-192	Sequence 192, App
462	164	12.6	460	6	5270178-15	Patent No. 5270178	535	145.5	11.2	299	4	US-09-312-283C-332	Sequence 332, App
463	164	12.6	460	6	5270178-16	Patent No. 5270178	536	144	11.1	235	4	US-09-902-540-15031	Sequence 15031, A
464	164	12.6	460	6	5270178-13	Patent No. 5270178	537	143.5	11.1	620	1	US-08-325-071-65	Sequence 65, Appl
465	164	12.6	460	6	5270178-14	Patent No. 5270178	538	143.5	11.1	620	3	US-08-461-004A-65	Sequence 65, Appl

539	143.5	11.1	650	1	US-08-325-071-56	Sequence 56, Appl	612	133.5	10.3	1481	2	US-08-599-654-40	Sequence 40, Appl
540	143.5	11.1	650	3	US-08-461-004A-56	Sequence 56, Appl	613	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
541	143.5	11.1	688	1	US-08-325-071-57	Sequence 57, Appl	614	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
542	143.5	11.1	688	3	US-08-461-004A-57	Sequence 57, Appl	615	133.5	10.3	1481	3	US-08-944-868A-40	Sequence 40, Appl
543	143.5	11.1	3647	4	US-09-949-016-10932	Sequence 10932, A	616	133.5	10.3	1587	4	US-09-845-583A-10	Sequence 10, Appl
544	143	11.0	491	3	US-08-030-335-2	Sequence 2, Appl	617	133.5	10.3	1587	4	US-09-561-709B-3	Sequence 3, Appl
545	143	11.0	748	2	US-08-920-234-2	Sequence 2, Appl	618	132	10.2	229	3	US-09-188-930-192	Sequence 192, App
546	143	11.0	748	2	US-08-937-931-4	Sequence 4, Appl	619	132	10.2	1138	1	US-08-323-474-8	Sequence 8, Appl
547	143	11.0	748	3	US-09-285-502-4	Sequence 4, Appl	620	132	10.2	1138	2	US-08-469-537A-98	Sequence 98, Appl
548	143	11.0	748	3	US-09-030-335-9	Sequence 9, Appl	621	132	10.2	1138	2	US-08-320-240A-5	Sequence 5, Appl
549	143	11.0	748	3	US-09-709-126-4	Sequence 4, Appl	622	132	10.2	1150	4	US-09-949-016-7769	Sequence 7769, Ap
550	143	11.0	748	3	US-09-871-385A-4	Sequence 4, Appl	623	132	10.2	1451	4	US-09-060-299-25	Sequence 25, Appl
551	143	11.0	761	3	US-09-949-016-10631	Sequence 10631, A	624	132	10.2	1451	4	US-09-402-923A-25	Sequence 25, Appl
552	143	11.0	799	3	US-09-030-335-4	Sequence 4, Appl	625	132	10.2	1584	4	US-09-060-299-39	Sequence 39, Appl
553	142.5	11.0	278	3	US-09-724-864-52	Sequence 52, Appl	626	132	10.2	1584	4	US-09-402-923A-39	Sequence 39, Appl
554	141	10.9	1358	1	US-08-404-665-4	Sequence 4, Appl	627	132	10.2	1591	4	US-09-060-299-4	Sequence 4, Appl
555	141	10.9	1358	1	US-08-404-665-4	Sequence 4, Appl	628	132	10.2	1591	4	US-09-060-299-43	Sequence 43, Appl
556	141	10.9	1358	1	US-08-404-781-4	Sequence 4, Appl	629	132	10.2	1591	4	US-09-402-923A-4	Sequence 4, Appl
557	140.5	10.8	650	1	US-08-325-071-59	Sequence 59, Appl	630	132	10.2	1591	4	US-09-060-299-3	Sequence 3, Appl
558	140.5	10.8	650	3	US-08-461-004A-59	Sequence 59, Appl	631	132	10.2	1615	4	US-09-402-923A-3	Sequence 3, Appl
559	139.5	10.8	44	6	5177197-48	Patent No. 5177197	632	132	10.2	1615	4	US-09-060-299-29	Sequence 29, Appl
560	139.5	10.8	44	6	5177197-48	Patent No. 5177197	633	132	10.2	1639	4	US-09-402-923A-29	Sequence 29, Appl
561	139	10.7	77	1	US-08-264-534-1	Sequence 1, Appl	634	132	10.2	1639	4	US-09-949-016-10117	Sequence 10117, A
562	139	10.7	77	1	US-08-083-590A-14	Sequence 14, Appl	635	131.5	10.1	765	4	US-09-590-656-2	Sequence 2, Appl
563	139	10.7	77	1	US-08-465-500-1	Sequence 1, Appl	636	131	10.1	704	4	US-09-733-764-2	Sequence 2, Appl
564	139	10.7	77	2	US-08-346-126-1	Sequence 1, Appl	637	131	10.1	704	4	US-08-444-792-4	Sequence 4, Appl
565	139	10.7	77	2	US-08-346-126-1	Sequence 1, Appl	638	131	10.1	718	1	US-08-445-042-4	Sequence 4, Appl
566	139	10.7	77	3	US-08-532-384-14	Sequence 14, Appl	639	131	10.1	784	4	US-09-949-016-9467	Sequence 9467, Ap
567	139	10.7	77	3	US-08-893-828-1	Sequence 1, Appl	640	131	10.1	784	4	US-07-728-215-32	Sequence 32, Appl
568	139	10.7	100	3	US-09-249-697A-3	Sequence 3, Appl	641	131	10.1	788	2	US-08-938-085A-32	Sequence 32, Appl
569	139	10.7	100	3	US-09-363-316B-3	Sequence 3, Appl	642	131	10.1	788	3	US-09-409-648-3	Sequence 3, Appl
570	139	10.7	100	4	US-10-136-227A-3	Sequence 3, Appl	643	131	10.1	788	3	US-09-409-648-4	Sequence 4, Appl
571	139	10.7	100	4	US-09-981-649A-3	Sequence 3, Appl	644	131	10.1	788	4	US-10-072-843-32	Sequence 32, Appl
572	138	10.6	2254	4	US-09-949-016-9270	Sequence 9270, Ap	645	131	10.1	788	4	US-10-072-843-32	Sequence 32, Appl
573	137.5	10.6	889	5	PCT-US93-11725-2	Sequence 2, Appl	646	131	10.1	788	4	US-10-072-843-32	Sequence 32, Appl
574	137	10.6	221	2	US-08-480-229C-29	Sequence 29, Appl	647	131	10.1	788	4	US-10-072-843-32	Sequence 32, Appl
575	137	10.6	221	2	US-08-659-235C-29	Sequence 29, Appl	648	131	10.1	788	4	US-09-054-272-8	Sequence 8, Appl
576	137	10.6	480	2	US-08-480-229C-10	Sequence 10, Appl	649	131	10.1	788	4	US-09-054-272-44	Sequence 44, Appl
577	137	10.6	480	2	US-08-659-235C-10	Sequence 10, Appl	650	131	10.1	788	4	US-10-219-631A-32	Sequence 32, Appl
578	137	10.6	730	3	US-08-872-757-2	Sequence 2, Appl	651	131	10.1	788	4	US-09-949-016-5901	Sequence 5901, Ap
579	137	10.6	730	3	US-09-850-048A-2	Sequence 2, Appl	652	131	10.1	977	4	US-09-590-656-1	Sequence 1, Appl
580	136.5	10.5	243	3	US-09-191-647-14	Sequence 14, Appl	653	131	10.1	977	4	US-09-733-764-1	Sequence 1, Appl
581	136.5	10.5	243	3	US-09-540-245A-14	Sequence 14, Appl	654	131	10.1	1124	1	US-08-323-474-2	Sequence 2, Appl
582	136.5	10.5	243	3	US-09-540-153-14	Sequence 14, Appl	655	131	10.1	1124	1	US-09-949-016-5946	Sequence 5946, Ap
583	136.5	10.5	650	1	US-08-325-071-67	Sequence 67, Appl	656	131	10.1	1124	5	PCT-US93-06093-2	Sequence 2, Appl
584	136.5	10.5	650	3	US-08-461-004A-67	Sequence 67, Appl	657	131	10.1	1157	4	US-09-949-016-9568	Sequence 9568, Ap
585	136.5	10.5	1799	4	US-09-845-583A-6	Sequence 6, Appl	658	131	10.1	1615	4	US-09-544-398B-3	Sequence 3, Appl
586	136	10.5	749	2	US-08-937-931-8	Sequence 8, Appl	659	131	10.1	1615	4	US-09-544-398B-4	Sequence 4, Appl
587	136	10.5	749	3	US-09-285-502-8	Sequence 8, Appl	660	131	10.1	1615	4	US-09-543-771B-3	Sequence 3, Appl
588	136	10.5	749	3	US-09-709-126-8	Sequence 8, Appl	661	131	10.1	1615	4	US-09-543-771B-4	Sequence 4, Appl
589	136	10.5	749	3	US-09-871-385A-8	Sequence 8, Appl	662	130.5	10.1	690	4	US-09-907-794A-49	Sequence 49, Appl
590	136	10.5	1171	1	US-08-445-135-1	Sequence 1, Appl	663	130.5	10.1	690	4	US-09-905-125A-49	Sequence 49, Appl
591	136	10.5	1854	4	US-09-949-016-11625	Sequence 11625, A	664	130.5	10.1	690	4	US-09-902-775A-49	Sequence 49, Appl
592	135.5	10.4	1798	4	US-09-845-583B-8	Sequence 8, Appl	665	130.5	10.1	690	4	US-09-906-700-49	Sequence 49, Appl
593	135.5	10.4	1798	4	US-09-561-709B-11	Sequence 11, Appl	666	130.5	10.1	690	4	US-09-903-603A-49	Sequence 49, Appl
594	135.5	10.4	1798	4	US-09-917-254-87	Sequence 87, Appl	667	130.5	10.1	690	4	US-09-904-920A-49	Sequence 49, Appl
595	135	10.4	448	4	US-09-949-016-10130	Sequence 10130, A	668	130.5	10.1	690	4	US-09-909-064-49	Sequence 49, Appl
596	135	10.4	513	2	US-08-480-229C-14	Sequence 14, Appl	669	130.5	10.1	690	4	US-09-905-381A-49	Sequence 49, Appl
597	135	10.4	513	2	US-08-659-235C-14	Sequence 14, Appl	670	130.5	10.1	690	4	US-09-906-618-49	Sequence 49, Appl
598	134	10.3	78	1	US-08-264-534-2	Sequence 2, Appl	671	130	10.0	717	4	US-09-949-016-11182	Sequence 11182, A
599	134	10.3	78	1	US-08-083-590A-15	Sequence 15, Appl	672	129.5	10.0	114	2	US-08-733-564-1	Sequence 1, Appl
600	134	10.3	78	1	US-08-465-500-2	Sequence 2, Appl	673	129.5	10.0	115	1	US-08-312-870-9	Sequence 9, Appl
601	134	10.3	78	2	US-08-346-126-2	Sequence 2, Appl	674	129	9.9	1725	4	US-09-562-702A-20	Sequence 20, Appl
602	134	10.3	78	2	US-08-346-126-2	Sequence 2, Appl	675	129	9.9	1725	4	US-09-561-818A-20	Sequence 20, Appl
603	134	10.3	78	3	US-08-532-384-15	Sequence 15, Appl	676	129	9.9	1786	4	US-09-562-702A-18	Sequence 18, Appl
604	134	10.3	78	3	US-08-893-828-2	Sequence 2, Appl	677	129	9.9	1786	4	US-09-561-818A-18	Sequence 18, Appl
605	134	10.3	1586	4	US-09-060-299-44	Sequence 44, Appl	678	128	9.9	699	1	US-09-949-016-6138	Sequence 6138, Ap
606	134	10.3	1586	4	US-09-402-923A-44	Sequence 44, Appl	679	127.5	9.8	356	1	US-08-228-162-2	Sequence 2, Appl
607	134	10.3	1614	4	US-09-060-299-42	Sequence 42, Appl	680	127.5	9.8	721	4	US-09-949-016-11031	Sequence 11031, A
608	134	10.3	1614	4	US-09-402-923A-42	Sequence 42, Appl	681	127.5	9.8	799	1	US-08-054-077C-2	Sequence 2, Appl
609	134	10.3	3084	4	US-09-562-702A-12	Sequence 12, Appl	682	127.5	9.8	1576	4	US-09-562-702A-24	Sequence 24, Appl
610	134	10.3	3106	4	US-09-562-702A-10	Sequence 10, Appl	683	127.5	9.8	1576	4	US-09-561-818A-24	Sequence 24, Appl
611	133.5	10.3	1481	2	US-08-616-844-40	Sequence 40, Appl	684	127.5	9.8	1584	4	US-09-562-702A-28	Sequence 28, Appl

685	127.5	9.8	1609	4	US-09-562-702A-22	Sequence 22, Appl	758	119	9.2	496	4	US-09-949-016-11306	Sequence 11306, A
686	127.5	9.8	1609	4	US-09-561-818A-22	Sequence 22, Appl	759	119	9.2	496	5	PCT-US94-00253-1	Sequence 1, Appl
687	127.5	9.8	1609	4	US-09-538-092-900	Sequence 900, App	760	119	9.2	583	4	US-09-902-540-10714	Sequence 10714, A
688	127.5	9.8	1617	4	US-09-562-702A-26	Sequence 26, Appl	761	119	9.2	830	6	5378464-2	Patent No. 5378464
689	127.5	9.8	2123	4	US-09-949-016-7517	Sequence 7517, Ap	762	119	9.2	830	6	5378464-2	Patent No. 5378464
690	127.5	9.8	3070	4	US-09-961-403-7	Sequence 7, Appl	763	119	9.2	849	4	US-09-949-016-10271	Sequence 10271, A
691	127.5	9.8	3088	4	US-09-562-702A-8	Sequence 8, Appl	764	119	9.2	902	4	US-09-644-600-10	Sequence 10, Appl
692	127.5	9.8	3089	4	US-09-562-702A-4	Sequence 4, Appl	765	119	9.2	902	4	US-09-654-600A-10	Sequence 10, Appl
693	127.5	9.8	3110	4	US-09-562-702A-2	Sequence 2, Appl	766	119	9.2	1572	4	US-09-562-702A-32	Sequence 32, Appl
694	127.5	9.8	3110	4	US-09-562-702A-6	Sequence 6, Appl	767	119	9.2	1572	4	US-09-561-818A-28	Sequence 28, Appl
695	127.5	9.8	3110	4	US-09-561-709B-7	Sequence 7, Appl	768	119	9.2	1605	4	US-09-562-702A-30	Sequence 30, Appl
696	127.5	9.8	3110	4	US-09-917-254-86	Sequence 86, Appl	769	119	9.2	1605	4	US-09-561-818A-26	Sequence 26, Appl
697	127.5	9.8	3110	4	US-09-949-016-5937	Sequence 5937, Ap	770	118.5	9.1	410	6	5177197-1	Patent No. 5177197
698	127.5	9.8	3111	2	US-08-460-309-4	Sequence 4, Appl	771	118.5	9.1	410	6	5177197-1	Patent No. 5177197
699	127.5	9.8	3111	2	US-08-125-077-4	Sequence 4, Appl	772	118.5	9.1	495	4	US-10-006-011A-4	Sequence 4, Appl
700	126.5	9.8	281	3	US-08-652-877-7	Sequence 7, Appl	773	118.5	9.1	705	4	US-10-006-011A-3	Sequence 3, Appl
701	126.5	9.8	281	3	US-08-476-515A-7	Sequence 7, Appl	774	118.5	9.1	769	4	US-08-454-455-6	Sequence 6, Appl
702	126.5	9.8	610	1	US-08-365-470-3	Sequence 3, Appl	775	118.5	9.1	831	4	US-09-949-016-10169	Sequence 10169, A
703	126.5	9.8	610	3	US-09-309-668-19	Sequence 19, Appl	776	118.5	9.1	1113	4	US-09-959-392-4	Sequence 4, Appl
704	126.5	9.8	610	3	US-09-409-490A-89	Sequence 89, Appl	777	118.5	9.1	1172	1	US-08-313-288B-19	Sequence 19, Appl
705	126.5	9.8	610	4	US-09-949-016-5942	Sequence 5942, Ap	778	118.5	9.1	1172	4	US-09-949-016-6333	Sequence 6333, Ap
706	126.5	9.8	610	6	5217870-2	Sequence 5942, Ap	779	118.5	9.1	4391	4	US-10-006-011A-2	Sequence 2, Appl
707	126.5	9.8	610	6	5217870-2	Patent No. 5217870	780	118	9.1	577	2	US-07-728-215-29	Sequence 29, Appl
708	126.5	9.8	647	4	US-09-949-016-10272	Sequence 10272, A	781	118	9.1	577	3	US-08-938-085A-29	Sequence 29, Appl
709	126	9.7	41	4	US-09-341-461-16	Sequence 16, Appl	782	118	9.1	577	4	US-10-072-84A-29	Sequence 29, Appl
710	126	9.7	155	4	US-09-270-767-32193	Sequence 32193, A	783	118	9.1	577	4	US-10-072-84A-29	Sequence 29, Appl
711	126	9.7	715	4	US-10-101-464A-924	Sequence 924, App	784	118	9.1	577	4	US-10-072-841A-29	Sequence 29, Appl
712	126	9.7	1135	2	US-08-469-537A-97	Sequence 97, Appl	785	118	9.1	577	4	US-10-219-631A-29	Sequence 29, Appl
713	125.5	9.7	2409	6	5180808-2	Sequence 97, Appl	786	118	9.1	830	5	PCT-US91-05059-2	Sequence 2, Appl
714	125.5	9.7	2409	6	5180808-2	Patent No. 5180808	787	118	9.1	933	2	US-08-313-200-1	Sequence 1, Appl
715	125	9.6	1765	4	US-09-562-702A-16	Sequence 16, Appl	788	118	9.1	933	4	US-09-251-039-2	Sequence 1, Appl
716	125	9.6	1765	4	US-09-561-818A-16	Sequence 16, Appl	789	118	9.1	933	5	PCT-US93-03837-1	Sequence 1, Appl
717	125	9.6	1786	4	US-09-562-702A-14	Sequence 14, Appl	790	118	9.1	1172	4	US-09-560-385A-32	Sequence 32, Appl
718	125	9.6	1786	4	US-09-561-818A-14	Sequence 14, Appl	791	118	9.1	1193	4	US-09-560-385A-30	Sequence 30, Appl
719	125	9.6	1786	4	US-09-561-709B-9	Sequence 9, Appl	792	118	9.1	1257	1	US-08-340-428B-49	Sequence 49, Appl
720	125	9.6	1786	4	US-09-538-092-869	Sequence 869, App	793	117.5	9.1	42	4	US-09-341-461-14	Sequence 14, Appl
721	124.5	9.6	179	4	US-09-148-545-177	Sequence 177, App	794	117.5	9.1	1073	4	US-09-949-016-9771	Sequence 9771, Ap
722	124.5	9.6	265	2	US-08-937-931-6	Sequence 6, Appl	795	117.5	9.1	1342	4	US-09-561-709B-13	Sequence 13, Appl
723	124.5	9.6	265	3	US-09-385-502-6	Sequence 6, Appl	796	117	9.0	933	4	US-09-949-016-5953	Sequence 5953, Ap
724	124.5	9.6	265	3	US-09-709-126-6	Sequence 6, Appl	797	117	9.0	933	4	US-09-949-016-7322	Sequence 7322, Ap
725	124.5	9.6	265	3	US-09-871-385A-6	Sequence 6, Appl	798	117	9.0	1621	4	US-09-949-016-8450	Sequence 8450, Ap
726	124.5	9.6	1761	4	US-09-561-709B-1	Sequence 1, Appl	799	116.5	9.0	42	6	5177197-41	Patent No. 5177197
727	123.5	9.5	197	4	US-09-370-838-206	Sequence 206, App	800	116.5	9.0	42	6	5177197-41	Patent No. 5177197
728	123.5	9.5	197	4	US-09-854-133-206	Sequence 206, App	801	116.5	9.0	131	2	US-08-650-598-3	Sequence 3, Appl
729	123.5	9.5	652	3	US-09-110-116-1	Sequence 1, Appl	802	116.5	9.0	1101	4	US-09-561-709B-5	Sequence 5, Appl
730	123.5	9.5	652	3	US-08-556-322-2	Sequence 2, Appl	803	116	8.9	794	4	US-09-949-016-10746	Sequence 10746, A
731	123	9.5	991	4	US-09-949-016-7768	Sequence 7768, Ap	804	116	8.9	1118	1	US-07-934-393B-2	Sequence 2, Appl
732	123	9.5	1551	4	US-09-949-016-6785	Sequence 6785, Ap	805	116	8.9	1118	1	US-08-278-089A-2	Sequence 2, Appl
733	122.5	9.4	441	4	US-09-949-016-10792	Sequence 10792, A	806	116	8.9	1118	2	US-08-838-957A-2	Sequence 2, Appl
734	122.5	9.4	560	4	US-09-949-016-6458	Sequence 6458, Ap	807	116	8.9	1122	1	US-08-278-089A-6	Sequence 6, Appl
735	122.5	9.4	560	4	US-09-912-559-3	Sequence 3, Appl	808	116	8.9	1122	2	US-08-838-957A-6	Sequence 6, Appl
736	122.5	9.4	560	4	US-09-312-559-4	Sequence 4, Appl	809	114.5	8.8	96	4	US-09-270-767-32102	Sequence 32102, A
737	122	9.4	1106	4	US-09-949-016-9626	Sequence 9626, Ap	810	114.5	8.8	830	1	US-08-110-158-4	Sequence 4, Appl
738	121	9.3	234	4	US-09-302-540-15175	Sequence 15175, A	811	114	8.8	788	2	US-07-728-215-27	Sequence 27, Appl
739	121	9.3	1101	2	US-08-469-537A-96	Sequence 96, Appl	812	114	8.8	788	3	US-08-938-085A-27	Sequence 27, Appl
740	120.5	9.3	1104	2	US-08-327-832-5	Sequence 5, Appl	813	114	8.8	788	4	US-10-072-84A-27	Sequence 27, Appl
741	120.5	9.3	1104	2	US-08-828-584-5	Sequence 5, Appl	814	114	8.8	788	4	US-10-072-841A-27	Sequence 27, Appl
742	120	9.3	788	1	US-08-454-455-4	Sequence 4, Appl	815	114	8.8	788	4	US-10-219-631A-27	Sequence 27, Appl
743	120	9.3	1111	1	US-08-317-450B-15	Sequence 15, Appl	816	114	8.8	788	4	US-10-219-631A-27	Sequence 27, Appl
744	120	9.3	1111	3	US-08-800-593-15	Sequence 15, Appl	817	114	8.8	1345	4	US-09-949-016-8313	Sequence 8313, Ap
745	120	9.3	1172	4	US-09-560-385A-28	Sequence 28, Appl	818	114	8.8	2214	1	US-08-727-034-7	Sequence 7, Appl
746	120	9.3	1193	1	US-08-317-450B-13	Sequence 13, Appl	819	114	8.8	2214	4	US-09-919-039-40	Sequence 40, Appl
747	120	9.3	1193	3	US-08-800-593-13	Sequence 13, Appl	820	114	8.8	2476	2	US-08-276-967-2	Sequence 2, Appl
748	120	9.3	1193	4	US-09-560-385A-26	Sequence 26, Appl	821	113.5	8.8	194	3	US-09-188-930-335	Sequence 335, App
749	119.5	9.2	439	4	US-09-949-016-9260	Sequence 9260, Ap	822	113.5	8.8	194	4	US-09-312-285C-335	Sequence 335, App
750	119	9.2	41	4	US-09-341-461-15	Sequence 15, Appl	823	113.5	8.8	240	4	US-10-006-011A-5	Sequence 5, Appl
751	119	9.2	314	2	US-08-460-309-19	Sequence 19, Appl	824	113.5	8.8	709	4	US-09-874-923-121	Sequence 121, App
752	119	9.2	314	2	US-08-125-077-19	Sequence 19, Appl	825	113	8.7	302	4	US-09-270-767-33326	Sequence 33326, A
753	119	9.2	486	1	US-08-462-128-37	Sequence 37, Appl	826	113	8.7	302	4	US-07-728-215-30	Sequence 30, Appl
754	119	9.2	486	1	US-08-463-180-37	Sequence 37, Appl	827	113	8.7	798	2	US-07-728-215-30	Sequence 30, Appl
755	119	9.2	486	2	US-08-001-078A-1	Sequence 1, Appl	828	113	8.7	798	3	US-08-938-085A-30	Sequence 30, Appl
756	119	9.2	486	2	US-08-897-443-4	Sequence 4, Appl	829	113	8.7	798	4	US-10-072-844-30	Sequence 30, Appl
757	119	9.2	486	2	US-08-463-218-1	Sequence 1, Appl	830	113	8.7	798	4	US-10-072-838-30	Sequence 30, Appl

831	113	8.7	798	4	US-10-072-841A-30	Sequence 30, Appl	904	108.5	8.4	589	2	US-08-429-998-6	Sequence 6, Appl
832	113	8.7	798	4	US-10-219-631A-30	Sequence 30, Appl	905	108.5	8.4	589	2	US-08-431-333-6	Sequence 6, Appl
833	113	8.7	798	4	US-09-949-016-6193	Sequence 6193, Ap	906	108.5	8.4	589	3	US-08-991-862-2	Sequence 2, Appl
834	113	8.7	846	3	US-07-728-215-33	Sequence 33, Appl	907	108.5	8.4	589	4	US-09-813-156-2	Sequence 2, Appl
835	113	8.7	846	3	US-08-938-085A-33	Sequence 33, Appl	908	108.5	8.4	589	4	US-09-456-886-2	Sequence 2, Appl
836	113	8.7	846	4	US-10-072-844-33	Sequence 33, Appl	909	108.5	8.4	589	4	US-09-824-647-2	Sequence 2, Appl
837	113	8.7	846	4	US-10-072-838-33	Sequence 33, Appl	910	108.5	8.4	589	5	PCT-US91-02321-6	Sequence 6, Appl
838	113	8.7	846	4	US-10-072-841A-33	Sequence 33, Appl	911	108.5	8.4	686	4	US-09-949-016-11203	Sequence 11203, A
839	113	8.7	846	4	US-10-219-631A-33	Sequence 33, Appl	912	108.5	8.4	696	3	US-09-351-414-2	Sequence 4, Appl
840	113	8.7	1042	4	US-09-959-392-2	Sequence 2, Appl	913	108.5	8.4	832	4	US-09-634-252A-4	Sequence 4, Appl
841	112.5	8.7	266	4	US-09-686-583B-31	Sequence 31, Appl	914	108.5	8.4	1153	4	US-09-560-385A-16	Sequence 16, Appl
842	112.5	8.7	285	4	US-09-686-583B-26	Sequence 26, Appl	915	108.5	8.4	1170	4	US-09-561-709B-12	Sequence 12, Appl
843	112.5	8.7	799	2	US-08-525-940-23	Sequence 23, Appl	916	108.5	8.4	1170	4	US-09-560-385A-14	Sequence 14, Appl
844	112.5	8.7	799	2	US-08-976-838-23	Sequence 23, Appl	917	108.5	8.4	5179	4	US-09-538-092-1258	Sequence 1258, Ap
845	112.5	8.7	881	2	US-08-525-940-21	Sequence 21, Appl	918	107.5	8.3	198	4	US-09-902-540-15333	Sequence 15333, A
846	112.5	8.7	881	2	US-08-976-838-21	Sequence 21, Appl	919	107.5	8.3	415	3	US-08-795-430-11	Sequence 11, Appl
847	112.5	8.7	915	2	US-08-525-940-18	Sequence 18, Appl	920	107.5	8.3	415	3	US-09-355-700-11	Sequence 11, Appl
848	112.5	8.7	915	2	US-08-976-838-18	Sequence 18, Appl	921	107.5	8.3	415	4	US-08-601-132-41	Sequence 41, Appl
849	112.5	8.7	915	3	US-09-214-555B-2	Sequence 2, Appl	922	107.5	8.3	415	4	US-08-671-573B-41	Sequence 41, Appl
850	112.5	8.7	915	3	US-09-214-555B-7	Sequence 7, Appl	923	107.5	8.3	415	4	US-09-631-092B-41	Sequence 41, Appl
851	112.5	8.7	2213	1	US-08-727-034-3	Sequence 3, Appl	924	107.5	8.3	415	4	US-09-534-376A-11	Sequence 11, Appl
852	112	8.6	855	2	US-09-027-337-2	Sequence 2, Appl	925	107.5	8.3	574	6	5378464-3	Patent No. 5378464
853	112	8.6	855	4	US-09-644-600-2	Sequence 2, Appl	926	107.5	8.3	574	6	5378464-3	Patent No. 5378464
854	112	8.6	855	4	US-09-654-600A-2	Sequence 2, Appl	927	107.5	8.3	1235	4	US-09-949-016-8455	Sequence 8455, Ap
855	112	8.6	1171	4	US-09-560-385A-36	Sequence 36, Appl	928	107.5	8.3	1235	4	US-09-949-016-8456	Sequence 8456, Ap
856	112	8.6	1192	4	US-09-560-385A-34	Sequence 34, Appl	929	107.5	8.3	2169	4	US-09-949-016-6930	Sequence 6930, Ap
857	111.5	8.6	42	2	US-08-751-305-7	Sequence 7, Appl	930	107.5	8.3	5405	3	US-08-718-388-9	Sequence 9, Appl
858	111.5	8.6	320	3	US-09-183-861-22	Sequence 22, Appl	931	107	8.2	45	1	US-08-278-089A-25	Sequence 25, Appl
859	111.5	8.6	320	3	US-09-183-861-55	Sequence 55, Appl	932	107	8.2	79	4	US-10-006-011A-7	Sequence 7, Appl
860	111.5	8.6	320	3	US-09-022-765-22	Sequence 22, Appl	933	107	8.2	160	3	US-09-191-647-5	Sequence 5, Appl
861	111.5	8.6	320	3	US-09-022-765-55	Sequence 55, Appl	934	107	8.2	160	3	US-09-540-245A-5	Sequence 5, Appl
862	111.5	8.6	320	4	US-09-551-974A-22	Sequence 22, Appl	935	107	8.2	160	3	US-09-540-153-5	Sequence 5, Appl
863	111.5	8.6	320	4	US-09-551-974A-55	Sequence 55, Appl	936	107	8.2	217	1	US-07-697-275-2	Sequence 2, Appl
864	111.5	8.6	320	4	US-09-565-501A-22	Sequence 22, Appl	937	107	8.2	217	1	US-08-400-421-2	Sequence 2, Appl
865	111.5	8.6	320	4	US-09-565-501A-55	Sequence 55, Appl	938	107	8.2	462	4	US-09-026-001A-16	Sequence 16, Appl
866	111.5	8.6	320	4	US-09-639-206A-22	Sequence 22, Appl	939	107	8.2	592	4	US-09-026-001A-14	Sequence 14, Appl
867	111.5	8.6	320	4	US-09-639-206A-55	Sequence 55, Appl	940	107	8.2	769	2	US-08-789-078-1	Sequence 1, Appl
868	111.5	8.6	320	4	US-09-874-923-22	Sequence 22, Appl	941	107	8.2	769	2	US-08-752-633-1	Sequence 1, Appl
869	111.5	8.6	320	4	US-09-874-923-55	Sequence 55, Appl	942	107	8.2	769	2	US-08-476-062A-45	Sequence 45, Appl
870	111.5	8.6	320	4	US-08-798-841-22	Sequence 22, Appl	943	107	8.2	769	2	US-07-728-215-31	Sequence 31, Appl
871	110.5	8.5	44	4	US-09-341-461-10	Sequence 10, Appl	944	107	8.2	769	3	US-08-938-085A-31	Sequence 31, Appl
872	110.5	8.5	265	4	US-09-270-767-43427	Sequence 43427, A	945	107	8.2	769	4	US-10-072-844-31	Sequence 31, Appl
873	110.5	8.5	379	4	US-09-907-794A-4	Sequence 4, Appl	946	107	8.2	769	4	US-10-072-838-31	Sequence 31, Appl
874	110.5	8.5	379	4	US-09-905-125A-4	Sequence 4, Appl	947	107	8.2	769	4	US-10-072-841A-31	Sequence 31, Appl
875	110.5	8.5	379	4	US-09-902-775A-4	Sequence 4, Appl	948	107	8.2	769	4	US-10-219-631A-31	Sequence 31, Appl
876	110.5	8.5	379	4	US-09-906-700-4	Sequence 4, Appl	949	107	8.2	769	5	PCT-US95-04886-1	Sequence 1, Appl
877	110.5	8.5	379	4	US-09-903-603A-4	Sequence 4, Appl	950	107	8.2	769	5	PCT-US96-01314-45	Sequence 45, Appl
878	110.5	8.5	379	4	US-09-904-920A-4	Sequence 4, Appl	951	107	8.2	1940	2	US-08-644-271-30	Sequence 30, Appl
879	110.5	8.5	379	4	US-09-909-064-4	Sequence 4, Appl	952	107	8.2	1940	2	US-09-077-955-34	Sequence 34, Appl
880	110.5	8.5	379	4	US-09-905-381A-4	Sequence 4, Appl	953	106.5	8.2	42	6	5177197-33	Patent No. 5177197
881	110.5	8.5	379	4	US-09-906-618-4	Sequence 4, Appl	954	106.5	8.2	42	6	5177197-33	Patent No. 5177197
882	110	8.5	41	6	5177197-37	Patent No. 5177197	955	106.5	8.2	154	3	US-09-191-647-10	Sequence 10, Appl
883	110	8.5	41	6	5177197-37	Patent No. 5177197	956	106.5	8.2	154	3	US-09-540-245A-10	Sequence 10, Appl
884	110	8.5	166	4	US-09-489-847-148	Sequence 148, App	957	106.5	8.2	154	3	US-09-540-153-10	Sequence 10, Appl
885	110	8.5	167	4	US-09-489-847-230	Sequence 230, App	958	106.5	8.2	219	1	US-08-152-019A-31	Sequence 31, Appl
886	110	8.5	321	4	US-09-270-767-45035	Sequence 45035, A	959	106.5	8.2	219	2	US-08-460-309-18	Sequence 18, Appl
887	110	8.5	589	1	US-07-668-648-2	Sequence 2, Appl	960	106.5	8.2	219	2	US-08-125-077-18	Sequence 18, Appl
888	110	8.5	589	2	US-08-429-998-2	Sequence 2, Appl	961	106.5	8.2	722	4	US-09-617-145-2	Sequence 2, Appl
889	110	8.5	589	2	US-08-431-333-2	Sequence 2, Appl	962	106.5	8.2	722	4	US-09-949-016-6418	Sequence 6418, Ap
890	110	8.5	589	5	PCT-US91-02321-2	Sequence 2, Appl	963	106.5	8.2	1155	4	US-09-560-385A-24	Sequence 24, Appl
891	110	8.5	691	4	US-09-949-016-7775	Sequence 7775, Ap	964	106.5	8.2	1167	4	US-09-560-385A-20	Sequence 20, Appl
892	109.5	8.4	484	2	US-08-252-493C-9	Sequence 9, Appl	965	106.5	8.2	1172	4	US-09-919-172-16	Sequence 16, Appl
893	109.5	8.4	484	3	US-09-276-197-9	Sequence 9, Appl	966	106.5	8.2	1174	4	US-09-560-385A-22	Sequence 22, Appl
894	109.5	8.4	676	3	US-08-630-172-10	Sequence 10, Appl	967	106.5	8.2	1186	4	US-09-560-385A-18	Sequence 18, Appl
895	109.5	8.4	676	3	US-09-375-419-10	Sequence 10, Appl	968	106.5	8.2	1276	3	US-08-937-236-3	Sequence 3, Appl
896	109.5	8.4	1277	3	US-08-937-236-6	Sequence 6, Appl	969	106.5	8.2	1291	3	US-08-569-214-3	Sequence 3, Appl
897	109.5	8.4	1292	3	US-08-569-214-5	Sequence 5, Appl	970	106.5	8.2	1291	3	US-08-937-236-2	Sequence 2, Appl
898	109.5	8.4	1292	3	US-08-569-214-6	Sequence 6, Appl	971	106.5	8.2	1295	3	US-08-569-214-2	Sequence 2, Appl
899	109.5	8.4	1292	3	US-08-937-236-5	Sequence 5, Appl	972	106	8.2	1036	4	US-09-949-016-6910	Sequence 6910, Ap
900	108.5	8.4	45	2	US-08-838-957A-24	Sequence 24, Appl	973	106	8.2	1049	4	US-09-949-016-11522	Sequence 11522, A
901	108.5	8.4	288	2	US-08-525-940-15	Sequence 15, Appl	974	105.5	8.1	37	4	US-09-060-299-10	Sequence 10, Appl
902	108.5	8.4	288	2	US-08-976-838-15	Sequence 15, Appl	975	105.5	8.1	37	4	US-09-402-923A-10	Sequence 10, Appl
903	108.5	8.4	589	1	US-07-668-648-6	Sequence 6, Appl	976	105.5	8.1	39	4	US-09-060-299-16	Sequence 16, Appl

977 105.5 8.1 39 4 US-09-402-923A-16 Sequence 16, Appl
 978 105.5 8.1 2211 3 US-09-738-884-1 Sequence 1, Appli
 979 105.5 8.1 2211 4 US-10-096-961A-1 Sequence 1, Appli
 980 105 8.1 161 4 US-10-293-622-4 Sequence 4, Appli
 981 105 8.1 345 4 US-10-293-622-2 Sequence 2, Appli
 982 105 8.1 469 4 US-09-902-540-16788 Sequence 16788, A
 983 105 8.1 2813 3 US-08-896-449A-2 Sequence 2, Appli
 984 105 8.1 2813 3 US-09-132-652-2 Sequence 2, Appli
 985 105 8.1 2813 4 US-09-886-900A-2 Sequence 2, Appli
 986 105 8.1 2813 4 US-09-662-478C-2 Sequence 2, Appli
 987 104.5 8.1 241 2 US-08-460-309-17 Sequence 17, Appl
 988 104.5 8.1 241 2 US-08-125-077-17 Sequence 17, Appl
 989 104.5 8.1 288 1 US-08-368-852-15 Sequence 15, Appl
 990 104.5 8.1 717 4 US-09-644-460-37 Sequence 37, Appl
 991 104.5 8.1 3075 2 US-08-460-309-5 Sequence 5, Appli
 992 104.5 8.1 3075 2 US-08-125-077-5 Sequence 5, Appli
 993 104 8.0 178 4 US-09-706-722A-7 Sequence 7, Appli
 994 104 8.0 455 4 US-09-866-028-50 Sequence 50, Appl
 995 104 8.0 455 4 US-09-944-457-50 Sequence 50, Appl
 996 104 8.0 908 5 PCT-US95-03747-3 Sequence 3, Appli
 997 104 8.0 1694 4 US-09-560-385A-12 Sequence 12, Appl
 998 104 8.0 1725 4 US-09-560-385A-10 Sequence 10, Appl
 999 103.5 8.0 115 4 US-09-270-767-42013 Sequence 42013, A
 1000 103.5 8.0 165 4 US-09-706-722A-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
 US-08-282-141-2
 ; Sequence 2, Application US/08282141
 ; Patent No. 5538861
 ; GENERAL INFORMATION:
 ; APPLICANT: Schneider, Claudio
 ; APPLICANT: Varnum, Brian
 ; APPLICANT: Avanzi, Giancarlo
 ; APPLICANT: Brancolini, Claudio
 ; APPLICANT: Manfioletti, Guidalberto
 ; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 Dehavilland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/282,141
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 678 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-282-141-2
 Query Match 100.0%; Score 1297; DB 1; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.3e-103;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 90 PRYLDCKVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCQDIDECADSEACGE 149

QY 61 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCQDIDECADSEACGE 120
 DB 150 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCQDIDECADSEACGE 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGJLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGJLK 269
 QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 227
 DB 270 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPTVIRLRFKRLQP 316
 RESULT 2
 US-08-435-434-2
 ; Sequence 2, Application US/08435434
 ; Patent No. 5714385
 ; GENERAL INFORMATION:
 ; APPLICANT: Mather, Jennie P.
 ; APPLICANT: Li, Ronghao
 ; APPLICANT: Chen, Jian
 ; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/435,434
 ; FILING DATE: 10-MAY-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION NUMBER:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 00,000
 ; REFERENCE/DOCKET NUMBER: 946-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 678 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; US-08-435-434-2
 Query Match 100.0%; Score 1297; DB 1; Length 678;
 Best Local Similarity 100.0%; Pred. No. 2.3e-103;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 150 GRLCDKDVNECSQENGGLQICHNKPFGSHCSHGFELSSDGRTCQDIDECADSEACGE 209
 QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGJLK 180
 DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGJLK 269

QY 181 LSQDMTCECILPCVPFSAKSVKSLYLGRMFGSGTPVIRLRFKRLQP 227
Db 270 LSQDMTCECILPCVPFSAKSVKSLYLGRMFGSGTPVIRLRFKRLQP 316

RESULT 3

US-08-435-436-2
; Sequence 2, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435, 436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-436-2

Query Match 100.0%; Score 1297; DB 1; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 270 LSQDMTCECILPCVPFSAKSVKSLYLGRMFGSGTPVIRLRFKRLQP 316

RESULT 4

US-08-438-863-2

; Sequence 2, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,863
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-863-2
Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PRYLDCKVNECSQENGGLQICHNKGSPHCSHGFSGLSSDGRTCQDIDECADSEACGE 60
Db 90 PRYLDCKVNECSQENGGLQICHNKGSPHCSHGFSGLSSDGRTCQDIDECADSEACGE 149
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Db 210 ARCKNLPGSYCLDEGFAYSQEKACRDVDECLQRCQCVNSPGSYTCHCDGRGGLK 269
QY 181 LSQDMTCECILPCVPFSAKSVKSLYLGRMFGSGTPVIRLRFKRLQP 227
Db 270 LSQDMTCECILPCVPFSAKSVKSLYLGRMFGSGTPVIRLRFKRLQP 316
RESULT 5
US-08-438-864-2
; Sequence 2, Application US/08438864
; Patent No. 5955420
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.

APPLICANT: Li, Ronghao
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,864
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402253
FILING DATE: 10-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 929P1-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-864-2

Query Match 100.0%; Score 1297; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
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DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQEVQVNSPGSYTCHCDGRGGLK 269
QY 181 LSQDMTCELDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
DB 270 LSQDMTCELDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316

RESULT 6
US-08-438-862-2
Sequence 2, Application US/08438862
Patent No. 6033660
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,862
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438-862-2

Query Match 100.0%; Score 1297; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKNGSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKNGSPYTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGCGCLQICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 209
QY 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQEVQVNSPGSYTCHCDGRGGLK 180
DB 210 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQEVQVNSPGSYTCHCDGRGGLK 269
QY 181 LSQDMTCELDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
DB 270 LSQDMTCELDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 316

RESULT 7
US-08-402-253-2
Sequence 2, Application US/08402253
Patent No. 6211142
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammonds, R. Glenn
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 678 amino acids
; TOPOLOGY: linear
; US-08-402-253-2

Query Match 100.0%; Score 1297; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKNKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKNKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNCSQENGCGCLOICHNKPFSFCHSCHSFGFELSSDGRGTCODIDECADSEACGE 120
DB 150 GRLCDKDVNCSQENGCGCLOICHNKPFSFCHSCHSFGFELSSDGRGTCODIDECADSEACGE 209
QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 180
DB 210 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 269
QY 181 LSQDMTCEIDILCPVPFSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
DB 270 LSQDMTCEIDILCPVPFSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 316

RESULT 8
US-08-443-866B-2
; Sequence 2, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-May-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000

; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0929D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-443-866B-2

Query Match 100.0%; Score 1297; DB 3; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.3e-103;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PRYLDCKNKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDCKNKYGSPTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149
QY 61 GRLCDKDVNCSQENGCGCLOICHNKPFSFCHSCHSFGFELSSDGRGTCODIDECADSEACGE 120
DB 150 GRLCDKDVNCSQENGCGCLOICHNKPFSFCHSCHSFGFELSSDGRGTCODIDECADSEACGE 209
QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 180
DB 210 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHDGRGLK 269
QY 181 LSQDMTCEIDILCPVPFSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
DB 270 LSQDMTCEIDILCPVPFSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 316

RESULT 9
US-08-628-747-2
; Sequence 2, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: One DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628,747
; FILING DATE: 17-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,253
; FILING DATE: 10-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
```

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; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 678 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-628-747-2

Query Match          99.4%; Score 1289; DB 3; Length 678;
Best Local Similarity 99.6%; Pred. No. 1.1e-102;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PRYLDICNKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 90 PRYLDICNKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 149

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 150 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 209

QY 121 ARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 180
DB 210 ARCKNLPGSYSLCDEGFAVSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGGLK 269

QY 181 LSQDMTCEILPCVPFSPVSAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
DB 270 LSQDMTCEILPCVPFSPVSAKSVKSLYLGRMFSGTPVIRLRFKRLQ 316

RESULT 10
US-08-282-141-3
; Sequence 3, Application US/08282141
; Patent No. 553861
; GENERAL INFORMATION:
; APPLICANT: Schneider, Claudio
; APPLICANT: Varnum, Brian
; APPLICANT: Avanzi, Giancarlo
; APPLICANT: Brancolini, Claudio
; APPLICANT: Manfioletti, Guidalberto
; TITLE OF INVENTION: Stimulating Factor for the AXL Receptor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,141
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-282-141-3

Query Match          85.8%; Score 1113; DB 1; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICNKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDPFAKCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 87 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 266

Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICNKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDPFAKCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 87 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 266

RESULT 11
US-08-435-434-1
; Sequence 1, Application US/08435434
; Patent No. 5714385
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,434
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-434-1

Query Match          85.8%; Score 1113; DB 1; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDICNKYGSPTTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEKNPDPFAKCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 120
DB 87 GRLCDKDVNECSQENGCGCLOICHNKPGSFHCSHGFSFELSSDGRTCQDIDECADSEACGE 266
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Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSQFQACHSGFSLASDGGTQCDIDECTDSDTCGD 206
Qy 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVQVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYCLDCEGYTSSKEKTCQDVDECOQDRCEQTCVNSPGSYTCHCDGRGGLK 266
Qy 181 LSQDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
Db 267 LSPDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 12
US-08-435-436-1
; Sequence 1, Application US/08435436
; Patent No. 5721139
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,436
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-435-436-1

Query Match 85.8%; Score 1113; DB 1; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKNKYGSPTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEKNPDKFACVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146
Qy 61 GRLCDKDVNECVQKNGGCSQVCHNKPFSQFQACHSGFSLASDGGTQCDIDECTDSDTCGD 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSQFQACHSGFSLASDGGTQCDIDECTDSDTCGD 206
Qy 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVQVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYCLDCEGYTSSKEKTCQDVDECOQDRCEQTCVNSPGSYTCHCDGRGGLK 266
Qy 181 LSQDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227

Db 267 LSPDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 13
US-08-438-863-1
; Sequence 1, Application US/08438863
; Patent No. 5849585
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Ronghao Li
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,863
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-438-863-1

Query Match 85.8%; Score 1113; DB 2; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKNKYGSPTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECMRKYGRPEKNPDKFACVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCVCTDGGW 146
Qy 61 GRLCDKDVNECVQKNGGCSQVCHNKPFSQFQACHSGFSLASDGGTQCDIDECTDSDTCGD 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSQFQACHSGFSLASDGGTQCDIDECTDSDTCGD 206
Qy 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQGRCEQVQVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYCLDCEGYTSSKEKTCQDVDECOQDRCEQTCVNSPGSYTCHCDGRGGLK 266
Qy 181 LSQDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
Db 267 LSPDMTCDILPCVPFSPVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 14
US-08-438-864-1
; Sequence 1, Application US/08438864
; Patent No. 5955420

```
;
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929p1-1
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-864-1

Query Match 85.8%; Score 1113; DB 2; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 60
Db 87 PRYQECMRKYGRPEKNPDPFAKCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146

QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSAKSLYLGRMFSGTPVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFSAKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 15
US-08-438-862-1
; Sequence 1, Application US/08438862
; Patent No. 6033660
; GENERAL INFORMATION:
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; APPLICANT: Chen, Jian
; TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS

;
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,864
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 946-1
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-438-862-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 60
Db 87 PRYQECMRKYGRPEKNPDPFAKCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146

QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFELSSDGRTCQDIDECADSEACGE 206

QY 121 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYCLDCEGFAYSSQEKACRDVDECLQRCQVCSNPGSYTCHCDGRGLK 266

QY 181 LSQDMTDCEDILPCVPFSAKSLYLGRMFSGTPVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFSAKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 16
US-08-628-747-1
; Sequence 1, Application US/08628747
; Patent No. 6169070
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie
; APPLICANT: Mather, Jennie P.
; APPLICANT: Li, Ronghao
; TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: One DNA Way
; CITY: South San Francisco
```



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; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-402-253-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKNKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWKYGRPEEKPNDFAKVCQNLDPDQCTPNPCDKKGTTHICQDLGMGNFFCVCTDGMG 146

Qy 61 GRLCDKDVNECSQNGGLQICHNKPFSFCHSGFELSSDGTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACHSGFSLASDGTCDIDECTDSDTCDG 206

Qy 121 ARCKNLPGSYSCLDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSCLDEGTYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266

Qy 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFSSMAKSVKSLYLGRMFSGTPVIRLRFKRLQP 313

RESULT 17
US-08-402-253-1
; Sequence 1, Application US/08402253
; Patent No. 6211142
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B

; STATE: California
; COUNTRY: United States
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 929
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 673 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-402-253-1

Query Match 85.8%; Score 1113; DB 3; Length 673;
Best Local Similarity 82.8%; Pred. No. 1.4e-87;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDCKNKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWKYGRPEEKPNDFAKVCQNLDPDQCTPNPCDKKGTTHICQDLGMGNFFCVCTDGMG 146

Qy 61 GRLCDKDVNECSQNGGLQICHNKPFSFCHSGFELSSDGTCDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCSQVCHNKPFSFQACHSGFSLASDGTCDIDECTDSDTCDG 206

Qy 121 ARCKNLPGSYSCLDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSCLDEGTYTSSKEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGLK 266

Qy 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTPVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFSSMAKSVKSLYLGRMFSGTPVIRLRFKRLQP 313

RESULT 18
US-08-443-866B-1
; Sequence 1, Application US/08443866B
; Patent No. 6255068
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
```


GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
FILING DATE: 10-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-435-436-3
Query Match 46.4%; Score 601.5; DB 1; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACODLMGNFF 52
DB 83 PKYLVLRLSFTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGGRLCDKDVNEC---SQENGGLQICHNKPFGSFHCSHGFSLSGRTQDI 109
DB 143 CTCKPGWQKEKCEFDINECKDPNSINGGCSQICDNTFGSYHCSCKNGFVMSLNKDKCKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDPECEPGRYVNLKSKSCDIEDCSNMCAQLCVNYPGG 262
QY 169 YTCHCDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSGTPVIRLRPK 223
DB 263 YTCYCDGKKGFKLAQDKQSCVSVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKR 316

RESULT 26

US-08-438-863-3
Sequence 3, Application US/08438863
Patent No. 5849585
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Ronghao Li
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,863
FILING DATE: 10-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-438-863-3
Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PRYLDICNKY-----GSPYTKNS--GFATCVQNLDPQCTPNPCDRKGTQACODLMGNFF 52
DB 83 PKYLVLRLSFTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
QY 53 CLCKAGGRLCDKDVNEC---SQENGGLQICHNKPFGSFHCSHGFSLSGRTQDI 109
DB 143 CTCKPGWQKEKCEFDINECKDPNSINGGCSQICDNTFGSYHCSCKNGFVMSLNKDKCKDV 202
QY 110 DECA-DSEACGEARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
DB 203 DECSLKPSICGTAVCKNIPGDPECEPGRYVNLKSKSCDIEDCSNMCAQLCVNYPGG 262
QY 169 YTCHCDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSGTPVIRLRPK 223
DB 263 YTCYCDGKKGFKLAQDKQSCVSVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKR 316

RESULT 27

US-08-438-864-3
Sequence 3, Application US/08438864
Patent No. 5955420
GENERAL INFORMATION:
APPLICANT: Chen, Jian
APPLICANT: Hammonds, R. Glenn
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

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/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ FILING DATE: 10-MAY-1995
/ APPLICATION NUMBER: US/08/438,864
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/402253
/ FILING DATE: 10-MAR-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wendy M. Lee
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 929P1-1
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 676 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-438-864-3

Query Match 46.4%; Score 601.5; DB 2; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLDCKNKY-----GSPYTKNS--GFATCVONLPDQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCDKGKASFT 142

QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPGRFHCSCGSHGSELSSDGRTCQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNSNGGCSQICDNTPGSYHCSCXKNGFVMLSNKKDKDV 202

QY 110 DECA-DSEACGEARCNLPGSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDFECPCPEGYRNLKSKSCDIDECSENCAQLCVNYPGG 262

QY 169 YTHCHDGRGLKLSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKGGFKLAQDKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 28
US-08-438-862-3
/ Sequence 3, Application US/08438862
/ Patent No. 6033660
/ GENERAL INFORMATION:
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ APPLICANT: Chen, Jian
/ TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
/ NUMBER OF SEQUENCES: 9
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: patin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/438,862
/ FILING DATE: 10-MAY-1995
/
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/
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 00,000
/ REFERENCE/DOCKET NUMBER: 946-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-1994
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 676 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-438-862-3

Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLDCKNKY-----GSPYTKNS--GFATCVONLPDQCTPNPCDRKGTQACQDLMGNFF 52
Db 83 PKYLVCLRSFQTGLFTAAARQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCDKGKASFT 142

QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPGRFHCSCGSHGSELSSDGRTCQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNSNGGCSQICDNTPGSYHCSCXKNGFVMLSNKKDKDV 202

QY 110 DECA-DSEACGEARCNLPGSYCLDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDFECPCPEGYRNLKSKSCDIDECSENCAQLCVNYPGG 262

QY 169 YTHCHDGRGLKLSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFGTPTVIRLRFK 223
Db 263 YTCYCDGKGGFKLAQDKSCVSVVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 29
US-08-628-747-3
/ Sequence 3, Application US/08628747
/ Patent No. 6169070
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Jian
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Hammonds, R. Glenn
/ APPLICANT: Mark, Melanie
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Li, Ronghao
/ TITLE OF INVENTION: RECEPTOR ACTIVATION BY GAS6
/ NUMBER OF SEQUENCES: 30
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: One DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: United States
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/628,747
/ FILING DATE: 17-APR-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/402,253
/ FILING DATE: 10-MAR-1995
/
```

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; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-628-747-3

Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

Qy 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLGNFF 52
Db 83 PKYLVLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPFGSHCSHGFSLSGRTSQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCCKNGFVMSLNKKDCKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
Qy 169 YTHCDGRGLKLSQDMTCEIDLPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 263 YTCYCDGKGLKLAQDKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 30
US-08-402-253-3
; Sequence 3, Application US/08402253
; Patent No. 6211142
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Godowski, Paul J.
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,253
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wendy M. Lee
; REGISTRATION NUMBER: 00,000

; APPLICATION NUMBER: US 08/438,861
; FILING DATE: 10-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P929P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-225-1994
; TELEFAX: 650-952-9881
; TELELEX: 910-371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-628-747-3

Query Match 46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

Qy 1 PRYLDCKIN-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTQACODLGNFF 52
Db 83 PKYLVLRSFQTGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMSCKDGKASFT 142
Qy 53 CLCKAGWGRGLCDKDVNEC---SQENGGLQICHNKPFGSHCSHGFSLSGRTSQDI 109
Db 143 CTCKPGWQEKCEFDINECKDPNNGGCSQICDNTPGSYHCCKNGFVMSLNKKDCKDV 202
Qy 110 DECA-DSEACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCKNIPGDCECEPEGYRYNLKSKSCEDIDECSENMCQALCVNYPGG 262
Qy 169 YTHCDGRGLKLSQDMTCEIDLPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 263 YTCYCDGKGLKLAQDKSCVSVCLPLNLDTKYELLYLAEQFAGV-VLYLKFR 316

RESULT 31
US-08-443-866B-3
; Sequence 3, Application US/08443866B
; Patent No. 6255088
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Hammonds, R. Glenn
; APPLICANT: Mark, Melanie R.
; TITLE OF INVENTION: RSE RECEPTOR ACTIVATION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,866B
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402253
; FILING DATE: 10-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: P0929D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 676 amino acids
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-443-866B-3

Query Match          46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
Db 83 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
QY 53 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
Db 143 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
QY 110 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
Db 203 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223
Db 263 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223

RESULT 33
5258288-1
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 675

5258288-1
Query Match          46.0%; Score 596.5; DB 6; Length 675;
Best Local Similarity 43.0%; Pred. No. 2.7e-43;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
Db 83 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
QY 53 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
Db 143 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
QY 110 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
Db 203 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223
Db 263 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223

RESULT 34
5258288-4
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO: 4:
; LENGTH: 652

5258288-4
Query Match          45.2%; Score 586.5; DB 6; Length 652;
Best Local Similarity 42.6%; Pred. No. 1.9e-42;
Matches 100; Conservative 46; Mismatches 76; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
Db 57 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
QY 53 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
Db 117 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
QY 110 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
Db 177 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223
Db 237 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223

RESULT 35
5258288-4
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO: 4:
; LENGTH: 652
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-443-866B-3

Query Match          46.4%; Score 601.5; DB 3; Length 676;
Best Local Similarity 43.4%; Pred. No. 1e-43;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
Db 83 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
QY 53 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
Db 143 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
QY 110 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
Db 203 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223
Db 263 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223

RESULT 33
5258288-1
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 675

5258288-1
Query Match          46.0%; Score 596.5; DB 6; Length 675;
Best Local Similarity 43.0%; Pred. No. 2.7e-43;
Matches 101; Conservative 40; Mismatches 81; Indels 13; Gaps 4;

QY 1 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
Db 83 PRLVLCINIKYSPYTKNSGFAT-----GFATCVQNLPDQCTPNPCDRKGTOACQDLMGNFF 52
QY 53 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
Db 143 CLCKAGWGRGLCDKQVNECSQE---SQENGGLQICHNKPFGSHFCHSGHSGFELSSDGRTCQDI 109
QY 110 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
Db 203 DECA-DSEACGEARCKNLPGSYCLDEGFAYSSQKACRDVDECLQGRCEQVQVNSPGS 168
QY 169 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223
Db 263 YTHCHDGRGGLKLSQDMTDCEDILPCVPFVSVAKSLSYLGRMFGSTPVIIRLFK 223

RESULT 33
5258288-1
; Patent No. 5258288
; APPLICANT: Wydro Robert; Cohen Edward; Dackowski William
; Stenflo John; Lundwall Ake; Dahlback Bjorn
; TITLE OF INVENTION: VECTOR CONTAINING DNA ENCODING MATURE
; HUMAN PROTEIN S
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/890,401
; FILING DATE: 25-JUL-1986
; SEQ ID NO: 1:
; LENGTH: 675
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```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11266
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11266

Query Match      26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348

QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11267
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11267

Query Match      26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348

QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11267
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11267

Query Match      26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348
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QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11365
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11365

Query Match      26.1%; Score 339; DB 4; Length 657;
Best Local Similarity 37.3%; Pred. No. 3.2e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348

QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11365
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11365

Query Match      26.1%; Score 339; DB 4; Length 657;
Best Local Similarity 37.3%; Pred. No. 3.2e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348

QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11366
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11366

Query Match      26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348

QY      46 DLMGNFFCLCKAGW---GRLCDKDVNECSQENG-CLQICHNKPGSFHCSCHSGFELS 100
DB      349 NSPGSFRCECKTGYFDGISRMC-VDVNECQRYPRGLCGHKCENTLGSYLSCSVGFRLS 407

QY      101 SDGRTCCDIDECADSEACGEARCKNLPGSYSLCDEGFAYSSQE-KACRDVDECLQGR-- 157
DB      408 VDGSRCEDEINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVGVTCEDIDECALPTGG 465

QY      158 --CEQVCVNSPGSYTCHDGRGGLKLSQMDTCDILPCV 195
DB      466 HICSYRCINIPGSFQSCPS-SGYRLAPNGRNCQDIDECV 504

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11366
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11366

Query Match      26.1%; Score 339; DB 4; Length 575;
Best Local Similarity 37.3%; Pred. No. 2.8e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY      6 CINKYSPYTKNSGFATCVQNL-----DOCTP--NPCDRKGTQACQ 45
DB      299 CINTGSS-----YTCQKNVPNCGRGYHLNBEGRTRCVDVDECAPPAEPCG-KG-HRCV 348
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[illegible]

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; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11369

Query Match      26.1%; Score 339; DB 4; Length 677;
Best Local Similarity 37.3%; Pred. No. 3.3e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKGSPYTKNSGFATCVONLP-----DOCTP--NPCDRKGTQACQ 45
Db 299 CINTGSG-----YTCQKNVPCGRGYHLNEEGTRCVDVDECAPPAPCG-KG-HRCV 348
QY 46 DLMGNFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPGSFHCSHSGFELS 100
Db 349 NSPGSFRCCKTYGYFDGIRMC--VDVNECQRYPGRLCGHKCENTLGSYLCSGVGFRLS 407
QY 101 SDGRTCODIDECADSEACGEARCKNLPSSYCLCDEGFAYSSOE--KACRDVDECLQGR-- 157
Db 408 VDRSCEDINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVDGVTCTEDIDECALPTGG 465
QY 158 --CEQVCVNSPGSYTHCDGRGGLKLSQDMTDCEDILPCV 195
Db 466 HICSYRCINIPGSPFCSCPS--SGYRLAPNGRNCQIDECV 504

Query Match      26.1%; Score 339; DB 4; Length 677;
Best Local Similarity 37.3%; Pred. No. 3.3e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKGSPYTKNSGFATCVONLP-----DOCTP--NPCDRKGTQACQ 45
Db 299 CINTGSG-----YTCQKNVPCGRGYHLNEEGTRCVDVDECAPPAPCG-KG-HRCV 348
QY 46 DLMGNFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPGSFHCSHSGFELS 100
Db 349 NSPGSFRCCKTYGYFDGIRMC--VDVNECQRYPGRLCGHKCENTLGSYLCSGVGFRLS 407
QY 101 SDGRTCODIDECADSEACGEARCKNLPSSYCLCDEGFAYSSOE--KACRDVDECLQGR-- 157
Db 408 VDRSCEDINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVDGVTCTEDIDECALPTGG 465
QY 158 --CEQVCVNSPGSYTHCDGRGGLKLSQDMTDCEDILPCV 195
Db 466 HICSYRCINIPGSPFCSCPS--SGYRLAPNGRNCQIDECV 504

Search completed: July 7, 2005, 09:41:26
Job time : 126.836 secs
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; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11370

Query Match      26.1%; Score 339; DB 4; Length 677;
Best Local Similarity 37.3%; Pred. No. 3.3e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKGSPYTKNSGFATCVONLP-----DOCTP--NPCDRKGTQACQ 45
Db 299 CINTGSG-----YTCQKNVPCGRGYHLNEEGTRCVDVDECAPPAPCG-KG-HRCV 348
QY 46 DLMGNFCLCKAGWG-----GRLCDKDVNECSQENG-CLQICHNKPGSFHCSHSGFELS 100
Db 349 NSPGSFRCCKTYGYFDGIRMC--VDVNECQRYPGRLCGHKCENTLGSYLCSGVGFRLS 407
QY 101 SDGRTCODIDECADSEACGEARCKNLPSSYCLCDEGFAYSSOE--KACRDVDECLQGR-- 157
Db 408 VDRSCEDINECSSSPCSQE--CANVYGSYQCYCRRGYQLSDVDGVTCTEDIDECALPTGG 465
QY 158 --CEQVCVNSPGSYTHCDGRGGLKLSQDMTDCEDILPCV 195
Db 466 HICSYRCINIPGSPFCSCPS--SGYRLAPNGRNCQIDECV 504

Query Match      26.1%; Score 339; DB 4; Length 677;
Best Local Similarity 37.3%; Pred. No. 3.3e-21;
Matches 82; Conservative 23; Mismatches 71; Indels 44; Gaps 12;

QY 6 CINKGSPYTKNSGFATCVONLP-----DOCTP--NPCDRKGTQACQ 45
Db 299 CINTGSG-----YTCQKNVPCGRGYHLNEEGTRCVDVDECAPPAPCG-KG-HRCV 348
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Search completed: July 7, 2005, 09:41:26
Job time : 126.836 secs
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RESULT 50

US-09-949-016-11371

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:31:46 ; Search time 394.132 Seconds
(without alignments)
222.507 Million cell updates/sec

Title: US-10-671-019-16

Perfect score: 1297

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-1

Query Match      100.0%; Score 1297; DB 16; Length 686;
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Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 270 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 316

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; Publication No. US20030100497A1
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3233P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657

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; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3233P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657

US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3233P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYLDCKINKYSPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQENGGLQICHNKPFSFHCSCHSFGFELSSDGRTCQDIDECADSEACGE 206
QY 121 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
Db 207 ARCKNLPGSYSCLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 227
Db 267 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFSGTPVIRLRFKRLQ 313

RESULT 5
US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3233P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
```

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; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-084-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECMKYGRPEENKPNDFAKCVQNLDPQCTPNPCDKKGTHICQDLGMGNFFCVCTDGGW 146
QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFGSCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCGQVCHNKPFGSQACCHSGFSLASDGTQCDIDECTSDTCGD 206
QY 121 ARCKNLPGSYSLCLDEGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGGLK 180
Db 207 ARCKNLPGSYSLCLDEGYTSSKEKTCQDVDECCQDRCQTCVNSPGSYTCHCDGRGGGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFGTGVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFVSMAKSVKSLYLGRMFGTGVIRLRFKRLQP 313

RESULT 6
US-10-223-088-48
; Sequence 48, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
```

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; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-088-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRLDCINKYGSPTKNSGFATCVQNLDPQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECMKYGRPEENKPNDFAKCVQNLDPQCTPNPCDKKGTHICQDLGMGNFFCVCTDGGW 146
QY 61 GRLCDKDVNECSQENGCGCLQICHNKPFGSCHSGFELSSDGRTCQDIDECADSEACGE 120
Db 147 GRLCDKDVNECVQKNGGCGQVCHNKPFGSQACCHSGFSLASDGTQCDIDECTSDTCGD 206
QY 121 ARCKNLPGSYSLCLDEGFAYSSOEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGGLK 180
Db 207 ARCKNLPGSYSLCLDEGYTSSKEKTCQDVDECCQDRCQTCVNSPGSYTCHCDGRGGGLK 266
QY 181 LSQDMTDCEDILPCVPFVSVAKSVKSLYLGRMFGTGVIRLRFKRLQP 227
Db 267 LSPDMTDCEDILPCVPFVSMAKSVKSLYLGRMFGTGVIRLRFKRLQP 313

RESULT 7
US-10-223-090-48
; Sequence 48, Application US/10223090
; Publication No. US20030105013A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C2
; CURRENT APPLICATION NUMBER: US/10/223,090
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
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; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-089-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 1 PRYLDICNKYSGPYTKNSGFATCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 PRYQECMRKYGRPEKNPFAKCVQNLDPDOCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 146
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 GRLCDKDVNECSQENGCLQICHNKPGSFHCSHGSELSGRTQODIDECADSEACGE 120
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 147 GRLCDKDVNECVKNGGCSQVCHNKPGSFQACHSGFSLASDGTQCDIDECTSDTCGD 206
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 121 ARCKNLPGSYSLCDEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGLK 180
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 207 ARCKNLPGSYSLCDEGYTSSKEKTCQDVDECOQDRCEQTCVNSPGSYTCHCDGRGLK 266
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 181 LSPDMTDCEDILPCVPFSPVAKSVKSLYLGRMFGTGPVIRLRFKRLQP 227
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 LSPDMTDCEDILPCVPFSPMAKSVKSLYLGRMFGTGPVIRLRFKRLQP 313
   ||| :|: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-223-081-48
; Sequence 48, Application US/10223081
; Publication No. US20030186866A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P2235P1C7
; CURRENT APPLICATION NUMBER: US/10/223,081
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383

US-10-223-082-48
; Sequence 48, Application US/10223082
; Publication No. US20030191059A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C3
; CURRENT APPLICATION NUMBER: US/10/223,082
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
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; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-223-082-48

Query Match      85.8%; Score 1113; DB 14; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWRKYGRPEEKNDPFAKCVQNLPDQCTPNPCDKKGTHICQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFHCSHGFEISSDRTQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQVQNGGCSQVCHNKPGSFQACCHSGFSLASDGTQCDIDECTSDTCGD 206

QY 121 ARCKNLPGSYSLCDGEGFAYSSQEKACRDVDECLQRCQVQVNSPGSYTCHCDGRGGLK 180
Db 207 ARCKNLPGSYSLCDGEGYTSSEKTKCQDVDECOQRCQVQVNSPGSYTCHCDGRGGLK 266

QY 181 LSQDMTDCEDILPCVPFSSVAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 227
Db 267 LSPDMTDCEDILPCVPFSSMAKSVKSLYLGRMFSGTVPVIRLRFKRLQ 313

RESULT 13
US-10-305-654-48
; Sequence 48, Application US/10305654
; Publication No. US20030224984A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hans-Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Paoni, N. F.
; APPLICANT: Stephan, J-P. F.
; APPLICANT: Watanabe, C.K.
; APPLICANT: Wood, W.I.
; APPLICANT: Williams, P.M.
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235R1C1
; CURRENT APPLICATION NUMBER: US/10/305,654
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
; US-10-305-654-48

Query Match      85.8%; Score 1113; DB 15; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKNKYSGPYTKNSGFATCVQNLPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
Db 87 PRYQECWRKYGRPEEKNDPFAKCVQNLPDQCTPNPCDKKGTHICQDLGMGNFFCVCTDGGW 146

QY 61 GRLCDKDVNECSQENGGLQICHNKPGSFHCSHGFEISSDRTQDIDECADSEACGE 120
Db 147 GRLCDKDVNECSQVQNGGCSQVCHNKPGSFQACCHSGFSLASDGTQCDIDECTSDTCGD 206

; US-10-081-056-48
; Sequence 48, Application US/10081056
; Publication No. US20040043927A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scott A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235P1C1
; CURRENT APPLICATION NUMBER: US/10/081,056
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/230,978
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
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; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-081-056-48

Query Match 85.8%; Score 1113; DB 15; Length 673;
Best Local Similarity 82.8%; Pred. No. 4.9e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKYKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 87 PRYQECMRKYGRPEEKNPDPFAKCVQNLDPDQCTPNPCDKKGTHICQDLGMGNFFCVCTDGMG 146
QY 61 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGTQCDIDECADSEACGE 120
DB 147 GRLCDKDVNECVQNGGCSQVCHNKPFSQACCHSGFSLASDGTQCDIDECTSDTCGD 206
QY 121 ARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSNPGSYTCHCDGRGGLK 180
DB 207 ARCKNLPGSYSLCDEGGYTSSEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 266
QY 181 LSQDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSGTPIRLRFRKRLQ 227
DB 267 LSPDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSGTPIRLRFRKRLQ 313

RESULT 15
US-10-367-094-31
; Sequence 31, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(697)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-367-094-31

Query Match 85.8%; Score 1113; DB 16; Length 697;
Best Local Similarity 82.8%; Pred. No. 5.1e-84;
Matches 188; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 PRYLDCKYKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFFCLCKAGWG 60
DB 120 PRYQECMRKYGRPEEKNPDPFAKCVQNLDPDQCTPNPCDKKGTHICQDLGMGNFFCVCTDGMG 179
QY 61 GRLCDKDVNECSQENGGLQICHNKPFSCHSGFELSSDGTQCDIDECADSEACGE 120
DB 180 GRLCDKDVNECVQNGGCSQVCHNKPFSQACCHSGFSLASDGTQCDIDECTSDTCGD 239
QY 121 ARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSNPGSYTCHCDGRGGLK 180
DB 240 ARCKNLPGSYSLCDEGGYTSSEKTCQDVDECCQDRCEQTCVNSPGSYTCHCDGRGGLK 299
QY 181 LSQDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSGTPIRLRFRKRLQ 227
DB 300 LSPDMTCEIDILPCVPFSSVAKSVKSLYLGRMFGSGTPIRLRFRKRLQ 346

RESULT 16
US-10-723-860-467
; Sequence 467, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 467
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-467

Query Match 46.4%; Score 601.5; DB 16; Length 650;
Best Local Similarity 43.4%; Pred. No. 1.4e-41;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;

QY 1 PRYLDCKYKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFF 52
DB 57 PRYLDCKYKSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTQACQDLGMGNFF 116
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSCHSGFELSSDGTQCDID 109
DB 117 CTCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSCHSGFELSSDGTQCDID 176
QY 110 DECA-DSEACGAEARCKNLPGSYSLCDEGFAYSSOEKACRDVDECLQRCCEQVCSNPGS 168

Db 177 DECSLKPSICGTAVCCKNIIPGDFECECEPEGYRNLKSKSCEDIDECSENCAQLCVNYPGG 236
QY 169 YTHCDGRCGLKLSQDMDCEDILPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 237 YTCYDGRKGFKAQDQKSECVSVVCLPLNLDTKYELLYLAEPQFAGV-VLYLKFR 290

RESULT 17
US-10-952-459-30
; Sequence 30, Application US/10952459
; Publication No. US20050074805A1
; GENERAL INFORMATION:
; APPLICANT: Kochan, Jarema Peter
; APPLICANT: Martin, Mitchell Lee
; APPLICANT: Rosinski, James Andrew
; TITLE OF INVENTION: Specific Markers for Diabetes
; FILE REFERENCE: 21270US1
; CURRENT APPLICATION NUMBER: US/10/952,459
; CURRENT FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-952-459-30

Query Match 46.4%; Score 601.5; DB 17; Length 676;
Best Local Similarity 43.4%; Pred. No. 1.4e-41;
Matches 102; Conservative 45; Mismatches 75; Indels 13; Gaps 5;
QY 1 PLYLDCINKY-----GSPYTKNS--GFATCVQNLDPDQCTPNPCDRKGTFQACDLMGNFF 52
Db 83 PXYLCLRSFQGLFTAAQSTNAYPDLRSCVNAIPDQCSPLPCNEDGYMCKDGKASFT 142
QY 53 CLCKAGWGRLCDKDVNEC---SQENGGLQICHNKPFSFHGSCSHGSELSDGRTGRTCODI 109
Db 143 CTCCKPQWQKECFDINECKDPNSINGGCSQICDNTPGSYHSCCKNGFWMLSNKKDKDV 202
QY 110 DSCA-DSEACGARKCNLPKGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGS 168
Db 203 DECSLKPSICGTAVCCKNIIPGDFECECEPEGYRNLKSKSCEDIDECSENCAQLCVNYPGG 262
QY 169 YTHCDGRCGLKLSQDMDCEDILPCVPFSAVSKSLYLGRMFSGTPVIRLRFK 223
Db 263 YTCYDGRKGFKAQDQKSECVSVVCLPLNLDTKYELLYLAEPQFAGV-VLYLKFR 316

RESULT 18
US-10-367-094-34
; Sequence 34, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-34

Query Match 27.8%; Score 361; DB 16; Length 510;
Best Local Similarity 35.7%; Pred. No. 9.7e-22;
Matches 81; Conservative 0; Mismatches 0; Indels 146; Gaps 1;
QY 1 PLYLDCINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTFQACDLMGNFFCLCKAGWG 60

Db 74 PXYLDCINKYSPYTKNSGFATCVQNLDPDQCTPNPCDRKGTFQA----- 116
QY 61 GRLCDKDVNECSQENGGLQICHNKPFSFHGSCSHGSELSDGRTGRTCODIDECADSEACGE 120
Db 117 ----- 116
QY 121 ARCKNLPGSYCLCDEGFAYSSQEKACRDVDECLQGRCEQVCVNSPGSYTCHCDGRGLK 180
Db 117 ----- 116
QY 181 LSQDMDCEDILPCVPFSAVSKSLYLGRMFSGTPVIRLRFKRLQP 227
Db 117 -----DILPCVPFSAVSKSLYLGRMFSGTPVIRLRFKRLQP 154

RESULT 19
US-09-855-824-4
; Sequence 4, Application US/09855824
; Publication No. US20030166048A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001233
; CURRENT APPLICATION NUMBER: US/09/855,824
; CURRENT FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-824-4

Query Match 27.6%; Score 357.5; DB 10; Length 911;
Best Local Similarity 38.6%; Pred. No. 3.4e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
QY 14 YTKNSGFATCVQNLDPDQCTPN--PCDRKGTOACODLMGNFFCLCKAGW----GGRLCDKD 67
Db 232 YALHADGRTCTET-----CAVNVGGCDR---TCKDXTATGVRCSCPVGFLOPDGKTC-KD 282
QY 68 VNECSQENGGLQICHNKPFSFHGSCSHGSELSDGRTGRTCODIDECADSEACGEARCKNLP 127
Db 283 INECLMNVGGCDHFCRNTVSGFEGCCQXGKHLTDERTCQDIDECSPERTCDHI-CINSP 341
QY 128 GSYGCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGGGLKLSQD 184
Db 342 GSFQCLCRRGYTLYGTH--CGDVDECSMNNGSCGQGVNTRGSEYECVCP--PGRRLHWN 397
QY 185 MDCEDILPCVPFSAVSKSLYLGRM 211
Db 398 QKDCVMNGLCLSRKASQAQALSCGKV 424

RESULT 20
US-10-476-542-4
; Sequence 4, Application US/10476542
; Publication No. US20040242473A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL001233-US
; CURRENT APPLICATION NUMBER: US/10/476,542
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/US02/22278
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/855,824
; PRIOR FILING DATE: 2001-05-16

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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 911
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-476-542-4

Query Match      27.6%; Score 357.5; DB 16; Length 911;
Best Local Similarity 38.6%; Pred. No. 3.4e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLGMGNFFCLCKAGW-----GGRLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR-----TCKDTATGVRCSCPVGFLLQPDGKTC-KD 282
QY 68 VNECSQENGGCLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNGGCDHFCRNTVSGFECGCKGHKLLTDERTCQDIDECSPERTCDHI-CINSP 341
QY 128 GYSVCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGLKLSQD 184
Db 342 GSFQCLCRGGTYLGTTH--CGDVDECSMNGSCQGCNVTRGSEYCVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSLYLGRM 211
Db 398 QKDCVEMNGCLSRKASQAQALSCGKV 424

RESULT 21
US-09-930-512-67
; Sequence 67, Application US/09930512
; Publication No. US20040010118A1
; GENERAL INFORMATION:
; APPLICANT: Zethusen, Bryan D
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly
; APPLICANT: Spaderna, Steven
; APPLICANT: Gangolli, Baha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Burgess, Catherine E
; APPLICANT: Majumder, Kumud
; APPLICANT: Shimkets, Richard
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine
; APPLICANT: Szekeres, Edward S
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Liu, Xiaohong
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Ellerman, Karen
; APPLICANT: Smithson, Glennda
; APPLICANT: Peyman, John
; APPLICANT: Stone, David
; APPLICANT: Macdougall, John
; TITLE OF INVENTION: No. US20040010118A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-091
; CURRENT APPLICATION NUMBER: US/09/930,512
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/225,692
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/225,837
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/225,693
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/226,236
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/226,353
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/227,085
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/227,395
; PRIOR FILING DATE: 2000-08-23
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; PRIOR APPLICATION NUMBER: 60/227,492
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/227,600
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/275,952
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-930-512-67

Query Match      27.6%; Score 357.5; DB 11; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLGMGNFFCLCKAGW-----GGRLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR-----TCKDTATGVRCSCPVGFLLQPDGKTC-KD 282
QY 68 VNECSQENGGCLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNGGCDHFCRNTVSGFECGCKGHKLLTDERTCQDIDECSPERTCDHI-CINSP 341
QY 128 GYSVCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHCDGRGLKLSQD 184
Db 342 GSFQCLCRGGTYLGTTH--CGDVDECSMNGSCQGCNVTRGSEYCVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSLYLGRM 211
Db 398 QKDCVEMNGCLSRKASQAQALSCGKV 424

RESULT 22
US-10-406-073-13
; Sequence 13, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; FILE REFERENCE: MPI02-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-406-073-13

Query Match      27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLGMGNFFCLCKAGW-----GGRLCDKD 67
Db 232 YALHADGRTCIET-----CAVNNGGCDR-----TCKDTATGVRCSCPVGFLLQPDGKTC-KD 282
QY 68 VNECSQENGGCLQICHNKPFSCHSGFELSSDGRTCQDIDECADSEACGEARCKNLP 127
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Db 283 INECLMNGGCDHFCRNTVSGSFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY 128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

RESULT 23
US-10-231-913-88
; Sequence 88, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Boldog, Ference L.
; APPLICANT: Colman, Steven D.
; APPLICANT: Eissen, Andrew J.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-231-913-88

Query Match 27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
QY 14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTQACQDLMGNFFCLCKAGW----GGRLCDKD 67

Db 232 YALHADGRTCTIET-----CAVNNGGCDR-----TCXDTATGVRCSVPVGTLPDQDKTC-KD 282
QY 68 VNECSQENGGLQICHNKPFGSFHCSHGFLSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNGGCDHFCRNTVSGSFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY 128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424

RESULT 24
US-10-029-020-35
; Sequence 35, Application US/10029020
; Publication No. US2004003971A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 961
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-020-35

Query Match 27.6%; Score 357.5; DB 15; Length 961;
Best Local Similarity 38.6%; Pred. No. 3.6e-21;
Matches 80; Conservative 23; Mismatches 81; Indels 23; Gaps 10;
QY 14 YTKNSGFATCVQNLPDQCTPN--PCDRKGTQACQDLMGNFFCLCKAGW----GGRLCDKD 67
Db 232 YALHADGRTCTIET-----CAVNNGGCDR-----TCXDTATGVRCSVPVGTLPDQDKTC-KD 282
QY 68 VNECSQENGGLQICHNKPFGSFHCSHGFLSSDGRTCQDIDECADSEACGEARCKNLP 127
Db 283 INECLMNGGCDHFCRNTVSGSFECGCGKHLLTDERTCQDIDECSEFERTCDHI-CINSP 341
QY 128 GSYSCLCDEGFA-YSSQEKACRDVDECL--QGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
Db 342 GSFQCLCRRGVTLTGTH--CGDVDECSMNNGSCGQCVNTRGSEYECVCP--PGRRLHWN 397
QY 185 MDTCEDILPCVPFVSVAKSVKSLYLGRM 211
Db 398 QKDCVEMNGCLSRSKASQAQLSCGKV 424
RESULT 25


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US-10-016-248-77
; Sequence 77, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 1587
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-77

Query Match      27.3%; Score 354.5; DB 15; Length 1587;
Best Local Similarity 43.3%; Pred. No. 1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy      29  DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db      636  DECTQSPGLCGG--CKNLPGSFRCVCPAGFRGSACEDVDECAQEPFPCGPGRCNT 692

Qy      86  PGSFHCSHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db      693  AGSFHCACPAGFRSRGPGACQDVDECARSPPCTYGRCENTEGSFQCVCPMGFQNTAG 752

Qy      145  KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db      753  SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 810

RESULT 26
US-10-016-248-78
; Sequence 78, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-78

Query Match      27.3%; Score 353.5; DB 15; Length 888;
Best Local Similarity 43.3%; Pred. No. 7.1e-21;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy      29  DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db      470  DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDECAQEPFPCGPGRCNT 526

Qy      86  PGSFHCSHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db      527  AGSFHCACPAGFRSRGPGACQDVDECARSPPCTYGRCENTEGSFQCVCPMGFQNTAG 586

Qy      145  KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db      587  SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 644

US-10-016-248-75
; Sequence 75, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-75

Query Match      27.3%; Score 353.5; DB 15; Length 888;
Best Local Similarity 43.3%; Pred. No. 7.1e-21;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

Qy      29  DOCTNP--CDRKGTOACODLMGNFCLCKAGWGRLCDKDVNECSQENGCC-LQICHNK 85
Db      470  DECTQSPGLC---GRGACKNLPGSFRCVCPAGFRGSACEDVDECAQEPFPCGPGRCNT 526

Qy      86  PGSFHCSHSGFELSSDGRTCQDIDECADS--EACGEARCKNLPGSYSCLCDEGFAYSSQE 144
Db      527  AGSFHCACPAGFRSRGPGACQDVDECARSPPCTYGRCENTEGSFQCVCPMGFQNTAG 586

Qy      145  KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCED-ILPCVP 196
Db      587  SECEDVDECEHNLACPGQECVNSPGSFQCRCTCPSGHHLHGRCTDVEDCSSGAPPCGP 644
```

RESULT 28
US-09-855-824-6
; Sequence 6, Application US/09855824
; Publication No. US20030166048A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: CL001233
; CURRENT APPLICATION NUMBER: US/09/855,824
; CURRENT FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-824-6

Query Match 27.3%; Score 353.5; DB 10; Length 957;
Best Local Similarity 34.9%; Pred. No. 7.6e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDQCTPN--PCDRKGTOA 43
Db 199 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 254

QY 44 CQDLGNFFCLCKAGW-----GRLCDKDVNECSQENGGLQICHNKPFSFHCSCSHGPFEL 99
Db 255 CKDTSTGVHCSCTPTGTLQVDGKTC-KDIDECQTRNGGCHNPFCKNTVGSFDCSCCKGFKL 313

QY 100 SSDGRTCDIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 314 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 370

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 371 GCQQVCINTVGSYECQC--HPGFKLHWNNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 425

RESULT 29
US-10-476-542-6
; Sequence 6, Application US/10476542
; Publication No. US20040242473A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: CL001233-US
; CURRENT APPLICATION NUMBER: US/10/476,542
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: PCT/US02/22278
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 09/855,824
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 957
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-476-542-6

Query Match 27.3%; Score 353.5; DB 16; Length 957;
Best Local Similarity 34.9%; Pred. No. 7.6e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDQCTPN--PCDRKGTOA 43
Db 199 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 254

QY 44 CQDLGNFFCLCKAGW-----GRLCDKDVNECSQENGGLQICHNKPFSFHCSCSHGPFEL 99
Db 255 CKDTSTGVHCSCTPTGTLQVDGKTC-KDIDECQTRNGGCHNPFCKNTVGSFDCSCCKGFKL 313

QY 100 SSDGRTCDIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 314 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 370

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 371 GCQQVCINTVGSYECQC--HPGFKLHWNNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 425

RESULT 30
US-09-747-371-3
; Sequence 3, Application US/09747371
; Patent No. US20020006616A1
; GENERAL INFORMATION:
; APPLICANT: Mack, Kurt
; APPLICANT: Gish, Kurt
; TITLE OF INVENTION: No. US20020006616A1el Methods of Diagnosing Breast Cancer, Compos
; TITLE OF INVENTION: Screening for Breast Cancer Modulators
; FILE REFERENCE: A-69028/DUB/JJD
; CURRENT APPLICATION NUMBER: US/09/747,371
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/ US/00/06952
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-747-371-3

Query Match 27.3%; Score 353.5; DB 9; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYGSPTKNSGFATCVQN-----LPDOCTPN--PCDRKGTOA 43
Db 239 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRRLLMETCAVNNGGCDR---T 294

QY 44 CQDLGNFFCLCKAGW-----GRLCDKDVNECSQENGGLQICHNKPFSFHCSCSHGPFEL 99
Db 295 CKDTSTGVHCSCTPTGTLQVDGKTC-KDIDECQTRNGGCHNPFCKNTVGSFDCSCCKGFKL 353

QY 100 SSDGRTCDIDECADSEACGEARCKNLPGSYCLCDEGFA-YSSQEKACRDVDECL--QG 156
Db 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGTYLSFTH--CGDTNECSVNNG 410

QY 157 RCEQVCVNSPGSYTCHCDGRGGLKLSQDMDCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 411 GCQQVCINTVGSYECQC--HPGFKLHWNNKDCVEVKVGFPTSMTPRV-SLHCCKSGGG 465

RESULT 31
US-09-930-512-66
; Sequence 66, Application US/09930512
; Publication No. US20040010118A1
; GENERAL INFORMATION:
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Spytek, Kimberly
; APPLICANT: Spaderna, Steven
; APPLICANT: Gangolli, Esha A
; APPLICANT: Rastelli, Luca
; APPLICANT: Burgess, Catherine E
; APPLICANT: Majumder, Kumud
; APPLICANT: Shinkets, Richard
; APPLICANT: Mishra, Vishnu
; APPLICANT: Vernet, Corine
; APPLICANT: Szekeres, Edward S

APPLICANT: Grosse, William M
APPLICANT: Alsbrook II, John P
APPLICANT: Liu, Xiaohong
APPLICANT: Gerlach, Valerie L
APPLICANT: Ellerman, Karen
APPLICANT: Smithson, Glenda
APPLICANT: Peyman, John
APPLICANT: Stone, David
APPLICANT: MacDougall, John
TITLE OF INVENTION: No. US20040010118a1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-091
CURRENT APPLICATION NUMBER: US/09/930,512
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,692
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/225,837
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/225,693
PRIOR FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: 60/226,236
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/226,353
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 60/227,085
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/227,395
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 60/227,492
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/227,600
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: 60/275,952
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 997
TYPE: PRT
ORGANISM: Mus musculus
US-09-930-512-66

Query Match 27.3%; Score 353.5; DB 11; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;
QY 1 PRY-----LDCINKYSPYTKNSGFATCVQN-----LPDQCTPN--PCDRKGTQA 43
Db 239 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRLMETCAVNGGCDR---T 294
QY 44 CQDLGNFFCLCKAGW----GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFEL 99
Db 295 CKDTSTGVHSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKCNKTVGSPDCSKKGFKL 353
QY 100 SSDGRTCDIDECADSEACEARCKNLPGSYSLCDEGFA-YSSQEKACRDVDECL--OG 156
Db 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFIACNPGTYLFSFTH--CGDTNECSVNG 410
QY 157 RCEQVCVNSPGSYTCHDCGRGGLKLSQDMDTCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 411 GCQVCINTVGSVEQC--HPGFKLHNKKDCVEVGFPTSMTPRV-SLHCGKSGG 465

RESULT 32
US-10-231-913-90
Sequence 90, Application US/10231913
Publication No. US20040005576A1
GENERAL INFORMATION:
APPLICANT: Guo, Xiaojia S.
APPLICANT: Li, Li
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard A.
APPLICANT: Casman, Stacie J.
APPLICANT: Malyankar, Uriel M.

APPLICANT: Tchernev, Velizar T.
APPLICANT: Vernet, Corine A.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Alsbrook II, John P.
APPLICANT: Edinger, Schlomit
APPLICANT: Peyman, John A.
APPLICANT: Stone, David J.
APPLICANT: Ellerman, Karen
APPLICANT: Gangolli, Beha A.
APPLICANT: Boldog, Ference L.
APPLICANT: Colman, Steven D.
APPLICANT: Eisen, Andrew J.
APPLICANT: Liu, Xiaohong
APPLICANT: Padigaru, Muralidhara
APPLICANT: Spaderna, Steven K.
APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-216
CURRENT APPLICATION NUMBER: US/10/231,913
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: 60/251,660
PRIOR FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 60/255,029
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 60/260,326
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/263,800
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/269,942
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/286,183
PRIOR FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 60/313,627
PRIOR FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: 60/318,712
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
LENGTH: 997
TYPE: PRT
ORGANISM: Mus musculus
US-10-231-913-90
Query Match 27.3%; Score 353.5; DB 15; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;
QY 1 PRY-----LDCINKYSPYTKNSGFATCVQN-----LPDQCTPN--PCDRKGTQA 43
Db 239 PRYRLHADGRSCLEQEGTVLEGTESNATSVADGDKRVKRLMETCAVNGGCDR---T 294
QY 44 CQDLGNFFCLCKAGW----GRLCDKDVNECSQENGGLQICHNKPFSFCHSGFEL 99
Db 295 CKDTSTGVHSCPTGFTLQVDGKTC-KDIDECQTRNGGCHNFKCNKTVGSPDCSKKGFKL 353
QY 100 SSDGRTCDIDECADSEACEARCKNLPGSYSLCDEGFA-YSSQEKACRDVDECL--OG 156
Db 354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFIACNPGTYLFSFTH--CGDTNECSVNG 410
QY 157 RCEQVCVNSPGSYTCHDCGRGGLKLSQDMDTCEDILPCVPFVSVAKSVKSLYLGRMFSG 214
Db 411 GCQVCINTVGSVEQC--HPGFKLHNKKDCVEVGFPTSMTPRV-SLHCGKSGG 465

RESULT 33
US-10-029-020-37
Sequence 37, Application US/10029020
Publication No. US20040033971A1
GENERAL INFORMATION:
APPLICANT: Gangolli et al.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

```

; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-029-020-37

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Query Match 27.3%; Score 353.5; DB 15; Length 997;
Best Local Similarity 34.9%; Pred. No. 7.9e-21;
Matches 83; Conservative 31; Mismatches 89; Indels 35; Gaps 12;

QY 1 PRY-----LDCINKYSPYTKNSGFATCVQN-----LPDQTPN--PCDRKGTQA 43
||| : : : : : : : : : : : : : : : : : : : : : : : : :
239 PRYLRHADGRSCLEQEGTLEGTESNATSVADGDKVRKRLMETCAVNNGGCDR---T 294
||| : : : : : : : : : : : : : : : : : : : : : : : : :
44 CQDLMGNFCLCKAGW---GGRLCDKVNESQENGGLQICHNKPFGSCHSGFEL 99
: : : : : : : : : : : : : : : : : : : : : : : : :
295 CKDTSTGVHSCPTGTQLVDGKTC-KDIDECOTRNGGCNHFCKNTVGSFDCSKKGFKL 353
: : : : : : : : : : : : : : : : : : : : : : : : :
354 LTDEKSCQDVDECSLERTCDHS-CINHPGTFICACNPGVTLYSFTH--CGDTNECSVNNG 410
: : : : : : : : : : : : : : : : : : : : : : : : :
157 RCEQVNSPGSYTCHCDGRGGLKLSQDMDTCEDILPCVPFVSAKSVKSLYLGRMFSG 214
: : : : : : : : : : : : : : : : : : : : : : : : :
411 GCQQVCINTVGSYEQC--HPGFKLHWNKDCVKEVGFPPPTSMTPRV-SLHCCKSGGG 465
: : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 34
US-10-016-248-32
; Sequence 32, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 60/315,639
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-30

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; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-32

```

```

Query Match 27.3%; Score 353.5; DB 15; Length 1354;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

QY 29 DOCTPNP--CDRKGTOACQDLGMGNFFCLCKAGWGRLCDKVNESQENGGL-LOICHNK 85
||| : : : : : : : : : : : : : : : : : : : : : : : : :
560 DECTQSPGLC---GRGACKNLPFGSRFCVCPAGFRSACEEDVDECAQEPFPGPGRCNDT 616
||| : : : : : : : : : : : : : : : : : : : : : : : : :
86 PGSFHCSCHSGFELSSDGRTOIDECADS--EACGEARCKNLPGSYSLCDEGFAYSSQE 144
||| : : : : : : : : : : : : : : : : : : : : : : : : :
617 AGSFHCACPAGFRSRPGAPCQDVDECARSPPTCTYGRCENTEGSFQCVCPMGFQFNAAG 676
||| : : : : : : : : : : : : : : : : : : : : : : : : :
145 KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCE-ILPCVP 196
||| : : : : : : : : : : : : : : : : : : : : : : : : :
677 SECDVDECEHNLACPGQECVNSPGSFQCRACPSGHHLHGRCTDVEDCSSGAPPGP 734
||| : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 35
US-10-016-248-30
; Sequence 30, Application US/10016248
; Publication No. US20040033491A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-218
; CURRENT APPLICATION NUMBER: US/10/016,248
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/254,329
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/291,037
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/255,648
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: 60/297,173
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: 60/309,258
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/326,393
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/315,639
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-016-248-30

```

```

Query Match 27.3%; Score 353.5; DB 15; Length 1356;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 77; Conservative 22; Mismatches 66; Indels 13; Gaps 9;

QY 29 DOCTPNP--CDRKGTOACQDLGMGNFFCLCKAGWGRLCDKVNESQENGGL-LOICHNK 85
||| : : : : : : : : : : : : : : : : : : : : : : : : :
560 DECTQSPGLC---GRGACKNLPFGSRFCVCPAGFRSACEEDVDECAQEPFPGPGRCNDT 616
||| : : : : : : : : : : : : : : : : : : : : : : : : :
86 PGSFHCSCHSGFELSSDGRTOIDECADS--EACGEARCKNLPGSYSLCDEGFAYSSQE 144
||| : : : : : : : : : : : : : : : : : : : : : : : : :
617 AGSFHCACPAGFRSRPGAPCQDVDECARSPPTCTYGRCENTEGSFQCVCPMGFQFNAAG 676
||| : : : : : : : : : : : : : : : : : : : : : : : : :
145 KACRDVDECLQG-RCE-QVCVNSPGSYTCH-CDGRGGLKLSQ--DMDTCE-ILPCVP 196
||| : : : : : : : : : : : : : : : : : : : : : : : : :
677 SECDVDECEHNLACPGQECVNSPGSFQCRACPSGHHLHGRCTDVEDCSSGAPPGP 734
||| : : : : : : : : : : : : : : : : : : : : : : : : :

```


; TITLE OF INVENTION: PROTEINS IN VASCULAR ENDOTHELIUM
; FILE REFERENCE: MPI02-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FASTSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 764
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-17

Query Match 26.9%; Score 349; DB 15; Length 764;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67
DB 207 YAPHSDDRTCIET-----CAVNNGGCDR----TCKDTATGVRCSGCPVGFLLQPDGKTC-KD 257
QY 68 VNECSQNGGCLQICHNKPGECHSGFELSSDGRGTCODIDECADSEAGEARCKNLP 127
DB 258 INECLVNNGGCDHFCRNTVSGFCGCRKGYKLLTDBRTCODIDECSPERTCDHI-CINSP 316
QY 128 GSYSCLCDEGF-AYSSQEKACRDVDEC--LQGRCEQVCVNSPGSYTCHDCDGRGGLKLSQD 184
DB 317 GSFQCLCHRGYILYGTTH--CGDVDECSMSNGSCDQCQVNTKGSYECVCP--PGRRLHWN 372
QY 185 MOTCEDILPC-----VPSVAKSVKSLYL 208
DB 373 RKDCVETGKLSRAKTSAPRAQLSCSKAGGVESCF 407

RESULT 42
US-10-406-073-2
; Sequence 2, Application US/10406073
; Publication No. US20030219813A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Ruey-Bing
; APPLICANT: NG, Chi Kin Domingos
; APPLICANT: TOMLINSON, James E.
; APPLICANT: KOMUVES, Laszlo G.
; APPLICANT: TOPPER, James N.
; APPLICANT: ROBISON, Keith E.
; APPLICANT: Millennium Pharmaceuticals Inc.
; TITLE OF INVENTION: IDENTIFICATION OF A FAMILY OF SECRETED
; FILE REFERENCE: MPI02-048PIRNM
; CURRENT APPLICATION NUMBER: US/10/406,073
; CURRENT FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/369876
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 988
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-406-073-2

Query Match 26.9%; Score 349; DB 15; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67
DB 232 YAPHSDDRTCIET-----CAVNNGGCDR----TCKDTATGVRCSGCPVGFLLQPDGKTC-KD 282
QY 68 VNECSQNGGCLQICHNKPGECHSGFELSSDGRGTCODIDECADSEAGEARCKNLP 127

; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-216
; CURRENT APPLICATION NUMBER: US/10/231,913
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 60/251,660
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 60/255,029
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/260,326
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/263,800
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/269,942
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/286,183
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 60/313,627
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/318,712
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 988
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-231-913-18

Query Match 26.9%; Score 349; DB 15; Length 988;
Best Local Similarity 37.7%; Pred. No. 1.9e-20;
Matches 81; Conservative 22; Mismatches 78; Indels 34; Gaps 11;

QY 14 YTKNSGFATCVQNLDPDOCTPN--PCDRKGTQACQDLMGNFFCLCKAGW-----GGRLCDKD 67


```

; TITLE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-015-115-56

Query Match 26.9%; Score 348.5; DB 15; Length 3002;
Best Local Similarity 42.9%; Pred. No. 6.2e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLGNFFCLCKAGWG---RLCDKDVNECSOENGGLQICHNKPFSHCSCGPFELS 100
Db 1302 CYNLIGKYQCACNPGYHSTPDLFCVDIDECSIMNGGCTFTCTNSGSEYSCQPGFALM 1361

QY 101 SDGRTCODIDEACDS-EACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDE----- 152
Db 1362 PDQRSCDTIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNI 1421

QY 153 CLOGRCEQVCVNSPGSYTCHD---GRGGLKLSQDMDTCE 189
Db 1422 CLSGTCE---NTKGSFICHCDMGYSKKGKGTGCTDINECE 1458

RESULT 47
US-10-408-765A-195
; Sequence 195, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-195

Query Match 26.9%; Score 348.5; DB 16; Length 3002;
Best Local Similarity 42.9%; Pred. No. 6.2e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLGNFFCLCKAGWG---RLCDKDVNECSOENGGLQICHNKPFSHCSCGPFELS 100
Db 1302 CYNLIGKYQCACNPGYHSTPDLFCVDIDECSIMNGGCTFTCTNSGSEYSCQPGFALM 1361

QY 101 SDGRTCODIDEACDS-EACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDE----- 152
Db 1362 PDQRSCDTIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNI 1421

QY 153 CLOGRCEQVCVNSPGSYTCHD---GRGGLKLSQDMDTCE 189
Db 1422 CLSGTCE---NTKGSFICHCDMGYSKKGKGTGCTDINECE 1458

RESULT 48
US-10-723-860-499
; Sequence 499, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 499
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-499

Query Match 26.9%; Score 348.5; DB 16; Length 3002;
Best Local Similarity 42.9%; Pred. No. 6.2e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLGNFFCLCKAGWG---RLCDKDVNECSOENGGLQICHNKPFSHCSCGPFELS 100
Db 1302 CYNLIGKYQCACNPGYHSTPDLFCVDIDECSIMNGGCTFTCTNSGSEYSCQPGFALM 1361

QY 101 SDGRTCODIDEACDS-EACGEARCKNLPGSYSLCDEGFAYSSQEKACRDVDE----- 152
Db 1362 PDQRSCDTIDECEDNPNICDGGQCTNIPGEYRCLCYDGFMASEDMKTCVDVNECDLNPNI 1421

QY 153 CLOGRCEQVCVNSPGSYTCHD---GRGGLKLSQDMDTCE 189
Db 1422 CLSGTCE---NTKGSFICHCDMGYSKKGKGTGCTDINECE 1458

RESULT 49
US-10-478-451-10
; Sequence 10, Application US/10478451
; Publication No. US20040259172A1
; GENERAL INFORMATION:
; APPLICANT: Osteometer BioTech A/S
; APPLICANT: Christgau, Stephan
; TITLE OF INVENTION: ASSAY OF ISOMERISED AND/OR OPTICALLY INVERTED PROTEINS AND
; FILE REFERENCE: PJS/P8489WO
; CURRENT APPLICATION NUMBER: US/10/478,451
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: GB0112626.7
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-478-451-10
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; ORGANISM: Fibrillin-1 Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: A47221
; DATABASE ENTRY DATE: 2000-07-21
US-10-478-451-10

Query Match      26.9%; Score 348.5; DB 16; Length 3002;
Best Local Similarity 42.9%; Pred. No. 6.2e-20;
Matches 69; Conservative 18; Mismatches 55; Indels 19; Gaps 5;

QY 44 CQDLNMFCLCKAGWG---RLCDXDVNECSQENGGLQICHNKPQSFHCSCHSGFELS 100
Db 1302 CVNLIGKYQCACNPGYHSTPDRLCFVDVIDECSTIMNGGCTFCTNSGSEYECSCQPGFALM 1361
QY 101 SDGRTQDDIDEADS-EAGEARCKNLPGSYSLCDDEGFAYSSQEKACRDVDE----- 152
Db 1362 PDQRCTDIDECDNPNICGGQCTNIPGEYRCLCYDGFWASEDMKTCVDVNECDLNPN 1421
QY 153 CLQGRCEQVCVNSPGSYTCHCD---GRGGLKLSQDMDTCE 189
Db 1422 CLSGTCE---NTKGSFICHCDMGYSKKGKTGCTDINECE 1458

RESULT 50
US-10-239-663-57
; Sequence 57, Application US/10239663
; Publication No. US20030139572A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 57
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-663-57
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```
Query Match      26.8%; Score 348; DB 14; Length 387;
Best Local Similarity 41.1%; Pred. No. 8.8e-21;
Matches 74; Conservative 16; Mismatches 60; Indels 30; Gaps 9;

QY 24 VQNLPDQCTPN---PCDRKGTQACQDLNMGFFCLCKAGW-----GGRLCDXDVNECSQENG 77
Db 213 IMSAPETCAVNGGCDR---TCKDTATGVRCSCPVGFTLQPDGKTC-KDINECLVNNGG 267
QY 78 CLQICHNKPQSFHCSGFELSDDGRTQDDIDEADSEACGEARCKNLPGSYSLCDDEG 137
Db 268 CHFCRNTVGSFECGRKGKLLTDERTCQDDIDECSFERTCDHI-CINSPGFSQCLCHRG 326
QY 138 F-AYSSQEKACRDVDEEC--LQGRCEQVCVNSPGSYTC-----HCDGRGGLKL 181
Db 327 YILYGTTH--CGDVDECSMNSGCDQGCYVNTKGSYECVCPGPRRLHWNGKDCVGRGSLLL 384
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Search completed: July 7, 2005, 10:31:22
Job time : 407.132 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:49:00 ; Search time 25.7967 Seconds
(without alignments)
224.889 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYLGL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003s:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	518	ABO84421	Human can
2	72	100.0	624	ADQ67207	Novel hum
3	72	100.0	678	AAR99414	Human gas
4	72	100.0	678	AAR99414	Human gas
5	72	100.0	678	AAW46463	Human gro
6	72	100.0	678	AAW46463	Human gro
7	72	100.0	678	AAW46463	Human gro
8	72	100.0	678	AAW46463	Human gro
9	72	100.0	678	AAW46463	Human gro
10	72	100.0	678	AAW46463	Human gro
11	72	100.0	678	AAW46463	Human gro
12	69	95.8	673	ADW40823	Human gas
13	69	95.8	673	ADW40823	Human gas
14	69	95.8	673	ADW40823	Human gas
15	69	95.8	673	ADW40823	Human gas
16	69	95.8	673	ADW40823	Human gas
17	69	95.8	673	ADW40823	Human gas
18	69	95.8	673	ADW40823	Human gas
19	69	95.8	673	ADW40823	Human gas
20	69	95.8	673	ADW40823	Human gas
21	69	95.8	673	ADW40823	Human gas
22	69	95.8	673	ADW40823	Human gas
23	69	95.8	673	ADW40823	Human gas
24	69	95.8	673	ADW40823	Human gas
25	44	61.1	77	ADC94783	E. faeciu

26	44	61.1	374	4	AAU03812	Au03812 G protein
27	44	61.1	374	8	ADN23180	Adn23180 Bacterial
28	42	58.3	291	7	ADD31762	Add31762 Enterobac
29	42	58.3	1220	8	ADN07100	Adn07100 S. cerevi
30	42	58.3	1220	8	ADS43652	Ads43652 Bacterial
31	42	58.3	4345	4	ABB66417	Abb66417 Drosophil
32	41	56.9	364	6	ABM67414	Abm67414 Phototrab
33	41	56.9	527	8	ADO05107	Ado05107 Rift vall
34	41	56.9	1067	8	ADO05104	Ado05104 Rift vall
35	41	56.9	1173	8	ADS43524	Ads43524 Bacterial
36	41	56.9	1206	1	AAU03812	Au03812 G protein
37	41	56.9	1206	1	AAU03812	Au03812 G protein
38	41	56.9	1235	8	ADP98882	Adp98882 C. albica
39	41	56.9	3457	2	AAW84560	Aaw84560 Polyprote
40	41	56.9	3457	2	AAW84560	Aaw84560 Polyprote
41	40	55.6	174	4	ABG08969	Abg08969 Novel hum
42	40	55.6	394	4	ABG02533	Abg02533 Novel hum
43	40	55.6	969	5	ABP73632	Abp73632 Candida a
44	39	54.2	64	4	AM89790	Am89790 Human imm
45	39	54.2	369	3	AAU03812	Au03812 G protein
46	38	52.8	120	5	ABP04700	Abp04700 Human ORF
47	38	52.8	133	5	ABP62898	Abp62898 Human pol
48	38	52.8	307	8	ADS43968	Ads43968 Bacterial
49	38	52.8	349	6	ABR53899	AbR53899 Protein g
50	38	52.8	349	7	ADK64826	Adk64826 Disease c
51	38	52.8	374	3	AAU03812	Au03812 G protein
52	38	52.8	382	8	ADJ76321	Adj76321 Marker ge
53	38	52.8	393	3	AAU03812	Au03812 G protein
54	38	52.8	406	3	AAU03812	Au03812 G protein
55	37	51.4	62	4	AM28773	Am28773 Peptide #
56	37	51.4	62	4	AM28773	Am28773 Peptide #
57	37	51.4	62	4	AM28773	Am28773 Peptide #
58	37	51.4	225	3	AAU03812	Au03812 G protein
59	37	51.4	258	8	ADN18230	Adn18230 Bacterial
60	37	51.4	266	7	ABO61682	AbO61682 Klebsiell
61	37	51.4	307	5	ABP53034	Abp53034 Yeast RNA
62	37	51.4	307	8	ADN19329	Adn19329 Bacterial
63	37	51.4	316	7	ADC95392	Adc95392 E. faeciu
64	37	51.4	334	2	AAU03812	Au03812 G protein
65	37	51.4	334	2	AAU03812	Au03812 G protein
66	37	51.4	384	3	AAU03812	Au03812 G protein
67	37	51.4	433	5	ABP64887	Abp64887 Human pro
68	37	51.4	456	7	ADL46379	Adl46379 UDP-N-ace
69	37	51.4	461	3	AAU03812	Au03812 G protein
70	37	51.4	480	3	AAU03812	Au03812 G protein
71	37	51.4	506	8	ADS29909	Ads29909 Bacterial
72	37	51.4	512	5	ABU55533	Abu55533 Lactococc
73	37	51.4	529	5	ABU55533	Abu55533 Lactococc
74	37	51.4	771	4	ABM64331	Abm64331 Drosophil
75	37	51.4	812	5	ABG92717	Abg92717 Coccidiol
76	37	51.4	1702	2	AAU03812	Au03812 G protein
77	36.5	50.7	54	5	ABP00991	Abp00991 Human ORF
78	36.5	50.7	966	7	ADC83634	Adc83634 LTRPC3-re
79	36	50.0	12	2	AAU17975	Aay17975 Peptide S
80	36	50.0	74	7	ABO62312	AbO62312 Klebsiell
81	36	50.0	84	4	ABB15173	Abb15173 Human ner
82	36	50.0	207	6	ABU35512	Abu35512 Protein e
83	36	50.0	226	6	ABU35512	Abu35512 Protein e
84	36	50.0	297	4	ABU46976	Abu46976 A. aeolic
85	36	50.0	394	5	AAU16591	Aau16591 Pseudozym
86	36	50.0	400	6	ABM73084	Abm73084 Staphyloc
87	36	50.0	410	4	AAU35435	Aau35435 Haemophil
88	36	50.0	432	6	ABU26432	Abu26432 Protein e
89	36	50.0	515	4	ABG12419	Abg12419 Novel hum
90	36	50.0	529	6	ABU49551	Abu49551 Protein e
91	36	50.0	551	3	ABU19526	Abu19526 Arabidops
92	36	50.0	551	4	ABM82992	Abm82992 Arabidops
93	36	50.0	605	5	ABB47309	Abb47309 Listeria
94	36	50.0	608	4	AAU94640	Aau94640 Human pro
95	36	50.0	629	4	AAU02721	Aau02721 C-termina
96	36	50.0	641	5	ABU57280	Abu57280 Mouse lac
97	36	50.0	719	4	ABM8053	Abm8053 Drosophil
98	36	50.0	875	5	ABB09317	Abb09317 Human TIC

99	36	50.0	876	7	ADB37641	Neural th	172	35	48.6	421	6	ADA76252	Human PRO
100	36	50.0	876	7	ADB37636	Neural th	173	35	48.6	421	6	ADA18902	Human PRO
101	36	50.0	900	2	AAY30338	A multifu	174	35	48.6	421	6	ADA61525	Homo sapi
102	36	50.0	900	4	AAB20179	S. cerevi	175	35	48.6	421	6	ADB19310	Novel hum
103	36	50.0	900	4	AAB20178	S. cerevi	176	35	48.6	421	6	ADB27851	Human PRO
104	36	50.0	900	4	AAB20176	Saccharom	177	35	48.6	421	6	ADA86330	Novel hum
105	36	50.0	900	4	AAB20177	S. cerevi	178	35	48.6	421	6	ADA86330	Novel hum
106	36	50.0	900	8	ADS43839	Bacterial	179	35	48.6	421	6	ADB15894	Human PRO
107	36	50.0	930	7	ADN95169	Human BEC	180	35	48.6	421	6	ADA47680	Human PRO
108	36	50.0	931	5	ABO93119	Human tra	181	35	48.6	421	6	ADA67475	Human PRO
109	36	50.0	931	7	ADB37609	Neural th	182	35	48.6	421	6	ADB30482	Human PRO
110	36	50.0	931	8	ADH51626	Human 156	183	35	48.6	421	6	ADA85778	Novel hum
111	36	50.0	1086	8	ADN23310	Bacterial	184	35	48.6	421	6	ADA96990	Human PRO
112	36	50.0	1145	8	ADN73071	Thale cre	185	35	48.6	421	6	ADA79294	Human PRO
113	36	50.0	15281	2	AAR44929	T. niveum	186	35	48.6	421	6	ADA87433	Novel hum
114	35.5	49.3	116	3	AGS34529	Arabidops	187	35	48.6	421	6	ADB16635	Human PRO
115	35.5	49.3	119	5	ABP33627	Human ORF	188	35	48.6	421	6	ADA91727	Novel hum
116	35.5	49.3	239	3	AGS24805	Arabidops	189	35	48.6	421	6	ADB14790	Human PRO
117	35.5	49.3	239	3	AGS40407	Arabidops	190	35	48.6	421	6	ADB18751	Novel hum
118	35.5	49.3	267	8	ADS43476	Bacterial	191	35	48.6	421	6	ADA93966	Human PRO
119	35	48.6	50	8	ABO56052	Human gen	192	35	48.6	421	6	ADB19862	Novel hum
120	35	48.6	78	5	ABP11021	Human ORF	193	35	48.6	421	6	ADB13174	Human PRO
121	35	48.6	93	8	ADI57735	Human bre	194	35	48.6	421	6	ABO43299	Novel hum
122	35	48.6	209	4	ABG16149	Novel hum	195	35	48.6	421	6	ADA74428	Human PRO
123	35	48.6	217	3	AGS31815	Arabidops	196	35	48.6	421	6	ADA24661	Human PRO
124	35	48.6	223	3	AGS31814	Arabidops	197	35	48.6	421	6	ADA82185	Human PRO
125	35	48.6	279	7	ABO84175	Bacteriom	198	35	48.6	421	6	ADA75148	Human PRO
126	35	48.6	303	6	ADA33592	Acinetoba	199	35	48.6	421	6	ADA85226	Novel hum
127	35	48.6	332	7	ABO60744	Klebsiell	200	35	48.6	421	6	ADA84674	Novel hum
128	35	48.6	358	3	AGS31813	Arabidops	201	35	48.6	421	6	ADB29930	Human PRO
129	35	48.6	361	8	ABM84676	Human dia	202	35	48.6	421	6	ADA80458	Human PRO
130	35	48.6	361	8	ABM82804	Human dia	203	35	48.6	421	6	ADA75700	Human PRO
131	35	48.6	362	7	ADD49055	Human NOV	204	35	48.6	421	6	ADA46925	Human PRO
132	35	48.6	366	8	ADS30288	Bacterial	205	35	48.6	421	6	ADB25221	Human PRO
133	35	48.6	367	4	ABBS2488	Escherich	206	35	48.6	421	6	ADB26747	Human PRO
134	35	48.6	379	2	AAR64159	Human ela	207	35	48.6	421	6	ADB31034	Human PRO
135	35	48.6	379	2	AAR94367	Human ela	208	35	48.6	421	6	ADA60962	Homo sapi
136	35	48.6	379	7	ADD49057	Human NOV	209	35	48.6	421	6	ADB24109	Human PRO
137	35	48.6	379	7	ADJ69755	Human hea	210	35	48.6	421	6	ADA96438	Human PRO
138	35	48.6	379	8	ADG25245	Human leu	211	35	48.6	421	6	ADA81010	Human PRO
139	35	48.6	379	8	ADJ66663	Nipl prot	212	35	48.6	421	6	ADA95886	Human PRO
140	35	48.6	379	8	ADJ66641	Leukocyte	213	35	48.6	421	6	ADA8195	Human PRO
141	35	48.6	379	8	ADJ75603	Marker ge	214	35	48.6	421	6	ADB26195	Human PRO
142	35	48.6	379	8	ADN04567	Antipsori	215	35	48.6	421	6	ADB21680	Novel hum
143	35	48.6	379	8	ADQ30590	Pancreas	216	35	48.6	421	7	ADA77459	Human PRO
144	35	48.6	379	8	ADP24496	PRO poly	217	35	48.6	421	7	ADB18199	Human PRO
145	35	48.6	382	8	ADN25725	Bacterial	218	35	48.6	421	7	ADA86882	Novel hum
146	35	48.6	386	6	ADA36269	Acinetoba	219	35	48.6	421	7	ADA87985	Novel hum
147	35	48.6	391	1	AAP70479	Sequence	220	35	48.6	421	7	ADA46373	Novel hum
148	35	48.6	391	2	AAR25305	HRSV majo	221	35	48.6	421	7	ADB28403	Human PRO
149	35	48.6	391	2	AAR24184	Bovine RS	222	35	48.6	421	7	ADB28955	Human PRO
150	35	48.6	391	2	AAR50001	HRSV majo	223	35	48.6	421	7	ADA76907	Human PRO
151	35	48.6	391	5	ABG99060	N protein	224	35	48.6	421	7	ADA89537	Novel hum
152	35	48.6	391	8	ADJ97186	Human res	225	35	48.6	421	7	ADA97542	Human PRO
153	35	48.6	391	8	ADJ97186	Human res	226	35	48.6	421	7	ADB27299	Human PRO
154	35	48.6	396	8	ADN49106	Bovine re	227	35	48.6	421	7	ADB22232	Novel hum
155	35	48.6	397	2	AAR21328	Sequence	228	35	48.6	421	7	ADA66923	Human PRO
156	35	48.6	410	6	ABU40555	Protein e	229	35	48.6	421	7	ADB23557	Human PRO
157	35	48.6	413	7	ADP05967	Bacterial	230	35	48.6	421	7	ADB32579	Novel hum
158	35	48.6	421	2	AAY05767	Human ost	231	35	48.6	421	7	ADB15342	Human PRO
159	35	48.6	421	3	AAY88377	PRO216 (o	232	35	48.6	421	7	ADB38594	Novel hum
160	35	48.6	421	3	AAB33417	Human PRO	233	35	48.6	421	7	ADB38042	Novel hum
161	35	48.6	421	3	AAB24435	Human PRO	234	35	48.6	421	7	ADB66514	Novel hum
162	35	48.6	421	4	AAL12322	Human PRO	235	35	48.6	421	7	ADB89594	Human PRO
163	35	48.6	421	4	AAB20340	Human PRO	236	35	48.6	421	7	ADB90326	Human PRO
164	35	48.6	421	5	AAB081955	Human PRO	237	35	48.6	421	7	ADB39427	Novel hum
165	35	48.6	421	6	ABO17766	Novel hum	238	35	48.6	421	7	ADB47050	Novel hum
166	35	48.6	421	6	ABU81020	Human PRO	239	35	48.6	421	7	ADB86657	Human PRO
167	35	48.6	421	6	ABU66720	Human PRO	240	35	48.6	421	7	ADB77262	Novel hum
168	35	48.6	421	6	ABU59801	Novel sec	241	35	48.6	421	7	ADB34419	Human PRO
169	35	48.6	421	6	ABO24991	Human sec	242	35	48.6	421	7	ADB35523	Human PRO
170	35	48.6	421	6	ABU66996	Human sec	243	35	48.6	421	7	ADB33867	Human PRO
171	35	48.6	421	6	ADA45821	Novel hum	244	35	48.6	421	7	ADB34971	Human PRO

245	35	48.6	421	7	ADB36075	Human PRO	318	35	48.6	421	7	ADN16510	Novel hum
246	35	48.6	421	7	ADB46470	Novel hum	319	35	48.6	421	7	ADN15329	Novel hum
247	35	48.6	421	7	ADC50343	Novel hum	320	35	48.6	421	7	ADN14777	Novel hum
248	35	48.6	421	7	ADC71890	Novel hum	321	35	48.6	421	7	ADI64003	Novel hum
249	35	48.6	421	7	ADC59869	Novel hum	322	35	48.6	421	8	ADC81039	Novel hum
250	35	48.6	421	7	ADC52876	Novel hum	323	35	48.6	421	8	ADD76487	Human PRO
251	35	48.6	421	7	ADC57230	Novel hum	324	35	48.6	421	8	ADD87851	Human PRO
252	35	48.6	421	7	ADC60421	Novel hum	325	35	48.6	421	8	ADD86255	Human PRO
253	35	48.6	421	7	ADC50896	Novel hum	326	35	48.6	421	8	AD75703	Human PRO
254	35	48.6	421	7	ADC65423	Human PRO	327	35	48.6	421	8	AD75703	Human PRO
255	35	48.6	421	7	ADC54521	Novel hum	328	35	48.6	421	8	AD75703	Human PRO
256	35	48.6	421	7	ADC53482	Novel hum	329	35	48.6	421	8	AD75703	Human PRO
257	35	48.6	421	7	ADC59005	Novel hum	330	35	48.6	421	8	AD75703	Human PRO
258	35	48.6	421	7	ADC55883	Novel hum	331	35	48.6	421	8	AD75703	Human PRO
259	35	48.6	421	7	ADC58453	Novel hum	332	35	48.6	421	8	AD75703	Human PRO
260	35	48.6	421	7	ADC03127	Novel hum	333	35	48.6	421	8	AD75703	Human PRO
261	35	48.6	421	7	ADC90119	Novel hum	334	35	48.6	421	8	AD75703	Human PRO
262	35	48.6	421	7	ADC69538	Human PRO	335	35	48.6	421	8	AD75703	Human PRO
263	35	48.6	421	7	ADC48427	Human PRO	336	35	48.6	421	8	AD75703	Human PRO
264	35	48.6	421	7	ADC09956	Human PRO	337	35	48.6	421	8	AD75703	Human PRO
265	35	48.6	421	7	ADC04531	Novel hum	338	35	48.6	421	8	AD75703	Human PRO
266	35	48.6	421	7	ADC80487	Novel hum	339	35	48.6	421	8	AD75703	Human PRO
267	35	48.6	421	7	ADD10994	Human PRO	340	35	48.6	421	8	AD75703	Human PRO
268	35	48.6	421	7	ADC47875	Human PRO	341	35	48.6	421	8	AD75703	Human PRO
269	35	48.6	421	7	ADC79935	Novel hum	342	35	48.6	421	8	AD75703	Human PRO
270	35	48.6	421	7	ADC09404	Human PRO	343	35	48.6	421	8	AD75703	Human PRO
271	35	48.6	421	7	ADD41117	Novel hum	344	35	48.6	421	8	AD75703	Human PRO
272	35	48.6	421	7	ADD52256	Human PRO	345	35	48.6	421	8	AD75703	Human PRO
273	35	48.6	421	7	ADD52996	Human PRO	346	35	48.6	421	8	AD75703	Human PRO
274	35	48.6	421	7	ADD53548	Novel hum	347	35	48.6	421	8	AD75703	Human PRO
275	35	48.6	421	7	ADD51704	Human PRO	348	35	48.6	421	8	AD75703	Human PRO
276	35	48.6	421	7	ADD02503	Human PRO	349	35	48.6	421	8	AD75703	Human PRO
277	35	48.6	421	7	ADD01937	Human PRO	350	35	48.6	421	8	AD75703	Human PRO
278	35	48.6	421	7	ADD54119	Novel hum	351	35	48.6	421	8	AD75703	Human PRO
279	35	48.6	421	7	ADD92436	Human PRO	352	35	48.6	421	8	AD75703	Human PRO
280	35	48.6	421	7	ADD91332	Human PRO	353	35	48.6	421	8	AD75703	Human PRO
281	35	48.6	421	7	ADD03946	Human PRO	354	35	48.6	421	8	AD75703	Human PRO
282	35	48.6	421	7	ADD32243	Novel hum	355	35	48.6	421	8	AD75703	Human PRO
283	35	48.6	421	7	ADD22175	Human PRO	356	35	48.6	421	8	AD75703	Human PRO
284	35	48.6	421	7	ADD79399	Human PRO	357	35	48.6	421	8	AD75703	Human PRO
285	35	48.6	421	7	ADD41935	Human PRO	358	35	48.6	421	8	AD75703	Human PRO
286	35	48.6	421	7	ADD17752	Human PRO	359	35	48.6	421	8	AD75703	Human PRO
287	35	48.6	421	7	ADD91884	Human PRO	360	35	48.6	421	8	AD75703	Human PRO
288	35	48.6	421	7	ADD33347	Novel hum	361	35	48.6	421	8	AD75703	Human PRO
289	35	48.6	421	7	ADD33899	Novel hum	362	35	48.6	421	8	AD75703	Human PRO
290	35	48.6	421	7	ADD79951	Human PRO	363	35	48.6	421	8	AD75703	Human PRO
291	35	48.6	421	7	ADD92988	Human PRO	364	35	48.6	421	8	AD75703	Human PRO
292	35	48.6	421	7	ADD19408	Human PRO	365	35	48.6	421	8	AD75703	Human PRO
293	35	48.6	421	7	ADD18856	Human PRO	366	35	48.6	421	8	AD75703	Human PRO
294	35	48.6	421	7	ADD43052	Human PRO	367	35	48.6	421	8	AD75703	Human PRO
295	35	48.6	421	7	ADD95841	Human PRO	368	35	48.6	421	8	AD75703	Human PRO
296	35	48.6	421	7	ADD22727	Human PRO	369	35	48.6	421	8	AD75703	Human PRO
297	35	48.6	421	7	ADD78845	Human PRO	370	35	48.6	421	8	AD75703	Human PRO
298	35	48.6	421	7	ADD32795	Novel hum	371	35	48.6	421	8	AD75703	Human PRO
299	35	48.6	421	7	ADD42487	Human PRO	372	35	48.6	421	8	AD75703	Human PRO
300	35	48.6	421	7	ADD80503	Human PRO	373	35	48.6	421	8	AD75703	Human PRO
301	35	48.6	421	7	ADD89531	Human PRO	374	35	48.6	421	8	AD75703	Human PRO
302	35	48.6	421	7	ADD40815	Human PRO	375	35	48.6	421	8	AD75703	Human PRO
303	35	48.6	421	7	ADD04614	Human PRO	376	35	48.6	421	8	AD75703	Human PRO
304	35	48.6	421	7	ADD92743	Human PRO	377	35	48.6	421	8	AD75703	Human PRO
305	35	48.6	421	7	ADD21452	Novel hum	378	35	48.6	421	8	AD75703	Human PRO
306	35	48.6	421	7	ADD23093	Novel hum	379	35	48.6	421	8	AD75703	Human PRO
307	35	48.6	421	7	ADD97428	Human PRO	380	35	48.6	421	8	AD75703	Human PRO
308	35	48.6	421	7	ADD80492	Human PRO	381	35	48.6	421	8	AD75703	Human PRO
309	35	48.6	421	7	ADD79940	Human PRO	382	35	48.6	421	8	AD75703	Human PRO
310	35	48.6	421	7	ADD55232	Novel hum	383	35	48.6	421	8	AD75703	Human PRO
311	35	48.6	421	7	ADD55784	Novel hum	384	35	48.6	421	8	AD75703	Human PRO
312	35	48.6	421	7	ADD164952	Novel hum	385	35	48.6	421	8	AD75703	Human PRO
313	35	48.6	421	7	ADD163451	Novel hum	386	35	48.6	421	8	AD75703	Human PRO
314	35	48.6	421	7	ADD81865	Novel hum	387	35	48.6	421	8	AD75703	Human PRO
315	35	48.6	421	7	ADD81313	Novel hum	388	35	48.6	421	8	AD75703	Human PRO
316	35	48.6	421	7	ADD82482	Novel hum	389	35	48.6	421	8	AD75703	Human PRO
317	35	48.6	421	7	ADD15881	Novel hum	390	35	48.6	421	8	AD75703	Human PRO

331	35	48.6	421	8	ADI114637	Adi114637	Novel hum	464	35	48.6	775	6	ADB24479	ADB24479	Human PRO
332	35	48.6	421	8	ADI18232	Adi18232	Novel hum	465	35	48.6	775	6	ADA82003	Ada82003	Human PRO
333	35	48.6	421	8	ADJ163513	Adj163513	Novel hum	466	35	48.6	775	6	ADA74966	Ada74966	Human PRO
334	35	48.6	421	8	ADJ77408	Adj77408	Human PRO	467	35	48.6	775	6	ADA85044	Ada85044	Novel hum
335	35	48.6	421	8	ADJ65530	Adj65530	Human PRO	468	35	48.6	775	6	ADA84492	Ada84492	Novel hum
336	35	48.6	421	8	ADM27666	Adm27666	Human PRO	469	35	48.6	775	6	ADB29748	Adb29748	Human PRO
337	35	48.6	421	8	ADM42390	Adm42390	Human PRO	470	35	48.6	775	6	ADA80276	Ada80276	Human PRO
338	35	48.6	421	8	ADM28252	Adm28252	Human PRO	471	35	48.6	775	6	ADA75518	Ada75518	Human PRO
339	35	48.6	421	8	ADQ18584	Adq18584	Human sof	472	35	48.6	775	6	ADA46743	Ada46743	Human PRO
340	35	48.6	421	8	ADI95734	Adi95734	Human PRO	473	35	48.6	775	6	ADB25039	Adb25039	Human PRO
341	35	48.6	421	8	ADI96286	Adi96286	Novel hum	474	35	48.6	775	6	ADA93215	Ada93215	Human PRO
342	35	48.6	421	8	ADT94397	Adt94397	Human PRO	475	35	48.6	775	6	ADB26565	Adb26565	Human PRO
343	35	48.6	437	3	AAB43755	Aab43755	Human can	476	35	48.6	775	6	ADB30852	Adb30852	Human PRO
344	35	48.6	444	7	ADG40032	Adg40032	Murine Sp	477	35	48.6	775	6	ADA60780	Ada60780	Homo sapi
345	35	48.6	445	7	ABO75589	AbO75589	Pseudomon	478	35	48.6	775	6	ADB23927	Adb23927	Human PRO
346	35	48.6	451	8	ADN04632	Adn04632	Antipsori	479	35	48.6	775	6	ADA96256	Ada96256	Human PRO
347	35	48.6	451	8	ADP24649	Adp24649	PRO polyp	480	35	48.6	775	6	ADA80828	Ada80828	Human PRO
348	35	48.6	452	2	AAV09553	Aay09553	Streptoco	481	35	48.6	775	6	ADA95704	Ada95704	Human PRO
349	35	48.6	452	5	ABP25517	Abp25517	Streptoco	482	35	48.6	775	6	ADB26013	Adb26013	Human PRO
350	35	48.6	452	6	ABU46730	Abu46730	Protein e	483	35	48.6	775	6	ADB21498	Adb21498	Novel hum
351	35	48.6	457	6	ABP76802	Abp76802	N. gonorr	484	35	48.6	775	7	ADA77277	Ada77277	Human PRO
352	35	48.6	457	6	ABP80055	Abp80055	N. gonorr	485	35	48.6	775	7	ADB18017	Adb18017	Human PRO
353	35	48.6	460	4	ABE67576	AbE67576	Drosophil	486	35	48.6	775	7	ADA86700	Ada86700	Novel hum
354	35	48.6	460	7	ABO70261	AbO70261	Pseudomon	487	35	48.6	775	7	ADA87803	Ada87803	Novel hum
355	35	48.6	465	6	ADA34854	Ada34854	Acinetoba	488	35	48.6	775	7	ADA46191	Ada46191	Novel hum
356	35	48.6	469	5	ABG93131	Abg93131	S. cerevi	489	35	48.6	775	7	ADB28221	Adb28221	Human PRO
357	35	48.6	469	6	ABR52710	AbR52710	Protein s	490	35	48.6	775	7	ADB28773	Adb28773	Human PRO
358	35	48.6	469	7	ADK61927	Adk61927	Disease t	491	35	48.6	775	7	ADA76725	Ada76725	Human PRO
359	35	48.6	516	5	ABR91350	AbR91350	Herbicida	492	35	48.6	775	7	ADA88355	Ada88355	Novel hum
360	35	48.6	517	8	ADN10645	Adn10645	Nicotiana	493	35	48.6	775	7	ADA97360	Ada97360	Human PRO
361	35	48.6	529	5	ABB47666	Abb47666	Listeria	494	35	48.6	775	7	ADB27117	Adb27117	Human PRO
362	35	48.6	529	6	ABU32537	Abu32537	Protein e	495	35	48.6	775	7	ADB22050	Adb22050	Novel hum
363	35	48.6	606	7	ADH86208	Adh86208	Enterococ	496	35	48.6	775	7	ADA66741	Ada66741	Human PRO
364	35	48.6	662	8	ADN74701	Adn74701	Thale cre	497	35	48.6	775	7	ADB22602	Adb22602	Human PRO
365	35	48.6	715	6	ABU40115	Abu40115	Protein e	498	35	48.6	775	7	ADB23375	Adb23375	Human PRO
366	35	48.6	719	5	ABB91351	Abb91351	Herbicida	499	35	48.6	775	7	ADA92097	Ada92097	Novel hum
367	35	48.6	735	4	AAU36496	Aau36496	Pseudomon	500	35	48.6	775	7	ADB15160	Adb15160	Human PRO
368	35	48.6	735	6	ABU38864	Abu38864	Protein e	501	35	48.6	775	7	ADB38412	Adb38412	Novel hum
369	35	48.6	759	8	ADS43027	AdS43027	Bacterial	502	35	48.6	775	7	ADB37860	Adb37860	Novel hum
370	35	48.6	771	8	ADS24420	AdS24420	Bacterial	503	35	48.6	775	7	ADB66332	Adb66332	Novel hum
371	35	48.6	772	4	ABB12438	Abb12438	Human bon	504	35	48.6	775	7	ADB89412	Adb89412	Human PRO
372	35	48.6	775	4	AAU12231	Aau12231	Human PRO	505	35	48.6	775	7	ADB90144	Adb90144	Human PRO
373	35	48.6	775	4	ABB71228	Abb71228	Drosophil	506	35	48.6	775	7	ADB39245	Adb39245	Novel hum
374	35	48.6	775	6	ABO17675	AbO17675	Novel hum	507	35	48.6	775	7	ADB46868	Adb46868	Novel hum
375	35	48.6	775	6	ABU80929	Abu80929	Human PRO	508	35	48.6	775	7	ADB86475	Adb86475	Human PRO
376	35	48.6	775	6	ABU66629	Abu66629	Human PRO	509	35	48.6	775	7	ADB77080	Adb77080	Novel hum
377	35	48.6	775	6	ABU59710	Abu59710	Novel sec	510	35	48.6	775	7	ADB34237	Adb34237	Human PRO
378	35	48.6	775	6	ABO24900	AbO24900	Human sec	511	35	48.6	775	7	ADB35341	Adb35341	Human PRO
379	35	48.6	775	6	ABU66905	Abu66905	Human sec	512	35	48.6	775	7	ADB33685	Adb33685	Human PRO
380	35	48.6	775	6	ADA45639	Ada45639	Novel hum	513	35	48.6	775	7	ADB34789	Adb34789	Human PRO
381	35	48.6	775	6	ADA76070	Ada76070	Human PRO	514	35	48.6	775	7	ADB35893	Adb35893	Human PRO
382	35	48.6	775	6	ADA18720	Ada18720	Human PRO	515	35	48.6	775	7	ADB46288	Adb46288	Novel hum
383	35	48.6	775	6	ADA61343	Ada61343	Homo sapi	516	35	48.6	775	7	ADC50161	Adc50161	Novel hum
384	35	48.6	775	6	ADB19128	Adb19128	Novel hum	517	35	48.6	775	7	ADC71708	Adc71708	Novel hum
385	35	48.6	775	6	ADB27669	Adb27669	Human PRO	518	35	48.6	775	7	ADC52694	Adc52694	Novel hum
386	35	48.6	775	6	ADA86148	Ada86148	Novel hum	519	35	48.6	775	7	ADC59687	Adc59687	Novel hum
387	35	48.6	775	6	ADB15712	Adb15712	Human PRO	520	35	48.6	775	7	ADC57048	Adc57048	Novel hum
388	35	48.6	775	6	ADA47498	Ada47498	Human PRO	521	35	48.6	775	7	ADC60239	Adc60239	Novel hum
389	35	48.6	775	6	ADA67293	Ada67293	Human PRO	522	35	48.6	775	7	ADC50714	Adc50714	Novel hum
390	35	48.6	775	6	ADB30300	Adb30300	Human PRO	523	35	48.6	775	7	ADC65241	Adc65241	Human PRO
391	35	48.6	775	6	ADA85596	Ada85596	Novel hum	524	35	48.6	775	7	ADC54339	Adc54339	Novel hum
392	35	48.6	775	6	ADA96808	Ada96808	Human PRO	525	35	48.6	775	7	ADC53300	Adc53300	Novel hum
393	35	48.6	775	6	ADA79112	Ada79112	Human PRO	526	35	48.6	775	7	ADC58823	Adc58823	Novel hum
394	35	48.6	775	6	ADA87251	Ada87251	Novel hum	527	35	48.6	775	7	ADC55701	Adc55701	Novel hum
395	35	48.6	775	6	ADB16453	Adb16453	Human PRO	528	35	48.6	775	7	ADC58271	Adc58271	Novel hum
396	35	48.6	775	6	ADA91545	Ada91545	Novel hum	529	35	48.6	775	7	ADD02945	Add02945	Novel hum
397	35	48.6	775	6	ADB14608	Adb14608	Human PRO	530	35	48.6	775	7	ADC89937	Adc89937	Novel hum
398	35	48.6	775	6	ADB18569	Adb18569	Novel hum	531	35	48.6	775	7	ADC69356	Adc69356	Human PRO
399	35	48.6	775	6	ADA93784	Ada93784	Human PRO	532	35	48.6	775	7	ADC48245	Adc48245	Human PRO
400	35	48.6	775	6	ADB19680	Adb19680	Novel hum	533	35	48.6	775	7	ADD09774	Add09774	Human PRO
401	35	48.6	775	6	ADB12992	Adb12992	Human PRO	534	35	48.6	775	7	ADD04349	Add04349	Novel hum
402	35	48.6	775	6	ABO43208	AbO43208	Novel hum	535	35	48.6	775	7	ADC80305	Adc80305	Novel hum
403	35	48.6	775	6	ADA74246	Ada74246	Human PRO	536	35	48.6	775	7	ADD10812	Add10812	Human PRO

537	35	48.6	775	7	ADC47693	Adc47693	Human PRO	610	35	48.6	775	8	ADE91457	Novel hum
538	35	48.6	775	7	ADC79753	Adc79753	Novel hum	611	35	48.6	775	8	ADG02036	Human PRO
539	35	48.6	775	7	ADD09222	AdD09222	Human PRO	612	35	48.6	775	8	ADG21822	Novel hum
540	35	48.6	775	7	ADD40935	AdD40935	Novel hum	613	35	48.6	775	8	ADG19892	Human PRO
541	35	48.6	775	7	ADD52074	AdD52074	Human PRO	614	35	48.6	775	8	ADf97798	Human PRO
542	35	48.6	775	7	ADD52814	AdD52814	Human PRO	615	35	48.6	775	8	ADG24015	Novel hum
543	35	48.6	775	7	ADD53366	AdD53366	Human PRO	616	35	48.6	775	8	ADf98369	Human PRO
544	35	48.6	775	7	ADD51522	AdD51522	Human PRO	617	35	48.6	775	8	ADG03200	Human PRO
545	35	48.6	775	7	ADD02321	AdD02321	Human PRO	618	35	48.6	775	8	ADf98921	Human PRO
546	35	48.6	775	7	ADD01755	AdD01755	Human PRO	619	35	48.6	775	8	ADf16506	Human PRO
547	35	48.6	775	7	ADD53937	AdD53937	Novel hum	620	35	48.6	775	8	ADG04965	Human PRO
548	35	48.6	775	7	ADD92254	AdD92254	Human PRO	621	35	48.6	775	8	ADG19232	Human PRO
549	35	48.6	775	7	ADD91150	AdD91150	Human PRO	622	35	48.6	775	8	ADG13069	Human PRO
550	35	48.6	775	7	ADG03764	AdG03764	Human PRO	623	35	48.6	775	8	ADG08126	Novel hum
551	35	48.6	775	7	ADG32061	AdG32061	Novel hum	624	35	48.6	775	8	ADG15296	Human PRO
552	35	48.6	775	7	ADG21993	AdG21993	Human PRO	625	35	48.6	775	8	ADf96694	Human PRO
553	35	48.6	775	7	ADG79217	AdG79217	Human PRO	626	35	48.6	775	8	ADG05879	Human PRO
554	35	48.6	775	7	ADG41753	AdG41753	Human PRO	627	35	48.6	775	8	ADG23463	Novel hum
555	35	48.6	775	7	ADG17570	AdG17570	Human PRO	628	35	48.6	775	8	ADG03752	Human PRO
556	35	48.6	775	7	ADD91702	AdD91702	Human PRO	629	35	48.6	775	8	ADG24653	Novel hum
557	35	48.6	775	7	ADG33165	AdG33165	Novel hum	630	35	48.6	775	8	ADG06950	Novel hum
558	35	48.6	775	7	ADG33717	AdG33717	Novel hum	631	35	48.6	775	8	ADG07502	Novel hum
559	35	48.6	775	7	ADD79769	AdD79769	Human PRO	632	35	48.6	775	8	ADG54997	Novel hum
560	35	48.6	775	7	ADD92806	AdD92806	Human PRO	633	35	48.6	775	8	ADG60661	Novel hum
561	35	48.6	775	7	ADG19226	AdG19226	Human PRO	634	35	48.6	775	8	ADG61765	Novel hum
562	35	48.6	775	7	ADG18674	AdG18674	Human PRO	635	35	48.6	775	8	ADG81966	Human PRO
563	35	48.6	775	7	ADG42870	AdG42870	Human PRO	636	35	48.6	775	8	ADG57205	Novel hum
564	35	48.6	775	7	ADG95659	AdG95659	Human PRO	637	35	48.6	775	8	ADG56653	Novel hum
565	35	48.6	775	7	ADG22545	AdG22545	Human PRO	638	35	48.6	775	8	ADG55549	Novel hum
566	35	48.6	775	7	ADG78663	AdG78663	Human PRO	639	35	48.6	775	8	ADG58309	Novel hum
567	35	48.6	775	7	ADG32813	AdG32813	Novel hum	640	35	48.6	775	8	ADG70675	Novel hum
568	35	48.6	775	7	ADG42305	AdG42305	Novel hum	641	35	48.6	775	8	ADG57757	Novel hum
569	35	48.6	775	7	ADG80321	AdG80321	Human PRO	642	35	48.6	775	8	ADG53341	Novel hum
570	35	48.6	775	7	ADG89349	AdG89349	Human PRO	643	35	48.6	775	8	ADG71227	Novel hum
571	35	48.6	775	7	ADG40633	AdG40633	Human PRO	644	35	48.6	775	8	ADG81414	Human PRO
572	35	48.6	775	7	ADG04432	AdG04432	Human PRO	645	35	48.6	775	8	ADH30376	Human PRO
573	35	48.6	775	7	ADG92561	AdG92561	Human PRO	646	35	48.6	775	8	ADH11743	Novel hum
574	35	48.6	775	7	ADG21270	AdG21270	Novel hum	647	35	48.6	775	8	ADG52165	Novel hum
575	35	48.6	775	7	ADG22911	AdG22911	Novel hum	648	35	48.6	775	8	ADG53893	Novel hum
576	35	48.6	775	7	ADG97246	AdG97246	Human PRO	649	35	48.6	775	8	ADG80862	Human PRO
577	35	48.6	775	7	ADG80310	AdG80310	Human PRO	650	35	48.6	775	8	ADG56101	Novel hum
578	35	48.6	775	7	ADG79758	AdG79758	Human PRO	651	35	48.6	775	8	ADH12367	Novel hum
579	35	48.6	775	7	ADH55050	AdH55050	Novel hum	652	35	48.6	775	8	ADG61213	Novel hum
580	35	48.6	775	7	ADH55602	AdH55602	Novel hum	653	35	48.6	775	8	ADH28300	Human PRO
581	35	48.6	775	7	ADf63821	Adf63821	Novel hum	654	35	48.6	775	8	ADG54445	Novel hum
582	35	48.6	775	7	ADf64770	Adf64770	Novel hum	655	35	48.6	775	8	ADG59485	Novel hum
583	35	48.6	775	7	ADf63269	Adf63269	Novel hum	656	35	48.6	775	8	ADf80909	Human PRO
584	35	48.6	775	7	ADH81683	AdH81683	Novel hum	657	35	48.6	775	8	ADG09652	Novel hum
585	35	48.6	775	7	ADH81131	AdH81131	Novel hum	658	35	48.6	775	8	ADf15123	Novel hum
586	35	48.6	775	7	ADH82300	AdH82300	Novel hum	659	35	48.6	775	8	ADG09000	Novel hum
587	35	48.6	775	7	ADN15699	AdN15699	Novel hum	660	35	48.6	775	8	ADf14455	Novel hum
588	35	48.6	775	7	ADN16328	AdN16328	Novel hum	661	35	48.6	775	8	ADf18050	Novel hum
589	35	48.6	775	7	ADN15147	AdN15147	Novel hum	662	35	48.6	775	8	ADf06531	Human tum
590	35	48.6	775	7	ADN14595	AdN14595	Novel hum	663	35	48.6	775	8	ADf63331	Novel hum
591	35	48.6	775	8	ADG08057	AdG08057	Novel hum	664	35	48.6	775	8	ADf77226	Human PRO
592	35	48.6	775	8	ADG76305	AdG76305	Human PRO	665	35	48.6	775	8	ADf65348	Human PRO
593	35	48.6	775	8	ADH87669	AdH87669	Human PRO	666	35	48.6	775	8	ADm27484	Human PRO
594	35	48.6	775	8	ADH86073	AdH86073	Human PRO	667	35	48.6	775	8	ADm42208	Human PRO
595	35	48.6	775	8	ADG75521	AdG75521	Human PRO	668	35	48.6	775	8	ADm28070	Human PRO
596	35	48.6	775	8	ADG23097	AdG23097	Human PRO	669	35	48.6	775	8	ADf95552	Human PRO
597	35	48.6	775	8	ADG23649	AdG23649	Human PRO	670	35	48.6	775	8	ADf96104	Novel hum
598	35	48.6	775	8	ADG24292	AdG24292	Human PRO	671	35	48.6	776	8	ADf49896	Novel hum
599	35	48.6	775	8	ADG87117	AdG87117	Human PRO	672	35	48.6	906	6	ABU29398	Oil-assoc
600	35	48.6	775	8	ADG88983	AdG88983	Human PRO	673	35	48.6	936	6	ABM0670	Protein e
601	35	48.6	775	8	ADG18122	AdG18122	Human PRO	674	35	48.6	1987	7	ABU63358	Tumour-as
602	35	48.6	775	8	ADG88431	AdG88431	Human PRO	675	35	48.6	2013	7	ABU63356	Human Sin
603	35	48.6	775	8	ADG94451	AdG94451	Human PRO	676	35	48.6	2014	7	ABU63356	Human Sin
604	35	48.6	775	8	ADG90862	AdG90862	Human PRO	677	35	48.6	2014	5	AAE24137	Amino aci
605	35	48.6	775	8	ADG95003	AdG95003	Human PRO	678	35	48.6	2014	6	ABP60434	Human ste
606	35	48.6	775	8	ADG93113	AdG93113	Human PRO	679	35	48.6	2014	7	ABU63359	Human Sin
607	35	48.6	775	8	ADf34694	Adf34694	Human PRO	680	35	48.6	2040	7	ABU63357	Human Sin
608	35	48.6	775	8	ADG92009	AdG92009	Novel hum	681	35	48.6	2041	6	ABP60435	Human ste
609	35	48.6	775	8	ADG90310	AdG90310	Human PRO	682	34.5	47.9	61	4	AAW92318	Human d19

829	34	47.2	446	2	AAV04289	Streptococ	902	34	47.2	854	4	AAW42224	AAW42224 Soybean r
830	34	47.2	450	2	AAW29454	Streptococ	903	34	47.2	877	4	AAW42214	AAW42214 Soybean r
831	34	47.2	450	2	AAW68551	S. pneumo	904	34	47.2	877	4	AAW42223	AAW42223 Soybean r
832	34	47.2	450	4	AAU37805	Streptococ	905	34	47.2	877	4	AAW42231	AAW42231 Soybean r
833	34	47.2	450	4	AAU38040	Streptococ	906	34	47.2	877	4	AAW42227	AAW42227 Soybean r
834	34	47.2	450	6	ABU01072	S. pneumo	907	34	47.2	877	4	AAW42225	AAW42225 Soybean r
835	34	47.2	450	6	ABU45941	Protein e	908	34	47.2	877	4	AAW42221	AAW42221 Soybean r
836	34	47.2	450	7	ADD15557	Streptococ	909	34	47.2	877	4	AAW42229	AAW42229 Soybean r
837	34	47.2	450	7	ADD15555	Streptococ	910	34	47.2	877	4	AAW42219	AAW42219 Soybean r
838	34	47.2	450	7	ADD15555	Streptococ	911	34	47.2	877	4	AAW42217	AAW42217 Soybean r
839	34	47.2	451	5	ABP30250	Streptococ	912	34	47.2	884	4	ABG22489	Novel hum
840	34	47.2	456	4	AAU33495	Enterococ	913	34	47.2	884	4	ABG30084	Novel hum
841	34	47.2	456	4	AAU35043	Enterococ	914	34	47.2	919	6	ABU21774	Protein e
842	34	47.2	456	6	ADL46377	Protein e	915	34	47.2	1081	5	ABP27331	Streptococ
843	34	47.2	456	6	ADL46377	Protein e	916	34	47.2	1081	5	ADK99301	Streptococ
844	34	47.2	456	8	ADO07009	Activator	917	34	47.2	1164	2	AAW33113	Thermococ
845	34	47.2	457	8	ADO23562	Novel hum	918	34	47.2	1374	5	ABP26112	Streptococ
846	34	47.2	460	8	ADR95741	Novel S.	919	34	47.2	1535	5	ABP73813	Candida a
847	34	47.2	462	8	ADR21900	Bacterial	920	34	47.2	1615	4	AAU03536	Human pro
848	34	47.2	463	8	ADO07006	E faecali	921	34	47.2	1879	5	ADL16684	Human nov
849	34	47.2	466	5	ABP27384	Streptococ	922	34	47.2	1879	8	ADN42338	Human nov
850	34	47.2	474	6	ABU33574	Protein e	923	34	47.2	2652	5	ABG31321	Predicted
851	34	47.2	475	6	ABM69249	Phototrab	924	34	47.2	2652	8	ADL02250	Human OCP
852	34	47.2	487	8	ADR94568	Novel S.	925	34	47.2	2764	4	ABM66967	Drosophil
853	34	47.2	496	5	ABP65142	Hypoxia-r	926	34	47.2	2802	4	AAE05485	Drosophil
854	34	47.2	496	6	ABP96793	Human COP	927	34	47.2	2802	4	ABM63789	Drosophil
855	34	47.2	496	7	ADP55870	Human PRO	928	34	47.2	2802	5	ABM08077	Drosophil
856	34	47.2	496	7	ADD45246	Human PRO	929	34	47.2	2828	5	ADL17071	Human NOV
857	34	47.2	496	7	ADD48382	Human PRO	930	34	47.2	2845	5	ABP70049	Human NOV
858	34	47.2	496	8	ADL82965	Human PRO	931	34	47.2	2853	6	ABR40110	Human cel
859	34	47.2	496	8	ADO19284	Human PRO	932	33.5	46.5	137	4	AAU18143	Novel hum
860	34	47.2	496	8	ADO19282	Human PRO	933	33.5	46.5	137	4	AAU18098	Novel hum
861	34	47.2	496	8	ADQ76758	Human glu	934	33.5	46.5	137	4	AAU18697	Renal and
862	34	47.2	496	8	ADR14665	Human NF-	935	33.5	46.5	137	4	AAU18650	Renal and
863	34	47.2	496	8	ADP25408	PRO polyp	936	33.5	46.5	137	4	AAU21589	Novel hum
864	34	47.2	502	4	ABP96833	Putative	937	33.5	46.5	137	4	AAU21746	Novel hum
865	34	47.2	509	6	ABM71923	Staphyloc	938	33.5	46.5	137	4	AAW99966	Human exp
866	34	47.2	512	5	ABP25416	Streptococ	939	33.5	46.5	137	4	AAW99938	Human exp
867	34	47.2	543	4	ABM48036	S. pneumo	940	33.5	46.5	137	4	AAW99965	Human exp
868	34	47.2	543	6	ABU01445	S. pneumo	941	33.5	46.5	137	4	AAW91804	Human imm
869	34	47.2	543	8	ABM92154	S. pneumo	942	33.5	46.5	137	4	AAW98875	Human imm
870	34	47.2	544	5	ABP74066	Candida a	943	33.5	46.5	137	4	ABM10183	Human CDN
871	34	47.2	547	8	ADK47203	Streptococ	944	33.5	46.5	137	4	ABM10420	Human CDN
872	34	47.2	578	2	AAW75085	Oxalyl-Co	945	33.5	46.5	137	4	AAW42390	Human pol
873	34	47.2	578	2	AAW22882	Human oxa	946	33.5	46.5	137	4	AAU87136	Novel cen
874	34	47.2	579	5	ABM48472	Listeria	947	33.5	46.5	137	4	AAU87136	Novel cen
875	34	47.2	587	3	AAV99819	Corn prot	948	33.5	46.5	137	4	AAU18418	Human end
876	34	47.2	587	8	ADH62812	Lactobaci	949	33.5	46.5	137	4	AAU18295	Human end
877	34	47.2	593	8	ADH62811	Lactobaci	950	33.5	46.5	137	4	ADG15142	Human 7 t
878	34	47.2	632	4	AG93218	C glutami	951	33.5	46.5	137	4	ADG15164	Human 7 t
879	34	47.2	632	8	ABM84849	Human dia	952	33.5	46.5	137	5	ABJ05725	Novel hum
880	34	47.2	685	2	AAV25683	Cockroach	953	33.5	46.5	137	5	ABJ05770	Novel hum
881	34	47.2	685	7	ADC34931	Cockroach	954	33.5	46.5	137	5	ABP66770	Human pol
882	34	47.2	686	8	ADH22525	Human tra	955	33.5	46.5	137	5	ABP67007	Human pol
883	34	47.2	686	8	ABM84848	Human dia	956	33.5	46.5	137	6	ABU97312	Human pol
884	34	47.2	758	4	AAU03389	Altenaria	957	33.5	46.5	137	6	ABU97265	Human pol
885	34	47.2	758	5	ABG92715	Listeria	958	33.5	46.5	137	7	ADC46230	Human neo
886	34	47.2	763	5	ABM50119	Listeria	959	33.5	46.5	137	7	ADC46387	Human neo
887	34	47.2	764	6	AAW60568	Down-regu	960	33.5	46.5	137	8	ADI54768	Novel hum
888	34	47.2	764	6	ADA10955	Human CDN	961	33.5	46.5	137	8	ADI54451	Novel hum
889	34	47.2	764	8	ADG47981	Human col	962	33.5	46.5	236	6	ABU18169	Protein e
890	34	47.2	792	5	AAU83419	Novel Lac	963	33.5	46.5	319	6	ABU18118	Protein e
891	34	47.2	805	8	ADK34373	Bacterial	964	33.5	46.5	322	7	AAW72332	Human OR-
892	34	47.2	827	4	ABM60840	Drosophil	965	33.5	46.5	322	7	ABO67653	Klebsiell
893	34	47.2	830	4	ABM10122	Soy bean	966	33.5	46.5	342	2	AAW59907	Human HNH
894	34	47.2	854	4	AAW42220	Soybean r	967	33.5	46.5	343	6	AAO19904	Human TM4
895	34	47.2	854	4	AAW42228	Soybean r	968	33.5	46.5	343	6	ABP81702	Human G p
896	34	47.2	854	4	AAW42222	Soybean r	969	33.5	46.5	343	8	ADO29418	Human GPC
897	34	47.2	854	4	AAW42226	Soybean r	970	33.5	46.5	347	8	ADO29145	Mouse nov
898	34	47.2	854	4	AAW42230	Soybean r	971	33.5	46.5	455	4	ABG04587	Novel hum
899	34	47.2	854	4	AAW42218	Soybean r	972	33.5	46.5	497	4	ABM57922	Drosophil
900	34	47.2	854	4	AAW42215	Soybean 2	973	33.5	46.5	815	7	ADB37640	Neural th
901	34	47.2	854	4	AAW42232	Soybean r	974	33.5	46.5	876	7	ADB37596	Neural th

975 33.5 46.5 876 7 ADB37574
976 33.5 46.5 893 7 ADB37638 Neural th
977 33.5 46.5 930 2 AAW55961
978 33.5 46.5 930 6 ABB99469
979 33.5 46.5 930 7 ADB37583
980 33.5 46.5 930 7 ADB37619
981 33.5 46.5 930 7 ADB37591 Neural th
982 33.5 46.5 930 7 ADB37631
983 33 45.8 27 2 AAR81819
984 33 45.8 45 4 AAM95235
985 33 45.8 45 4 ABB95932
986 33 45.8 61 4 AAU86767
987 33 45.8 61 7 ADB60101
988 33 45.8 67 4 AAM16772
989 33 45.8 67 4 ABB35758
990 33 45.8 67 4 AAM29259
991 33 45.8 67 4 ABB30592
992 33 45.8 67 4 ABB21182
993 33 45.8 67 4 AAM68948
994 33 45.8 67 4 AAM56566
995 33 45.8 67 4 AAG50611
996 33 45.8 67 4 AAM04489
997 33 45.8 67 5 ABB38532
998 33 45.8 68 5 ABB04063 Human ORF
999 33 45.8 73 5 ABE20834
1000 33 45.8 73 5 ABB64680 Human alb

ALIGNMENTS

RESULT 1
ASO8421
ID ABO84421 standard; protein; 518 AA.
XX ABO84421;
XX
DT 18-NOV-2004 (first entry)
DE Human cancer-associated protein HP7-153.1.
XX
KW Human; cancer-associated protein; cytostatic; cancer; leukaemia;
KW Lymphoma; CAP.
XX
OS Homo sapiens.
XX
FN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
DR N-PSDB; ABB32567.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 18; seqid 54; 310pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10

CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC a recombinant nucleic acid or expression vector, a microarray for detecting
CC cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence, selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP protein sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 518 AA;

Query Match 100.0%; Score 72; DB 8; Length 518;

Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15

Db 124 VPFSVAKSVKSLYL 138

RESULT 2

ADQ67207

ID ADQ67207 standard; protein; 624 AA.

XX ADQ67207;

XX 07-OCT-2004 (first entry)

XX Novel human protein sequence #2180.

XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
XX gene therapy; diagnostic marker; morbid state; osteoporosis;
XX neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
XX cancer.

OS Homo sapiens.

PN EP1440981-A2.

PD 28-JUL-2004.

XX 21-JAN-2004; 2004EP-00001196.

XX 21-JAN-2003; 2003JP-00102206.

PR 09-MAY-2003; 2003JP-00131392.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX
DR WPI; 2004-535376/52.
DR N-PSDB; ADQ65019.
XX
PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 4368; 2449pp; English.
XX
CC The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a protein
XX sequence of the invention.
XX
SQ Sequence 624 AA;

Query Match 100.0%; Score 72; DB 8; Length 624;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 230 VPFSVAKSVKSLYL 244
|||||
RESULT 3
AAR99414
ID AAR99414 standard; protein; 678 AA.
XX
AC AAR99414;
XX
DT 04-DEC-1996 (first entry)
XX
DE Human gas6 protein, an S protein homologue and axl receptor ligand.
XX
KW Axl receptor ligand; human protein S homologue; growth factor;
KW myeloid cell proliferation; myeloid malignancy; regulation; prevention;
KW recombinant production.
XX
OS Homo sapiens.
XX
PN US5538861-A.
XX
PD 23-JUL-1996.
XX
PF 29-JUL-1994; 94US-00282141.
XX
PR 29-JUL-1994; 94US-00282141.
XX
PA (AMGE/) AMGEN INC.
PA (SCHN/) SCHNEIDER C.
XX
PI Manfioletti G, Varnum BC, Schneider C, Avanzi G, Brancolini C;
XX
DR WPI; 1996-353825/35.
DR N-PSDB; AAT41544.
XX
PT DNA encoding gas6, the axl receptor ligand - useful to regulate growth of
PT myeloid cells and malignancies.
XX
PS Claim 1; Col 19-22; 36pp; English.
XX
CC AAR99414 is the gas6 protein (from the growth arrest specific gene number
CC 6). The gas6 protein has homology to human protein S which functions as a
CC cofactor in a protease cascade that regulates coagulation. Gas6
CC expression, as with gas1 and gas2, is associated with cell growth arrest
CC which suggests a possible role of gas6 in the regulation of cell growth.
CC In fact the gas6 protein is an axl receptor: (axlr) ligand and a growth

CC factor for any cells expressing axlr e.g. bone marrow, spleen, thymus,
CC ovary, heart, intestine and lung cells. The axl receptor is involved in
CC myeloid cell proliferation and myeloid malignancies, so gas6 may regulate
CC growth of such cells
XX
SQ Sequence 678 AA;

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 284 VPFSVAKSVKSLYL 298
|||||
RESULT 4
AAW46463
ID AAW46463 standard; protein; 678 AA.
XX
AC AAW46463;
XX
DT 15-MAY-1998 (first entry)
XX
DE Human growth arrest specific-gene 6 (gas6) protein.
XX
KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
KW receptor tyrosine kinase; regulation; protease cascade; insulin;
KW growth regulation; serum-free culture medium; human; Schwann cell;
KW receptor activator; erbB receptor; heregulin; cAMP level; proliferation;
KW treatment; nervous system injury.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 49..89 /note= "A domain of gas6"
FT Domain 90..117 /note= "B domain of gas6 comprising a thrombin sensitive
FT loop"
FT Domain 118..278 /note= "C domain of gas6, contains 4 epidermal growth
FT factor-like repeats"
FT Domain 279..678 /note= "D domain of gas6, homologous to steroid binding
FT hormone"
FT Domain 314..471 /note= "G domain 1"
FT Domain 503..671 /note= "G domain 2"
XX
PN US5714385-A.
XX
PD 03-FEB-1998.
XX
PF 10-MAY-1995; 95US-00435434.
XX
PR 10-MAY-1995; 95US-00435434.
XX
PA (GETH) GENENTECH INC.
XX
PI Chen J, Mather JP, Li R;
XX
DR WPI; 1998-129864/12.
XX
PT Medium for culturing human Schwann cells - is serum-free and contains Rse
PT receptor activator and other mitogens.
XX
PS Disclosure; Fig 2; 51pp; English.
XX
CC The present sequence represents a human growth arrest specific-gene 6
CC (gas6) protein which is able to activate the Rse and Axl receptor. Rse is
CC a receptor tyrosine kinase that is preferentially expressed in the adult

CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise cAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 XX
 XX Sequence 678 AA;

Query Match 100.0%; Score 72; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 |||||
 Db 284 VPFSVAKSVKSLYL 298

RESULT 5
 AAY29794
 ID AAY29794 standard; protein; 678 AA.

XX
 AC AAY29794;

XX 15-NOV-1999 (first entry)

XX Human growth arrest-specific gene 6 protein.

XX Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW Glial cell; Schwann cell; fusion protein.

XX Homo sapiens.

XX US955420-A.

XX 21-SEP-1999.

XX 10-MAY-1995; 95US-00438864.

XX 10-MAR-1995; 95US-00402253.

XX (GETH) GENENTECH INC.

XX Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;

XX WPI; 1999-539585/45.

XX Activation of the Rse receptor on a cell, useful for promoting cell
 PT proliferation and differentiation.

XX Disclosure; Fig 2; 48pp; English.

XX A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents human gas6 given in the present invention

XX Sequence 678 AA;

Query Match 100.0%; Score 72; DB 2; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 |||||
 Db 284 VPFSVAKSVKSLYL 298

RESULT 6
 AAY57383
 ID AAY57383 standard; protein; 678 AA.

XX
 AC AAY57383;

XX 19-JUN-2000 (first entry)

XX Amino acid sequence of human gas6 (h gas6) protein.

XX Nervous system; Schwann cell; mitogen; Rse/Axl receptor activator;
 KW central nervous system; peripheral nervous system; injury; trauma;
 KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 KW protein S.

XX Homo sapiens.

XX US6033660-A.

XX 07-MAR-2000.

XX 10-MAY-1995; 95US-00438862.

XX 10-MAY-1995; 95US-00438862.

XX (GETH) GENENTECH INC.

XX Mather JP, Chen J, Li R;

XX WPI; 2000-246046/21.

XX Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.

XX Disclosure; Fig 2; 52pp; English.

XX The invention relates to a method for treating nervous system injuries in
 CC mammals by administering human Schwann cells (SC) that have been cultured
 CC in serum-free medium. The serum-free medium is a nutrient solution
 CC supplemented with two mitogens, one of which, is a Rse/Axl receptor
 CC activator, to increase survival and proliferation of SC. The method is
 CC used to treat (or prevent) central or peripheral nervous system injury,
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
 CC or lesions associated with nutritional deficiencies, systemic disease,
 CC toxing or demyelination. Culturing cells in the specified medium allows
 CC proliferation of adult SC for use in autologous transplants. The present
 CC sequence represents a human gas6 (h gas6) protein, having 44% sequence
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
 CC survival factor for SCs in defined serum-free culture

XX Sequence 678 AA;

Query Match 100.0%; Score 72; DB 3; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 |||||
 Db 284 VPFSVAKSVKSLYL 298

RESULT 7
 ADL83231
 ID ADL83231 standard; protein; 678 AA.

XX
 AC ADL83231;

XX 17-JUN-2004 (first entry)

XX Human PRO12613, SEQ ID 433.

XX Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;
 KW Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;
 KW Gene Therapy; PRO; B cell related disorder; cancer;
 KW Immune-mediated inflammatory disease; human.
 XX Homo sapiens.
 OS WO2004024097-A2.
 XX 25-MAR-2004.
 XX 15-SEP-2003; 2003WO-US029097.
 XX 16-SEP-2002; 2002US-0411392P.
 XX (GETH) GENENTECH INC.
 PA Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;
 PI Wu TD;
 DR WPI; 2004-329389/30.
 DR N-PSDB; ADL83230.
 XX New PRO polypeptide, useful for diagnosing and treating a B cell related
 PT disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune
 PT mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.
 PS Claim 10; Fig 433; 695pp; English.
 XX The present invention relates to PRO proteins and their coding sequences.
 CC The PRO proteins are useful for diagnosing and treating a B cell related
 CC disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide
 CC antigen unresponsiveness, selective IgA deficiency, selective IGM
 CC deficiency, selective deficiency of IgG subclasses, immunodeficiency with
 CC hyper IGM, transient hypogammaglobulinemia of infancy, Burkitt's
 CC lymphoma, intermediate lymphoma, follicular lymphoma, type II
 CC hypersensitivity, rheumatoid arthritis, autoimmune mediated haemolytic
 CC anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or
 CC ankylosing spondylitis. The PRO proteins are also useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO
 CC coding sequences are useful as hybridization probes in chromosome and
 CC gene mapping, in preparing PRO proteins, or in generating transgenic
 CC animals or knockout animals, which in turn are useful in the development
 CC and screening of therapeutically useful reagents.
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 72; DB 8; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 15
 DB 284 VPFSVAKSVKSLYL 298
 RESULT 8
 ADM40825
 ID ADM40825 standard; protein; 678 AA.
 XX ADM40825;
 XX 01-JUL-2004 (first entry)
 DE Human Gas6 protein SEQ ID NO:3.
 KW growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
 KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
 KW receptor internalisation; cell proliferation; cell apoptosis prevention;
 KW signaling molecule; cell marker; human.
 XX

OS Homo sapiens.
 XX WO2004029209-A2.
 XX 08-APR-2004.
 XX 24-SEP-2003; 2003WO-US030330.
 XX 24-SEP-2002; 2002US-0413157P.
 XX (CENZ) CENTOCOR INC.
 PI Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
 DR WPI; 2004-316097/29.
 XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
 PT manufacturing medicines or for identifying inhibitors of Gas6 and its
 PT receptors.
 XX Disclosure; SEQ ID NO 3; 28pp; English.
 XX The present invention describes an isolated growth arrest specific gene 6
 CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
 CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
 CC ID NO:2, ADM40824), or a polyhistidine sequence. The variant Gas6
 CC polypeptide has 75% identity to native human Gas6 protein. Also
 CC described: (1) a recombinant DNA molecule encoding the amino acid
 CC sequence of the polypeptide described above; (2) a vector comprising the
 CC above nucleic acid; (3) a host cell comprising the vector, where the host
 CC cell is of mammalian origin; and (4) a composition comprising the
 CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
 CC activity. The composition is useful for manufacturing medicines or for
 CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
 CC may also be used for Gas6-dependent receptor phosphorylation, receptor
 CC internalisation, cell proliferation, prevention of cell apoptosis, or
 CC induction of signaling molecules or cell markers. The present sequence
 CC represents the human Gas6 protein from the present invention.
 XX Sequence 678 AA;
 SQ
 Query Match 100.0%; Score 72; DB 8; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 15
 DB 284 VPFSVAKSVKSLYL 298
 RESULT 9
 ADM60275
 ID ADM60275 standard; protein; 678 AA.
 XX ADM60275;
 AC 18-NOV-2004 (first entry)
 XX Human growth arrest-specific 6 (GAS6) protein.
 DE angiogenesis modulator; tumorigenesis modulator; angiogenesis; Ax1;
 KW tubulin cofactor D; transglutaminase 2; cytosine deaminase;
 KW peptidase M41; paraplegin; CD13 aminopeptidase; PPK-1; zip kinase; Gas6;
 KW SRm160; non-muscle myosin heavy chain; calmodulin 2; symporter;
 KW semaphorin; zinc finger helicase; plexin-A2; deoxycytidylate deaminase;
 KW sugar transporter; tumorigenesis; antiangiogenic; cytostatic;
 KW cerebroprotective; vasotropic; antiinfertility; cardiant;
 KW antibody therapy; antisense therapy; RNA interference therapy;
 KW RNAi therapy; cancer; stroke; infertility; heart disease; human.
 XX Homo sapiens.
 OS WO2004039955-A2.
 XX

XX growth arrest specific gene 6; Gas6; epitope tag; variant Gas6;
 KW anti-apoptotic; Gas6 inhibitor; Gas6-dependent receptor phosphorylation;
 KW receptor internalisation; cell proliferation; cell apoptosis prevention;
 KW signaling molecule; cell marker; human.
 OS Homo sapiens.
 XX WO2004029209-A2.
 PN XX
 PD 08-APR-2004.
 XX
 PF 24-SEP-2003; 2003WO-US030330.
 XX
 PR 24-SEP-2002; 2002US-0413157P.
 XX
 XX (CENZ) CENTOCOR INC.
 PA Yang J, Chen C, Hu B, Andrade-Gordon P, Jordan R;
 XX WPI; 2004-316097/29.
 DR
 XX New epitope-tagged Growth Arrest Specific Gene 6 (Gas6) proteins for
 PT manufacturing medicines or for identifying inhibitors of Gas6 and its
 PT receptors.
 XX
 PS Claim 2; SEQ ID NO 1; 28pp; English.
 XX
 CC The present invention describes an isolated growth arrest specific gene 6
 CC (Gas6) polypeptide, or its variant, with an epitope tag fused at the C-
 CC terminus. The epitope tag comprises a Flag sequence of 8 amino acids (SEQ
 CC ID NO:2, AWM40824), or a polyhistidine sequence. The variant Gas6
 CC polypeptide has 75% identity to native human Gas6 protein. Also
 CC described: (1) a recombinant DNA molecule encoding the amino acid
 CC sequence of the polypeptide described above; (2) a vector comprising the
 CC above nucleic acid; (3) a host cell comprising the vector, where the host
 CC cell is of mammalian origin; and (4) a composition comprising the
 CC polypeptide and a pharmaceutical carrier. Gas6 has anti-apoptotic
 CC activity. The composition is useful for manufacturing medicines or for
 CC identifying inhibitors of Gas6 and its receptors. The Gas6 polypeptide
 CC may also be used for Gas6-dependent receptor phosphorylation, receptor
 CC internalisation, cell proliferation, prevention of cell apoptosis, or
 CC induction of signaling molecules or cell markers. The present sequence
 CC represents the human Gas6 protein with an epitope tag fused at the C-
 CC terminus, from the present invention.
 XX
 SQ Sequence 686 AA;

Query Match 100.0%; Score 72; DB 8; Length 686;
 Best Local Similarity 100.0%; Pred. No. 0.00033;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 284 VPFSVAKSVKSLYL 298
 |||||

RESULT 12
 AA46462
 ID AA46462 standard; protein; 673 AA.
 XX
 AC AA46462;
 XX
 DT 15-MAY-1998 (first entry)
 XX
 DE Murine growth arrest specific-gene 6 (gas6) protein.
 XX
 KW Growth arrest specific-gene 6; gas6; Rsa; Axl; receptor; mitogenic agent;
 KW receptor tyrosine kinase; regulation; protease cascade; insulin;
 KW growth regulation; serum-free culture medium; human; Schwann cell;
 KW receptor activator; erbB receptor; heregulin; CAMP level; proliferation;
 KW treatment; nervous system injury.

OS Mus sp.
 XX US5714385-A.
 XX
 PD 03-FEB-1998.
 XX
 PF 10-MAY-1995; 95US-00435434.
 XX
 PR 10-MAY-1995; 95US-00435434.
 XX
 PA (GETH) GENENTECH INC.
 XX Chen J, Mather JP, Li R;
 PI WPI; 1998-129864/12.
 DR
 XX Medium for culturing human Schwann cells - is serum-free and contains Rse
 PT receptor activator and other mitogens.
 XX
 PS Disclosure; Fig 2; 51pp; English.
 XX
 CC The present sequence represents a murine growth arrest specific-gene 6
 CC (gas6) protein which is able to activate the Rsa and Axl receptor. Rse is
 CC a receptor tyrosine kinase that is preferentially expressed in the adult
 CC brain. Gas6 is a vitamin K dependent protein which may play a role in the
 CC regulation of a protease cascade relevant in growth regulation. The
 CC protein is used in a serum-free culture medium for culturing human
 CC Schwann cells, which does not support fibroblast growth. Gas6 functions
 CC as a mitogenic agent which is a Rse/Axl receptor activator. A second
 CC mitogenic agent e.g. insulin or an erbB receptor activator such as
 CC heregulin, is also required to raise CAMP levels and enhance survival or
 CC proliferation of human Schwann cells. The culture medium additionally
 CC comprises a molecule or composition that provides Fe ions to the Schwann
 CC cells, vitamin E, a protease inhibitor, and progesterone. The Schwann
 CC cells can be used to treat patients with nervous system injuries
 XX
 SQ Sequence 673 AA;

Query Match 95.8%; Score 69; DB 2; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 281 VPFSVAKSVKSLYL 295
 |||||

RESULT 13
 AA29793
 ID AA29793 standard; protein; 673 AA.
 XX
 AC AA29793;
 XX
 DT 15-NOV-1999 (first entry)
 XX
 DE Murine growth arrest-specific gene 6 protein.
 XX
 KW Rse receptor protein tyrosine kinase; Rse ligand; Rse-L; gas6;
 KW growth arrest-specific gene 6; proliferation; differentiation;
 KW glial cell; Schwann cell; fusion protein.
 XX
 OS Mus sp.
 XX US5955420-A.
 PN
 PD 21-SEP-1999.
 XX
 PF 10-MAY-1995; 95US-00438864.
 XX
 PR 10-MAR-1995; 95US-00402253.
 XX
 PA (GETH) GENENTECH INC.
 XX

PI Mark MR, Mather JP, Li R, Chen J, Hammonds RG, Godowski PJ;
 XX WPI: 1999-539585/45.
 XX
 XX Activation of the Rse receptor on a cell, useful for promoting cell
 PT proliferation and differentiation.
 XX
 XX Disclosure; Fig 2; 48pp; English.
 XX
 XX A method has been developed for activating the Rse receptor on a cell.
 CC The method comprises exposing the receptor to the exogenous growth arrest
 CC -specific gene 6 (gas6) polypeptide. The method is useful for enhancing
 CC cell proliferation and cell differentiation. The present sequence
 CC represents murine gas6 given in the present invention
 XX
 XX Sequence 673 AA;
 SQ

Query Match 95.8%; Score 69; DB 2; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 14
 AAB33459
 ID AAB33459 standard; protein; 673 AA.
 XX
 XX AAB33459;
 AC
 XX
 DT 29-JAN-2001 (first entry)
 XX
 XX Human PRO21 protein UNQ21 SEQ ID NO:231.
 DE
 XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; anti rheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW aniaemetic; hepatotropic; virucide; antiporiatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopaenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; Gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200053758-A2.
 FN
 XX
 XX 14-SEP-2000.
 PD
 XX
 XX 02-MAR-2000; 2000WO-US005841.
 PF
 XX
 XX 08-MAR-1999; 99WO-US005028.
 PR
 XX 10-MAR-1999; 99US-0123618P.
 PR
 XX 12-MAR-1999; 99US-0123957P.
 PR
 XX 23-MAR-1999; 99US-0125775P.
 PR
 XX 12-APR-1999; 99US-0128849P.
 PR
 XX 20-APR-1999; 99WO-US008615.
 PR
 XX 28-APR-1999; 99US-0131445P.
 PR
 XX 04-MAY-1999; 99US-0132371P.
 PR
 XX 14-MAY-1999; 99US-0134287P.
 PR
 XX 02-JUN-1999; 99WO-US012252.
 PR
 XX 23-JUN-1999; 99US-0141037P.
 PR
 XX 20-JUL-1999; 99US-0144758P.
 PR
 XX 26-JUL-1999; 99US-0145698P.
 PR
 XX 28-JUL-1999; 99US-0146222P.

PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-OCT-1999; 99US-0162506P.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 30-NOV-1999; 99WO-US028409.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000277.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US0003565.
 PR 18-FEB-2000; 2000WO-US0004341.
 PR 18-FEB-2000; 2000WO-US0004342.
 PR 22-FEB-2000; 2000WO-US0004414.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff JC, Lu Y, Fan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 XX WPI: 2000-572271/53.
 DR N-PSDB; AAC58624.
 DR
 XX

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
 Claim 33; Fig 92; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58397 to AAC58578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention

SQ Sequence 673 AA;

Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VPFSVAKSVKSLYLIG 15
 Db 281 VPFSMAKSVKSLYLIG 295
 ||||:|||||||

RESULT 15

AAY57382
 ID AAY57382 standard; protein; 673 AA.
 AC AAY57382;
 XX 19-JUN-2000 (first entry)
 DT
 XX Amino acid sequence of murine gas6 (m gas6) protein.
 DE
 XX Nervous system; Schwann cell; mitogen; Res/Axl receptor activator;
 KW central nervous system; peripheral nervous system; injury; trauma;
 KW nutritional deficiency; systemic disease; toxin; demyelination; gas6;
 KW protein S.
 XX
 OS Mus sp.
 XX
 PN US6033660-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 10-MAY-1995; 95US-00438862.
 XX
 PR 10-MAY-1995; 95US-00438862.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Mather JP, Chen J, Li R;
 XX
 DR WPI; 2000-246046/21.
 XX
 PT Repairing nervous system injuries in mammals, by administering human
 PT Schwann cells that have been propagated in medium supplemented with
 PT mitogens.
 XX
 PS Disclosure; Fig 2; 52pp; English.
 XX
 CC The invention relates to a method for treating nervous system injuries in
 CC mammals by administering human Schwann cells (SC) that have been cultured
 CC in serum-free medium. The serum-free medium is a nutrient solution
 CC supplemented with two mitogens, one of which, is a Res/Axl receptor
 CC activator, to increase survival and proliferation of SC. The method is
 CC used to treat (or prevent) central or peripheral nervous system injury,
 CC e.g. traumatic, ischemic, malignant, infectious or degenerative lesions,
 CC or lesions associated with nutritional deficiencies, systemic disease,
 CC toxins or demyelination. Culturing cells in the specified medium allows
 CC proliferation of adult SC for use in autologous transplants. The present
 CC sequence represents a murine gas6 (m gas6) protein, having 43% sequence
 CC identity to human protein S. Gas6 is demonstrated to be a potent growth/
 CC survival factor for SCs in defined serum-free culture
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 3; Length 673;
 Best Local Similarity 93.3%; Pred No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 VPFSVAKSVKSLYL 15
 Db 281 VPFSVAKSVKSLYL 295
 RESULT 16
 ABB84840
 ID ABB84840 standard; protein; 673 AA.
 XX
 AC ABB84840;
 XX
 DT 16-MAY-2002 (first entry)
 XX
 DE Human PRO21 protein sequence SEQ ID NO:48.
 KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
 KW

KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 KW age-related macular degeneration; arterial restenosis; angina;
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 KW wound healing; chromosome mapping; gene mapping.
 XX
 OS Homo sapiens.
 XX
 PN WO200200690-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 20-JUN-2001; 2001WO-US019692.
 XX
 PR 23-JUN-2000; 2000US-0213637P.
 PR 20-JUL-2000; 2000US-0219556P.
 PR 25-JUL-2000; 2000US-0220624P.
 PR 25-JUL-2000; 2000US-0220664P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 02-AUG-2000; 2000US-0222695P.
 PR 17-AUG-2000; 2000US-00643657.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 07-SEP-2000; 2000US-0230978P.
 PR 18-SEP-2000; 2000US-00664610.
 PR 24-OCT-2000; 2000US-0242922P.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 22-JAN-2001; 2001US-00767609.
 PR 28-FEB-2001; 2001US-00796498.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 09-MAR-2001; 2001US-00802706.
 PR 14-MAR-2001; 2001US-00808689.
 PR 22-MAR-2001; 2001US-00816744.
 PR 05-APR-2001; 2001US-00828366.
 PR 10-MAY-2001; 2001US-00854208.
 PR 10-MAY-2001; 2001US-00854280.
 PR 25-MAY-2001; 2001US-00866028.
 PR 25-MAY-2001; 2001US-00866034.
 PR 25-MAY-2001; 2001WO-US017092.
 PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-090516/12.
 DR N-PSDB; ABL88095.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides;
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal.
 XX
 PS Claim 11; Fig 48; 565pp; English.
 XX
 CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,

CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL8259 to ABL8267 represent primers and probes used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 673 AA;

Query Match 95.8%; Score 69; DB 5; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 ||||:|||||||
 Db 281 VPFSMAKSVKSLYL 295

RESULT 17
 ABB95446
 ID ABB95446 standard; protein; 673 AA.

XX AC ABB95446;
 XX DT 19-JUL-2002 (first entry)
 XX DE Human angiogenesis related protein PRO21 SEQ ID NO: 48.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiatic; cytotatic; antiangiogenic; hypotensive; vulnerary;
 KW antiarteriosclerotic.

XX OS Homo sapiens.

XX PN WO200208284-A2.

XX PD 31-JAN-2002.

XX PF 09-JUL-2001; 2001WO-US021735.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 28-JUL-2000; 2000WO-US020710.

XX PR 02-AUG-2000; 2000US-0222699P.

XX PR 17-AUG-2000; 2000US-00643657.

XX PR 23-AUG-2000; 2000WO-US023522.

XX PR 24-AUG-2000; 2000WO-US023328.

XX PR 07-SEP-2000; 2000US-0230978P.

XX PR 18-SEP-2000; 2000US-00664610.

XX PR 18-SEP-2000; 2000US-00665350.

XX PR 24-OCT-2000; 2000US-0242922P.

XX PR 08-NOV-2000; 2000US-00709238.

XX PR 08-NOV-2000; 2000WO-US030952.

XX PR 10-NOV-2000; 2000WO-US030873.

XX PR 01-DEC-2000; 2000WO-US032678.

XX PR 20-DEC-2000; 2000US-00747259.

XX PR 20-DEC-2000; 2000WO-US034956.

XX PR 22-JAN-2001; 2001US-00767609.

PR 30-MAY-2001; 2001US-00870574.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.

XX (GETH) GENENTECH INC.

PA (BAKE/) BAKER K P.

PA (FERR/) FERRARA N.

PA (GERB/) GERBER H.

PA (GERR/) GERRITSEN M E.

PA (GODD/) GODDARD A.

PA (GODO/) GODOWSKI P J.

PA (GURN/) GURNEY A L.

PA (HILL/) HILLAN K J.

PA (MARS/) MARSTERS S A.

PA (PANJ/) PAN J.

PA (PAON/) PAONI N F.

PA (STEP/) STEPHAN J F.

PA (WATA/) WATANABE C K.

PA (WILL/) WILLIAMS P M.

PA (WOOD/) WOOD W I.

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX WPI: 2002-171999/22.

DR N-PSDB; ABL95584.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 48; 567pp; English.

XX The present invention provides the protein and coding sequences of human

XX PRO proteins. These are useful for treating or diagnosing a

XX cardiovascular, endothelial or angiogenic disorder, including cardiac

XX hypertrophy, trauma, cancer, age-related macular degeneration,

XX atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,

XX angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

XX angiogenesis (such as breast carcinoma and liver carcinoma) and wound

XX healing. The present sequence is a PRO protein of the invention

XX Sequence 673 AA;

Query Match 95.8%; Score 69; DB 5; Length 673;

Best Local Similarity 93.3%; Pred. No. 0.0011;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 15
 ||||:|||||||
 Db 281 VPFSMAKSVKSLYL 295

RESULT 18
 ADD10337
 ID ADD10337 standard; protein; 673 AA.

XX AC ADD10337;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted/transmembrane PRO polypeptide #24.

XX human; secreted protein; transmembrane protein; cardiovascular disorder;

XX endothelial disorder; angiogenic disorder; myocardial infarction;

XX cardiac hypertrophy; trauma; cancer; age-related macular degeneration;

XX angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;

XX endothelial cell tube formation.

XX OS Homo sapiens.

PN US2003105011-A1.
 XX
 PD
 XX
 PF 05-JUN-2003.
 XX
 PF 16-AUG-2002; 2002US-00223084.
 XX
 PR 15-SEP-2000; 2000US-0232887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2003-810831/76.
 DR N-PSDB; ADD10336.
 DR
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 PT
 XX Claim 11; SEQ ID NO 48; 493pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 7; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLGL 15
 Db 281 VPFSMAKSVKSLYLGL 295
 ||||:|||||||
 ||||:|||||||
 RESULT 19
 ADD11297
 ID ADD11297 standard; protein; 673 AA.
 XX
 XX AC ADD11297;
 XX
 XX DT 01-JAN-2004 (first entry)
 XX
 XX DE Human secreted/transmembrane PRO polypeptide #24.
 XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003105013-A1.
 PN

XX 05-JUN-2003.
 XX
 PF 16-AUG-2002; 2002US-00223090.
 XX
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 XX (GETH) GENENTECH INC.
 PA
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2003-801242/75.
 DR N-PSDB; ADD11296.
 DR
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, useful for treating a cardiovascular, endothelial, or
 PT angiogenic disorder in a mammal, such as cancer or age-related macular
 PT degeneration.
 PT
 XX Claim 11; SEQ ID NO 48; 493pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 7; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYLGL 15
 Db 281 VPFSMAKSVKSLYLGL 295
 ||||:|||||||
 ||||:|||||||
 RESULT 20
 ADD37090
 ID ADD37090 standard; protein; 673 AA.
 XX
 XX AC ADD37090;
 XX
 XX DT 15-JAN-2004 (first entry)
 XX
 XX DE Human secreted/transmembrane PRO polypeptide #24.
 XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX
 OS Homo sapiens.
 XX
 XX US2003105012-A1.
 PN

PD 05-JUN-2003.
XX 16-AUG-2002; 2002US-00223088.
XX 15-SEP-2000; 2000US-0232887P.
XX 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
PI WPI; 2003-829354/77.
DR N-PSDB; ADD37089.
XX New isolated nucleic acids encoding a secreted and transmembrane
PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
PT disorder in a mammal, such as cancer or age-related macular degeneration.
XX Claim 11; SEQ ID NO 48; 492pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX Sequence 673 AA;
SQ Query Match 95.8%; Score 69; DB 7; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295
RESULT 21
ADE41298
ID ADE41298 standard; protein; 673 AA.
XX ADE41298;
AC ADE41298;
DT 29-JAN-2004 (first entry)
XX Human secreted/transmembrane PRO polypeptide #24.
XX human; secreted protein; transmembrane protein; cardiovascular disorder;
KW endothelial disorder; angiogenic disorder; myocardial infarction;
KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
KW endothelial cell tube formation.
OS Homo sapiens.
XX US2003100497-A1.
XX 29-MAY-2003.
PD

XX 16-AUG-2002; 2002US-00223085.
XX 20-JUN-2001; 2001WO-US019692.
PR 09-JUL-2001; 2001WO-US021735.
PR 20-FEB-2002; 2002US-00081056.
XX (GETH) GENENTECH INC.
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
PI Watanabe CK, Williams PM, Wood WI, Ye W;
PI WPI; 2004-008957/01.
DR N-PSDB; ADE41297.
XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO205 or
PT PRO214, useful in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and for treating disorders involving
PT angiogenesis.
XX Claim 11; SEQ ID NO 48; 492pp; English.
XX The invention relates to an isolated nucleic acid encoding a secreted and
CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
CC by the nucleic acid, or an agonist or antagonist, is used to treat a
CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
CC preferably a human. The human may have suffered a myocardial infarction
CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
CC degeneration. The cardiac hypertrophy is characterised by the presence of
CC an elevated level of PGP-2 alpha. A PRO polypeptide, given in the
CC specification, or an agonist is used to inhibit or stimulate endothelial
CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.
XX Sequence 673 AA;
SQ Query Match 95.8%; Score 69; DB 8; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.0011;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYL 15
Db 281 VPFSMAKSVKSLYL 295
RESULT 22
ADH43481
ID ADH43481 standard; protein; 673 AA.
XX ADH43481;
AC ADH43481;
DT 25-MAR-2004 (first entry)
XX Human PRO polypeptide #24.
XX Human; PRO; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
KW cell apoptosis; cell tube formation; angiogenesis;
KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
KW age-related macular degeneration; cytostatic; cardiant;
KW cerebroprotective; ophthalmological; vulnary.
OS Homo sapiens.
XX US2003224984-A1.
XX 04-DEC-2003.
PD

XX 26-NOV-2002; 2002US-00305654.
 XX 20-JUN-2001; 2001WO-US019692.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A; Paoni NP;
 PI Godowski PJ, Gurney AL, Hillan KU, Marsters SA, Pan J, Ye W;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI: 2004-042166/04.
 DR N-PSDB; ADH43480.
 XX
 XX New PRO polypeptides and nucleic acids encoding the polypeptides, useful
 PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
 PT or age-related macular degeneration.
 XX
 XX Claim 11; SEQ ID NO 48; 492pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the PRO
 CC polynucleotides encoding them. The invention also relates to treating
 CC cardiovascular, endothelial or angiogenic disorders in mammals,
 CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
 CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
 CC stimulating angiogenesis or smooth muscle cell growth by administering
 CC polypeptides of the invention. The PRO polypeptides and polynucleotides
 CC are useful for treating cardiovascular, endothelial or angiogenic
 CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
 CC cancer or age-related macular degeneration. The PRO polynucleotides are
 CC useful as hybridisation probes in chromosome and gene mapping and in
 CC generating antisense RNA and DNA, and for chromosome identification and
 CC tissue typing. The PRO polypeptides and polynucleotides are also useful
 CC in gene therapy and as molecular weight markers for protein
 CC electrophoresis purposes. This sequence represents a human PRO
 CC polypeptide of the invention.
 XX
 SQ Sequence 673 AA;
 Query Match 95.8%; Score 69; DB 8; Length 673;
 Best Local Similarity 93.3%; Pred. No. 0.0011;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSAKSVKSLYL 15
 DB 281 VPFSAKSVKSLYL 295
 RESULT 23
 ID ADK82826
 XX ADK82826 standard; protein; 673 AA..
 AC ADK82826;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human PRO polypeptide #24.
 XX
 KW Human; PRO; cardiovascular disorder; endothelial disorder;
 KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
 KW cell apoptosis; cell tube formation; angiogenesis;
 KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
 KW age-related macular degeneration; cytostatic; cardiant;
 KW cerebroprotective; ophthalmological; vulnary.
 XX
 OS Homo sapiens.
 XX
 XX US2004043927-A1.
 XX
 XX 04-MAR-2004.
 XX
 XX 20-FEB-2002; 2002US-00081056.
 XX

PR 19-SEP-1997; 97US-00333821.
 PR 29-JAN-1998; 98US-00015089.
 PR 10-SEP-1998; 98WO-US018824.
 PR 14-SEP-1998; 98WO-US019177.
 PR 16-SEP-1998; 98WO-US019330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 19-NOV-1998; 98US-00180997.
 PR 01-DEC-1998; 98WO-US025108.
 PR 22-DEC-1998; 98US-00218517.
 PR 05-JAN-1999; 99WO-US000106.
 PR 12-FEB-1999; 99US-00214186.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 09-MAR-1999; 99US-00254460.
 PR 12-MAR-1999; 99US-00267213.
 PR 12-APR-1999; 99WO-US0284291.
 PR 02-JUN-1999; 99WO-US012252.
 PR 14-JUN-1999; 99US-00332928.
 PR 14-JUN-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 01-SEP-1999; 99WO-US020111.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 15-OCT-1999; 99US-00403154.
 PR 18-OCT-1999; 99US-00403296.
 PR 18-OCT-1999; 99US-00403297.
 PR 10-NOV-1999; 99US-00423741.
 PR 12-NOV-1999; 99US-00423843.
 PR 29-NOV-1999; 99US-00423844.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 02-DEC-1999; 99WO-US028551.
 PR 02-DEC-1999; 99WO-US028564.
 PR 16-DEC-1999; 99WO-US028565.
 PR 20-DEC-1999; 99WO-US030095.
 PR 30-DEC-1999; 99WO-US030999.
 PR 30-DEC-1999; 99WO-US031243.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 05-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 01-MAR-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005601.
 PR 10-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006319.
 PR 20-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000WO-US007532.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00864610.
 PR 18-SEP-2000; 2000US-00663550.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 28-FEB-2001; 2001US-00796498.

CC leukaemia. These may also be used in screening for agents that modulate
 CC cancer. The present sequence is a mouse CAP protein sequence. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 703 AA;
 Query Match 95.8%; Score 69; DB 8; Length 703;
 Best Local Similarity 93.3%; Pred. NO. 0.0012;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 15
 Db 314 VPFSVAKSVKSLYL 328
 RESULT 25
 ID ADC94783 standard; protein; 77 AA.
 XX AC ADC94783;
 XX AC
 DT 01-JAN-2004 (first entry)
 XX
 DE E. faecium protein sequence SEQ ID 4410.
 XX
 KW Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
 KW abdominal-pelvic infection.
 XX
 OS Enterococcus faecium.
 XX
 PN US6583275-B1.
 XX
 PD 24-JUN-2003.
 XX
 PF 30-JUN-1998; 98US-00107532.
 XX
 PR 02-JUL-1997; 97US-0051571P.
 PR 14-MAY-1998; 98US-0085598P.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Doucette-Stamm LA, Bush D;
 XX
 DR WPI; 2003-799836/75.
 DR N-PSDB; ADC91129.
 XX
 PT New isolated nucleic acid derived from Enterococcus faecium encoding an
 PT Enterococcus faecium polypeptide useful for detection, prevention and
 PT treatment of a pathological condition resulting from a bacterial
 PT infection.
 XX
 PS Example 1; SEQ ID NO 4410; 243pp; English.
 XX
 CC The invention relates to an isolated nucleic acid derived from
 CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
 CC one of 10 fully defined sequences given in the (or comprising 40
 CC sequential nucleotides chosen from any of the nucleic acids, its
 CC complement or sequences hybridising to it). Also included are a
 CC recombinant vector comprising the nucleic acid operably linked to
 CC transcription regulatory element, a cell comprising the vector and a
 CC single-stranded probe comprising the nucleic acid. The nucleic acids are
 CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
 CC The nucleic acids are useful for diagnosing pathological conditions
 CC resulting from E. faecium bacterial infection (e.g. urinary tract
 CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
 CC infection) and for screening drugs such as agonists and antagonists. The
 CC nucleic acid is useful for recombinant production of Candida albicans -
 CC derived peptides or antisense polypeptides. Pharmaceutical compositions
 CC and vaccines containing the nucleic acid are useful for preventing or
 CC treating Enterococcus faecium infections. The present sequence represents
 CC one if the disclosed E. faecium proteins.

XX SQ Sequence 77 AA;
 Query Match 61.1%; Score 44; DB 7; Length 77;
 Best Local Similarity 57.1%; Pred. No. 4;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 14
 Db 44 IPISIAKKEVILYL 57
 RESULT 26
 ID AAU03812 standard; protein; 374 AA.
 XX AC AAU03812;
 XX AC
 DT 12-SEP-2001 (first entry)
 XX
 DE G protein-coupled receptor-like (GPCR-like) receptor protein #11.
 XX
 KW G protein-coupled receptor-like receptor; GPCR-like receptor; helminth;
 KW endoparasite; ectoparasite; invertebrate; insect; neurological disorder;
 KW neuromuscular disorder; human; nematode; lobster; locust; mollusc; leech;
 KW fruitfly.
 XX
 OS Homo sapiens.
 XX
 PN WO200138533-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 24-NOV-2000; 2000WO-US032225.
 XX
 PR 24-NOV-1999; 99US-0167523P.
 XX
 PA (PHAA) PHARMACIA & UPJOHN.
 XX
 PI Lowery DE, Geary TG, Kubiak TM, Larsen MJ;
 XX
 DR WPI; 2001-343952/36.
 DR N-PSDB; AAS07211.
 XX
 PT Using G-protein-coupled receptor (GPCR)-like receptors to identify
 PT candidate compounds for the treatment and prevention of invertebrate
 PT parasites, especially helminths and insects.
 XX
 PS Claim 6; Page 121-122; 219pp; English.
 XX
 CC The sequence represents a G protein-coupled receptor-like (GPCR-like)
 CC receptor protein. GPCR-like receptors and their associated nucleic acids
 CC may be used to identify candidate compounds for their ability to modulate
 CC the activity of GPCRs. The sequences therefore are useful for treating
 CC and preventing infection by endoparasitic and ectoparasitic invertebrate
 CC parasites, especially helminths and insects, and particularly ailments
 CC related to aberrant neurological and neuromuscular function
 XX
 SQ Sequence 374 AA;
 Query Match 61.1%; Score 44; DB 4; Length 374;
 Best Local Similarity 61.5%; Pred. No. 23;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 13
 Db 142 LPFAIAASVNSLY 154
 RESULT 27
 ID ADN23180 standard; protein; 374 AA.
 XX

AC ADN23180;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #5833.
DE
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 5833; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 374 AA;
XX
XX Query Match 61.1%; Score 44; DB 8; Length 374;
XX Best Local Similarity 61.5%; Pred. No. 23;
XX Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 VPFSVAKSVKSLY 13
XX :||:::| |||||
XX

Db 142 LPFAIAASVNSLY 154
RESULT 28
ADD31762
ID ADD31762 standard; protein; 291 AA.
XX
XX ADD31762;
XX AC
XX 15-JAN-2004 (first entry)
XX
XX Enterobacter cloacae beta-lactamase amino acid sequence SEQ ID NO:1.
DE recombination product; synthetic gene technology; beta-lactamase.
XX
XX Synthetic.
OS Enterobacter cloacae.
OS
XX WO2003064611-A2.
XX
XX 07-AUG-2003.
XX
XX 29-JAN-2003; 2003WO-US002612.
XX
XX 30-JAN-2002; 2002US-00062188.
XX
XX (EGEA-) EGEA BIOSCIENCES INC.
XX
XX Evans GA;
XX
XX WPI; 2003-663477/62.
XX
XX Creating recombination products between two distinct nucleotide
PT sequences, useful in the field of synthetic gene technology, and in
PT assembling a library, or a population or a collection of polypeptide
PT variants.
XX
XX Example 1; SEQ ID NO 1; 132pp; English.
XX
XX The present invention describes a method for creating a collection of
CC recombination products between two nucleotide sequences. The method
CC comprises combining an initial set of oligonucleotides corresponding to a
CC first nucleotide sequence with a subsequent set of oligonucleotides
CC corresponding to a distinct nucleotide sequence and further combining the
CC initial and subsequent sets of combination oligonucleotides having a
CC sequence region corresponding to the initial nucleotide sequence and a
CC sequence region corresponding to the second oligonucleotide sequence.
CC Also described is a method of creating a collection of recombination
CC products between two genes. The methods and compositions of the present
CC invention are useful in the field of synthetic gene technology, and more
CC specifically, to generating a collection of recombination products
CC between distinct nucleotide sequences. They can also be used in
CC assembling a library, or a population or a collection of polypeptide
CC variants that correspond to single or multiple polynucleotide
CC recombination products. The present sequence is used in the
CC exemplification of the present invention.
XX
XX SQ Sequence 291 AA;
XX
XX Query Match 58.3%; Score 42; DB 7; Length 291;
XX Best Local Similarity 64.3%; Pred. No. 41;
XX Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX 2 PFSVAKSVKSLYLG 15
XX :||:::| |||||
XX
XX 184 PAAVAKSLKTLALG 197
XX
XX RESULT 29
XX ADN07100
XX ID ADN07100 standard; protein; 1220 AA.
XX
XX AC ADN07100;

XX 17-JUN-2004 (first entry)
 XX S. cerevisiae histidine kinase Slnp protein.
 XX Histidine kinase; fungal infection; antifungal drug; yeast; Slnp.
 KW Saccharomyces cerevisiae.
 OS
 XX Key Location/Qualifiers
 FH Region 556..703
 FT /note="H-box"
 FT Binding-site 859..920
 FT /note="ATP-binding domain"
 FT Region 1081..1207
 FT /note="D-box"
 XX US6716625-B1.
 XX 06-APR-2004.
 XX 09-AUG-2000; 2000US-00636728.
 XX 16-APR-1997; 97US-00843530.
 XX 22-JUN-1999; 99US-00338156.
 XX (SELI/) SELITRENNIKOFF C.
 XX (POTT/) POTT G.
 XX Selitrennikoff C, Pott G;
 XX WPI; 2004-303092/28.
 XX New fungal histidine kinase polypeptides and nucleic acids, e.g. FOS-1 or
 PT COS-1, useful for eradicating, mitigating or preventing fungal
 PT infections, and in identifying antifungal drugs.
 XX Example 10; SEQ ID NO 32; 124pp; English.
 XX The invention relates to histidine kinases of Aspergillus and other
 CC fungal species and their corresponding nucleic acid sequences. The
 CC histidine kinase polypeptides and nucleic acids are useful for
 CC eradicating, mitigating or preventing fungal infections and in
 CC identifying antifungal drugs. The present sequence is saccharomyces
 CC cerevisiae histidine kinase Slnp protein. This sequence is used in the
 CC exemplification of the invention.
 XX Sequence 1220 AA;
 SQ
 Query Match 58.3%; Score 42; DB 8; Length 1220;
 Best Local Similarity 81.8%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKS 11
 DB 955 VKFSVAKSIKS 965
 RESULT 30
 ADS43652
 ID ADS43652 standard; protein; 1220 AA.
 XX AC
 XX ADS43652;
 XX 02-DEC-2004 (first entry)
 XX Bacterial polypeptide #22082.
 XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX Bacteria.
 XX US2003233675-A1.
 XX 18-DEC-2003.
 XX 20-FEB-2003; 2003US-00369493.
 XX 21-FEB-2002; 2002US-0360039P.
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 PI WPI; 2004-061375/06.
 DR
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 XX Claim 1; SEQ ID NO 22082; 122pp; English.
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX Sequence 1220 AA;
 SQ
 Query Match 58.3%; Score 42; DB 8; Length 1220;
 Best Local Similarity 81.8%; Pred. No. 2e+02;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKS 11
 DB 955 VKFSVAKSIKS 965
 RESULT 31
 ABB66417
 ID ABB66417 standard; protein; 4345 AA.
 XX AC
 XX ABB66417;
 XX 26-MAR-2002 (first entry)
 XX

DE Drosophila melanogaster polypeptide SEQ ID NO 26043.
XX
KW Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.

OS WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL10520.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX Disclosure; SEQ ID NO 26043; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 4345 AA;

Query Match 58.3%; Score 42; DB 4; Length 4345;
Best Local Similarity 63.6%; Pred. No. 8.4e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSL 12

Db 2115 PFAVAKNIKSI 2125

RESULT 32

ABM67414
ID ABM67414 standard; protein; 364 AA.

XX ABM67414;

XX 20-NOV-2003 (first entry)

XX Photorhabdus luminescens protein sequence #511.

XX Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.

XX Photorhabdus luminescens.

OS WO200294867-A2.

XX 28-NOV-2002.

XX 07-FEB-2002; 2002WO-IB003040.

XX 07-FEB-2001; 2001FR-00001659.

XX (INSP) INST PASTEUR.

PA (CNRS) CNRS CENT NAT RECH SCI.

XX Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;

PI Buchrieser C;

XX WPI; 2003-148459/14.

XX Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.

XX Claim 2; SEQ ID NO 511; 1205pp; French.

XX The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful
CC therapeutically (to treat microbial infection by bacteria or fungi that
CC are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC biopesticides. Other uses of the genes and the proteins are as virulence
CC factors and for identifying targets of human diseases for which P.
CC luminescens is a model (particularly plague and whooping cough). This
CC sequence represents one of the isolated P. luminescens proteins

XX Sequence 364 AA;

Query Match 56.9%; Score 41; DB 6; Length 364;
Best Local Similarity 50.0%; Pred. No. 80;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14

Db 78 VPTRVASAIKIYIL 91

RESULT 33

ADO05107
ID ADO05107 standard; protein; 527 AA.

XX ADO05107;

XX 12-AUG-2004 (first entry)

XX Rift valley fever virus (RVFV) GN surface envelope glycoprotein SeqID 5.
XX virus-like particle; VLP; viral core protein; VCP;
KW viral surface envelope glycoprotein; immunogenic; virucidal; vaccine;
KW infection; HIV; Ebola virus.

XX Rift Valley fever virus.

XX WO2004042001-A2.

XX 21-MAY-2004.

XX 19-MAY-2003; 2003WO-US015930.

XX 17-MAY-2002; 2002US-0381557P.

PR 11-MAR-2003; 2003US-0454115P.

PR 11-MAR-2003; 2003US-0454139P.
 PR 14-MAR-2003; 2003US-0454584P.
 PR 16-MAY-2003; 2003US-0381557P.
 XX
 XX (UYEM-) UNIV EMORY.

XX Compans RW, Yang C, Yao Q, Kang S;
 XX
 XX WPI; 2004-400659/37.

XX New virus-like particles for enhancing immune responses or for treating

PT or preventing viral infections (e.g. HIV), comprises a viral core
 PT protein, a viral surface envelope glycoprotein and, optionally, an
 PT adjuvant molecule.

XX Disclosure; SEQ ID NO 5; 74pp; English.

XX This invention relates to novel virus-like particles (VLPs).
 CC Specifically, it refers to VLPs that comprise a viral core protein (VCP)
 CC that can self-assemble into a VLP core, at least one viral surface
 CC envelope glycoprotein expressed on the surface of the VLP, (where the
 CC viral protein and the viral surface envelope glycoprotein are from
 CC different viruses) and optionally at least one adjuvant molecule
 CC expressed on the surface of the VLP. The present invention describes the
 CC development of immunogenic compositions comprising the VLP and a
 CC pharmaceutical carrier in order to generate an immunological response in
 CC the host or treat an appropriate condition. Accordingly, the methods and
 CC virucidal compositions thereof are useful for enhancing an immune
 CC response (e.g. antibody production, cytotoxic T-cell activity or cytokine
 CC activity) and for developing vaccines to treat and/or prevent viral
 CC infections such as those caused by HIV or Ebola virus. This polypeptide
 CC sequence is a Rift valley fever virus surface envelope glycoprotein of
 CC the invention.

XX Sequence 527 AA;

Query Match 56.9%; Score 41; DB 8; Length 527;
 Best Local Similarity 57.1%; Pred. No. 1.2e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
 |||:|:|:|:|:|:|:
 Db 190 VPFAVFKNSKKVYL 203

RESULT 34

ADO05104
 ID ADO05104 standard; protein; 1067 AA.

XX AC ADO05104;

XX DT 12-AUG-2004 (first entry)

DE Rift valley fever virus (RVFV) surface envelope glycoprotein SeqID 2.

XX virus-like particle; VLP; viral core protein; VCP;
 KW viral surface envelope glycoprotein; immunogenic; virucidal; vaccine;
 KW infection; HIV; Ebola virus.

XX OS Rift valley fever virus.

XX WO2004042001-A2.

XX PD 21-MAY-2004.

XX PF 19-MAY-2003; 2003WO-US015930.

XX PR 17-MAY-2002; 2002US-0381557P.

PR 11-MAR-2003; 2003US-0454115P.

PR 11-MAR-2003; 2003US-0454139P.

PR 14-MAR-2003; 2003US-0454584P.

PR 16-MAY-2003; 2003US-0381557P.

XX

PA (UYEM-) UNIV EMORY.

XX Compans RW, Yang C, Yao Q, Kang S;

XX WPI; 2004-400659/37.

XX New virus-like particles for enhancing immune responses or for treating
 PT or preventing viral infections (e.g. HIV), comprises a viral core
 PT protein, a viral surface envelope glycoprotein and, optionally, an
 PT adjuvant molecule.

XX Disclosure; SEQ ID NO 2; 74pp; English.

XX This invention relates to novel virus-like particles (VLPs).
 CC Specifically, it refers to VLPs that comprise a viral core protein (VCP)
 CC that can self-assemble into a VLP core, at least one viral surface
 CC envelope glycoprotein expressed on the surface of the VLP, (where the
 CC viral protein and the viral surface envelope glycoprotein are from
 CC different viruses) and optionally at least one adjuvant molecule
 CC expressed on the surface of the VLP. The present invention describes the
 CC development of immunogenic compositions comprising the VLP and a
 CC pharmaceutical carrier in order to generate an immunological response in
 CC the host or treat an appropriate condition. Accordingly, the methods and
 CC virucidal compositions thereof are useful for enhancing an immune
 CC response (e.g. antibody production, cytotoxic T-cell activity or cytokine
 CC activity) and for developing vaccines to treat and/or prevent viral
 CC infections such as those caused by HIV or Ebola virus. This polypeptide
 CC sequence is a Rift valley fever virus surface envelope glycoprotein of
 CC the invention.

XX Sequence 1067 AA;

Query Match 56.9%; Score 41; DB 8; Length 1067;
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14

Db 213 VPFAVFKNSKKVYL 226

RESULT 35

ADS43524
 ID ADS43524 standard; protein; 1173 AA.

XX AC ADS43524;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #21954.

XX Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.

XX PN US2003233675-A1.

XX PD 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
PT Claim 1; SEQ ID NO 21954; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1173 AA;

Query Match 56.9%; Score 41; DB 8; Length 1173;
Best Local Similarity 46.2%; Pred. No. 3e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLYL 14
Db 1089 PFSIARQTKSMWI 1101
||||:| |:::|

RESULT 36
AAP60679
ID AAP60679 standard; protein; 1206 AA.
XX AAP60679;
AC
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 22-AUG-1991 (first entry)
XX
DE Sequence of Rift Valley Fever Virus (RVFV) glycoproteins G1 and G2
DE encoded by the M portion of the genome.
XX
XX Vaccine; passive immunotherapy; antibody; immunoassay; diagnosis.
XX
XX Rift Valley fever virus.
XX
XX Key Location/Qualifiers
FH 154..690
FT Protein /label= G2
FT Protein 691..1206
FT /label= G1
XX
XX ZA8407007-A.
XX

PD 13-DEC-1985.
XX
XX 06-SEP-1984; 84ZA-00007007.
XX
PR 09-SEP-1983; 83US-00530887.
PR 23-AUG-1984; 84US-00642781.
XX
XX (MOLE-) MOLECULAR GENETICS INC.
XX
XX Purchio AF, Collett MS;
XX
XX WPI; 1986-088057/13.
DR N-PSDB; AAN60640.
XX
XX Rift valley fever virus vaccine prodn. - by culturing unicellular
PT organism, contg. recombinant vector, having specific DNA sequence coding,
PT and isolating polypeptide.
XX
XX Claim 136; Fig 2; 123pp; English.
XX
XX Glycoproteins G1 and G2 may be used as immunogens in vaccines to protect
CC against RVFV infections in humans or esp. animals, e.g. cattle and sheep.
CC The vaccines are safer than conventional vaccines made from attenuated
CC virus. The polypeptide may also be used to produce antibodies for use in
CC passive immunotherapy or as a diagnostic tool. (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 1206 AA;

Query Match 56.9%; Score 41; DB 1; Length 1206;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPPSVAKSVKSLYL 14
Db 343 VPPFAVFNKKVYL 356
||||:| |:::|

RESULT 37
AAP82995
ID AAP82995 standard; protein; 1206 AA.
XX AAP82995;
AC
XX 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 07-DEC-1990 (first entry)
XX
XX Rift Valley fever virus, M portion.
XX
XX RVFV; Bunyaviridae; M segment; antigen; glycoprotein; vaccine.
XX
XX Rift Valley fever virus.
XX
XX Key Location/Qualifiers
FH 154..634
FT Protein /label= G2
FT /note= "putative N-terminal; 53 kD unglycosylated"
FT Modified-site 438..440
FT /label= putative N-glycosylation site
FT /note= "in centre of G2"
FT Protein 691..1206
FT /label= G2
FT /note= "putative N-terminal; 57 kD unglycosylated"
FT Modified-site 794..796
FT /label= putative N-glycosylation site
FT /note= "in N-terminal of G1"
FT Modified-site 829..831
FT /label= putative N-glycosylation site
FT /note= "in N-terminal of G1"
FT Modified-site 1035..1037
FT /label= putative N-glycosylation site
FT /note= "in C-terminal of G1"
FT

FT Modified-site 1077. .1079
 FT /label= putative N-glycosylation site
 FT /note= "in C-terminal of G1"
 XX
 PN US4735800-A.
 XX
 PD 05-APR-1988.
 XX
 XX 23-AUG-1984; 84US-00642781.
 XX
 XX 09-SEP-1983; 83US-00530887.
 XX
 XX (MOLB-) MOLECULAR GENETICS INC.
 XX
 XX Collett MS, Purchio AF;
 XX
 XX WPI; 1988-112449/16.
 XX
 XX P-PSDB; AAP82995.
 XX
 XX DNA sequences coding for Rift Valley fever virus - useful for prodn. of
 XX polypeptide(s) for assay reagents and vaccines.
 XX
 XX Disclosure; Page ?; -pp; English.
 XX
 CC The sequence is deduced from DNA complementary to the complete medium (M)
 CC RVFV viral RNA. It encodes two glycoproteins, G1 and G2, which are virus-
 CC specific and are located on the outer surface of the viral particles. The
 CC purified proteins have been sequenced only at the N-terminal so that the
 CC positions given in the feature table are estimated for the C-terminals
 CC from the known mol. wts of the non- glycosylated proteins. Both G1 and G2
 CC have strikingly high Cys content (6% for G2 and 5% for G1). There is also
 CC protein coding information between G2 and G1, and prior to the G2 protein
 CC ; the role of these sequences is as yet unknown but they are thought to
 CC be involved in processing and/or transport to and from the Golgi
 CC apparatus where virus maturation occurs. The virus is a member of the
 CC arthropod-borne Bunyaviridae family, primarily affecting cloven-hoofed
 CC animals, but with increasing human involvement. The sequences encoding
 CC the G1 and G2 antigens can be cloned into expression vectors for prodn.
 CC of recombinant proteins which can be used to prepare vaccines against the
 CC infection. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
 CC MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 1206 AA;
 Query Match 56.9%; Score 41; DB 1; Length 1206;
 Best Local Similarity 57.1%; Pred. No. 3.1e+02;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VPFSVAKSVKSLYL 14
 DB 343 VPFAVFNKSKVYL 356
 RESULT 38
 ADP98882
 ID ADP98882 standard; protein; 1235 AA.
 XX
 AC ADP98882;
 XX
 XX 23-SEP-2004 (first entry)
 DT
 DE C. albicans specific gene, orf6.8631, protein sequence.
 XX
 XX Diploid fungal cell; allele; gene disruption cassette;
 KW promoter replacement fragment; antifungal; fungicide; gene therapy;
 KW infection; Candida albicans.
 XX
 XX Candida albicans.
 OS
 XX WO2004056965-A2.
 PN
 XX 08-JUL-2004.

XX 19-DEC-2003; 2003WO-US040618.
 XX
 XX 19-DEC-2002; 2002US-0434832P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX (ELIT-) ELITRA CANADA LTD.
 XX
 XX Roemer T, Jiang B, Boone C, Bussey H;
 XX
 XX WPI; 2004-500296/47.
 DR N-PSDB; ADP98572.
 XX
 XX Constructing a strain of diploid fungal cells in which both alleles of a
 XX gene are modified comprises modifying the alleles of a gene in the fungal
 XX cells by recombination using a gene disruption cassette and a promoter
 XX replacement fragment.
 XX
 XX Claim 44; SEQ ID NO 7057; 163pp; English.
 XX
 CC The invention relates to a novel method for constructing a strain of
 CC diploid fungal cells in which both alleles of a gene are modified. The
 CC method comprises modifying the alleles of a gene in diploid fungal cells
 CC by recombination using a gene disruption cassette and a promoter
 CC replacement fragment. The invention further comprises: assembling a
 CC collection of diploid fungal cells each of which comprises modified
 CC alleles of a different gene; a strain of diploid fungal cells comprising
 CC modified alleles of a gene, where the first allele of the gene is
 CC inactivated by a gene disruption cassette comprising a nucleotide
 CC sequence encoding an expressible selectable marker; and the expression of
 CC the second allele of the gene is regulated by a heterologous promoter
 CC that is operably linked to the coding region of the second allele of the
 CC gene, and where the gene encodes the polypeptide mentioned above; a
 CC collection of diploid fungal strains comprising the diploid strains cited
 CC above, where substantially all the different genes that encode the above
 CC amino acid sequences are modified and are present in different diploid
 CC strains in the collection; a nucleic acid molecule microarray comprising
 CC nucleic acid molecules, where each nucleic acid molecule comprises a
 CC nucleotide sequence that is hybridizable to a target nucleotide sequence
 CC comprising any of the 310 nucleotide sequences listed in the
 CC specification (ADP98516-ADP98825); identifying a gene that is essential
 CC to the survival or growth of a fungus, that contributes to the virulence
 CC and/or pathogenicity of a fungus, or that contributes to the resistance
 CC of a diploid fungus to an antifungal agent; identifying an antifungal
 CC agent that inhibits the growth of a diploid fungus, or a therapeutic
 CC agent for treatment of a mammalian disease; correlating changes in the
 CC levels of proteins or gene transcripts with the inhibition of growth or
 CC proliferation of a diploid fungal cell; a purified or isolated nucleic
 CC acid molecule comprising a nucleotide sequence encoding a gene product
 CC required for proliferation of Candida albicans, where the gene product
 CC consists of any of the above-mentioned amino acid sequences; a vector
 CC comprising a promoter operably linked to the nucleic acid molecule cited
 CC above; a host cell containing the vector; a purified or isolated
 CC polypeptide comprising any of the 61 amino acid sequences given in the
 CC specification (ADP96718-ADP96778); a fusion protein comprising a fragment
 CC of a first polypeptide fused to a second polypeptide, the fragment
 CC consisting of at least 6 consecutive residues of any of ADP98826-ADP99135
 CC ; producing a polypeptide; identifying a compound which modulates the
 CC activity of a gene product encoded by a nucleic acid comprising any of
 CC ADP98516-ADP98825; eliciting an immune response in an animal; a strain of
 CC Candida albicans, where a first allele of a gene comprising any of
 CC ADP98516-ADP98825 is inactive and a second allele of the gene is under
 CC the control of a heterologous promoter; identifying a compound or binding
 CC partner that binds to the polypeptide comprising any of ADP98826-
 CC ADP99135, or its fragment; identifying a compound having the ability to
 CC inhibit growth or proliferation of Candida albicans; inhibiting growth or
 CC proliferation of Candida albicans cells; manufacturing an antimycotic
 CC compound; treating an infection of a subject by Candida albicans;
 CC preventing or containing contamination of an object by Candida albicans,
 CC or for preventing or inhibiting formation on a surface of a biofilm
 CC comprising Candida albicans; a pharmaceutical composition comprising a
 CC therapeutic amount of an agent which reduces the activity or level of a
 CC gene product encoded by a nucleic acid comprising any of ADP98516-

ADP98825 in a pharmaceutical carrier; an antibody preparation which binds the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP9826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicide activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This sequence represents the protein of a Candida albicans fungal specific gene of the invention.

NOTE: This sequence was downloaded from an electronic sequence listing provided on the WIPO website.

XX SQ Sequence 1235 AA;

Query Match 56.9%; Score 41; DB 8; Length 1235;
Best Local Similarity 53.8%; Pred. No. 3.1e+02;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PFSVAKSVKSLYL 14
Db 52 PFNVDKSLQTIYL 64
|||:||||:|

RESULT 39
AAR62504
ID AAR62504 standard; protein; 3457 AA.

XX AC AAR62504;

DT 25-MAR-2003 (revised)
DT 18-MAY-1995 (first entry)

XX DE Large polyprotein sequence of Maize Chlorotic Dwarf Virus.

KW MCDV; maize chlorotic dwarf virus; coat protein; plasmid vector;
KW plant resistance; viral infection resistance; maize plant;
KW maize dwarf mosaic virus; MDV.

XX OS Maize chlorotic dwarf virus.

XX FH Key Location/Qualifiers

FT Region 439..829

FT /note= "antigenic region of cp2"

FT Cleavage-site 896..897

FT /label= dipeptide cleavage site

FT /note= "may be used by animal picornavirus 3C proteases"

FT Peptide 897..1098

FT /note= "putative cp3 region, one of the structural

FT proteins"

FT Peptide 897..911

FT /note= "N-terminus of cp3"

FT Cleavage-site 1098..1099

FT /label= dipeptide cleavage site

FT /note= "may be used by animal picornavirus 3C proteases"

FT Peptide 1099..1113

FT /note= "N-terminus of cp1"

FT Region 1205..1483

FT /note= "antigenic region of cpl"

XX WN WO9421796-A2.

XX 29-SEP-1994.

XX

PF 22-MAR-1994; 94WO-US003028.
XX
XX 24-MAR-1993; 93US-00038768.
XX
XX (PION-) PIONEER HI-BRED INT INC.
PA (USDA) US SEC OF AGRIC.
XX
XX Roth BA, Townsend R, McMullen MD;
XX
XX WPI; 1994-317016/39.
DR N-PSDB; AAQ74694.
XX

XX DNA encoding maize chlorotic dwarf virus proteins - used to provide plants with resistance to the virus and related viral infections.

XX Disclosure; Page 18-32; 40pp; English.

XX This sequence shows the large polyprotein of the Maize Chlorotic Dwarf Virus (MCDV). When cleaved it contains 3 structural proteins, cpl, cp2 and cp3. Depending on the exact location of cp2, the MCDV genome, can encode upto 78 kD of protein 5' of the capsid proteins (for which there are no corresponding animal picornavirus protein). The DNA is used for imparting resistance to MCDV or viruses to which MCDV infection or resistance provides cross-resistance, including maize dwarf mosaic strain A. Any or all of the three coat protein genes from MCDV can be used to provide protection for plants. (Updated on 25-MAR-2003 to correct CC PN field.)

XX SQ Sequence 3457 AA;

Query Match 56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSL 12
Db 1386 VPFSIAKTAKVL 1397
||||:|

RESULT 40

AAR84560
ID AAR84560 standard; protein; 3457 AA.

XX AC AAR84560;

DT 31-MAR-1999 (first entry)

XX DE Polyprotein encoded by the MCDV-T positive strand RNA genome.

KW Maize chlorotic dwarf virus strain Tennessee; MCDV-Tn; MCDV-M1;
KW coat protein; transgenic plant; resistance; MCDV-Tn infection.

XX Maize chlorotic dwarf virus.

XX OS US5866780-A.

XX PD 02-FEB-1999.

XX PF 04-APR-1995; 95US-00416603.

XX PR 04-APR-1995; 95US-00416603.

XX (NOVS) NOVARTIS FINANCE CORP.

XX PA Habera L, Law M, Reddick BB;

XX FI WPI; 1999-142034/12.

XX DR N-PSDB; AAX03390.

XX cDNA of maize chlorotic dwarf virus strain MCDV-Tn - and chimeric genes for producing e.g. MCDV-Tn-resistant transgenic plants.

XX Disclosure; Col 115-132; 73pp; English.

XX The present sequence represents the polyprotein encoded by contiguous
CC sequence of the maize chlorotic dwarf virus strain T (MCDV-T) genome. The
CC specification describes a MCDV strain that is distinct from known MCDV-T
CC and MCDV-M1 isolates, called MCDV Tennessee (MCDV-Tn). The specification
CC also provides the sequences for 3 MCDV-Tn coat proteins, which may be
CC expressed in transgenic plants to confer resistance to MCDV-Tn infection.
XX The coat proteins can also be produced recombinantly

SQ Sequence 3457 AA;
Query Match 56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 9.9e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
|||:|:|
Db 1386 VPFSIAKTAKVL 1397

RESULT 41
ABG08969
ID ABG08969 standard; protein; 174 AA.
XX
AC ABG08969;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #8960.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS73156.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 39328; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 174 AA;
Query Match 55.6%; Score 40; DB 4; Length 174;
Best Local Similarity 53.3%; Pred. No. 53;
Matches 8; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 VPFSVAKSVKSLYLIG 15
:|:|:|:|:|
Db 97 LPFTIAKRIK--YLIG 109

RESULT 42
ABG02533
ID ABG02533 standard; protein; 394 AA.
XX
AC ABG02533;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #2524.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS66720.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID NO 32892; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 394 AA;
Query Match 55.6%; Score 40; DB 4; Length 394;
Best Local Similarity 46.7%; Pred. No. 1.3e+02;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYLIG 15
Db 279 IPTTISEVTSILRG 293
RESULT 43
ABP73632
ID ABP73632 standard; protein; 969 AA.
XX
AC ABP73632;
XX
DT 30-JAN-2003 (first entry)
XX
DE Candida albicans essential protein SEQ ID NO 7469.
XX
DE Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; Candida albicans; fungicide; antifungal.
XX
OS Candida albicans.
XX
PN WO200253728-A2.
XX
PD 11-JUL-2002.
XX
PF 26-DEC-2001; 2001WO-US049486.
XX
PR 29-DEC-2000; 2000US-0259128P.
XX
PR 20-FEB-2001; 2001US-00792024.
XX
PR 22-AUG-2001; 2001US-0314050P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Roemer T, Jiang B, Boone C, Bussey H, Ohlseen KL;
XX
XX WPI; 2002-566694/60.
DR N-PSDB; ABZ32182.
XX
XX Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.
XX
PS Claim 44; SEQ ID NO 7469; 167pp + Sequence Listing; English.
XX
XX The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division

CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of C. albicans cells and for
CC treating infection by C. albicans. The present sequence is that of an
CC essential Candida albicans protein used in the method of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office
XX
SQ Sequence 969 AA;
Query Match 55.6%; Score 40; DB 5; Length 969;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
Qy 1 VPFSVAKSVKSLYLIG 15
Db 792 LPFGVAKESKSELG 806
RESULT 44
AAM89790
ID AAM89790 standard; protein; 64 AA.
XX
AC AAM89790;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:17383.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001354.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.

PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228524P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235835P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241807P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244611P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0245475P.
PR 08-NOV-2000; 2000US-0245476P.
PR 08-NOV-2000; 2000US-0245477P.
PR 08-NOV-2000; 2000US-0245478P.
PR 08-NOV-2000; 2000US-0245523P.
PR 08-NOV-2000; 2000US-0245524P.
PR 08-NOV-2000; 2000US-0245525P.
PR 08-NOV-2000; 2000US-0245526P.
PR 08-NOV-2000; 2000US-0245527P.
PR 08-NOV-2000; 2000US-0245528P.
PR 08-NOV-2000; 2000US-0245532P.
PR 08-NOV-2000; 2000US-0245609P.
PR 08-NOV-2000; 2000US-0245610P.
PR 08-NOV-2000; 2000US-0245611P.
PR 08-NOV-2000; 2000US-0245613P.
PR 17-NOV-2000; 2000US-0245207P.
PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Barash SC, Ruben SM;

XX WPI, 2001-483426/52.

DR N-PSDB; AAK62571.

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.

XX Claim 11; SEQ ID NO 17383; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK67694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention

XX Sequence 64 AA;

Query Match 54.2%; Score 39; DB 4; Length 64;
Best Local Similarity 53.8%; Pred. No. 27;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
||| : : :
Db 29 VPFLLSKKIKSKY 41

RESULT 45

AAB27329
ID AAB27329 standard; protein; 369 AA.

XX AC AAB27329;

XX DT 25-JAN-2001 (first entry)

XX DE N. tabacum NIM1 homologue SEQ ID NO: 74.

XX KW Systemic acquired resistance; SAR; signal transduction cascade;
KW disease resistance; tobacco; tomato; canola; sunflower; sugarbeet;
KW potato.

XX OS Nicotiana tabacum.

XX FN WO200053762-A2.

XX PD 14-SEP-2000.

XX PF 07-MAR-2000; 2000WO-EP001978.

XX PR 09-MAR-1999; 99US-00265149.

XX PA (NOVS) NOVARTIS AG.

XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX PI Salmeron JM, Weislo LJ, Willits MG, Mengiste T;

XX DR WPI; 2000-594322/56.

XX DR N-PSDB; AAA97234.

XX PT Novel plant genes for enhancing systemic acquired resistance gene
PT expression and broad spectrum disease resistance in plants, are homologs
PT of Arabidopsis NIM1 gene.

XX PS Claim 1; Page 151-152; 152pp; English.

XX CC The present invention is concerned with the isolation of NIM1 homologues
CC and their coding sequences from Arabidopsis thaliana, Brassica napus,
CC Nicotiana tabacum, Lycopersicon esculentum, Beta vulgaris, Helianthus
CC annuus and Solanum tuberosum. NIM1 is one of the proteins involved in the
CC signal transduction cascade leading to systemic acquired resistance (SAR)
CC in plants. This gives the plants an increased resistance to disease. The
CC protein and gene can be used to produce transgenic plants resistant to
CC diseases caused by viruses, such as tobacco or cucumber mosaic virus,
CC ringspot virus, pelargonium leaf curl virus, red clover mottle virus,
CC tomato bushy stunt virus, fungi, including Phytophthora parasitica and
CC Peronospora tabacina, bacteria such as Pseudomonas syringae and P.
CC tabaci, insects, including aphids and lepidoptera and nematodes such as
CC Meloidogyne incognita. In particular they can be used against disease
CC organisms of maize

XX SQ Sequence 369 AA;

Query Match 54.2%; Score 39; DB 3; Length 369;
Best Local Similarity 53.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13

Db 237 VPFEVAENIKLIW 249

RESULT 46

ABP04700
ID ABP04700 standard; protein; 120 AA.

XX AC ABP04700;

XX DT 24-JUN-2002 (first entry)

XX DE Human ORFX protein sequence SEQ ID NO:9382.

XX

KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

XX OS Homo sapiens.

XX FN WO200192523-A2.

XX PD 06-DEC-2001.

XX PF 29-MAY-2001; 2001WO-US010836.

XX PR 30-MAY-2000; 2000US-0206132P.

XX PR 29-AUG-2000; 2000US-0228716P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach MD;

XX DR WPI; 2002-106308/14.

XX DR N-PSDB; ABN20452.

XX FI Novel human polypeptides and polynucleotides useful for diagnosing,
FI preventing and treating cardiovascular disease, neurodegenerative,
FI hyperproliferative disorders and autoimmune disorders.

XX PS Disclosure; SEQ ID NO 9382; 1037pp; English.

XX CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification) . ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative diseases, diabetes mellitus, systemic
CC transplantation, cardiovascular diseases, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 120 AA;

Query Match 52.8%; Score 38; DB 5; Length 120;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SVAKSVKSLYLG 15

Db 95 AVSKKDKSLYLG 106

RESULT 47

ABP62898
ID ABP62898 standard; protein; 133 AA.

XX

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 08:53:50 ; Search time 4.03846 Seconds
(without alignments)
357.377 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYL 15

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	678	2 B48089	growth arrest-spec
2	69	95.8	673	2 A48089	growth arrest-spec
3	69	95.8	674	2 I55476	growth potentiatin
4	44	61.1	374	2 S28285	hypothetical prote
5	42	58.3	252	2 H72469	hypothetical prote
6	42	58.3	292	2 S35915	beta-lactamase (EC
7	42	58.3	1220	2 S48387	SLN1 protein - yea
8	41	56.9	354	2 C64352	hypothetical prote
9	41	56.9	1173	2 S48877	Ca2+-transporting
10	41	56.9	1197	1 VGVURF	M polyprotein - Ri
11	41	56.9	1206	1 VGVURV	M polyprotein - Ri
12	40	55.6	250	2 D70335	hypothetical prote
13	40	55.6	415	1 A48359	glutamy1-tRNA redu
14	39	54.2	421	2 T08268	conserved hypotet
15	39	54.2	461	2 T48015	hypothetical prote
16	39	54.2	1262	2 T25168	hypothetical prote
17	38	52.8	307	2 S60949	probable phosphate
18	38	52.8	317	2 C75012	hypothetical prote
19	38	52.8	330	2 B83902	transcription repr
20	38	52.8	349	2 S59308	probable membrane
21	38	52.8	390	2 T03841	patatin homolog -
22	38	52.8	401	2 T51407	proline-rich prote
23	38	52.8	508	1 PWRWA	H+-transporting tw
24	38	52.8	615	2 T29550	hypothetical prote
25	38	52.8	661	2 I56258	RP105 - mouse
26	37.5	52.1	296	2 G70446	hypothetical prote
27	37	51.4	258	1 OYECHP	imidazoleglycerol-
28	37	51.4	258	2 B90982	imidazoleglycerol-
29	37	51.4	258	2 H85827	imidazoleglycerol-

30	37	51.4	258	2 B54052	cyclase hiaF - Kle
31	37	51.4	259	2 T37185	probable GntR-fam1
32	37	51.4	271	2 S47620	beta-lactamase - P
33	37	51.4	300	2 S51044	beta-lactamase - P
34	37	51.4	300	2 A55792	beta-lactamase (EC
35	37	51.4	307	2 S53908	hypothetical prote
36	37	51.4	418	2 A53120	intracellular coag
37	37	51.4	435	2 AG1028	prepilin imported
38	37	51.4	506	2 G31090	H+-transporting tw
39	37	51.4	506	2 AE1807	ATP synthase chain
40	37	51.4	513	2 C86897	hypothetical prote
41	37	51.4	533	2 E97854	H+-transporting tw
42	37	51.4	1702	2 S42459	DNA-directed DNA p
43	36.5	50.7	437	2 T00127	hypothetical prote
44	36	50.0	81	2 C91278	hypothetical prote
45	36	50.0	81	2 C86119	hypothetical prote
46	36	50.0	81	2 D65233	hypothetical 9.6 k
47	36	50.0	90	2 AH1054	conserved hypotet
48	36	50.0	149	2 C90217	hypothetical prote
49	36	50.0	166	2 AB2147	hypothetical prote
50	36	50.0	226	2 A64209	ribosomal protein
51	36	50.0	297	2 A70347	UDP-N-acetylenolp
52	36	50.0	356	2 T22882	hypothetical prote
53	36	50.0	366	2 E97304	iron-regulated ABC
54	36	50.0	397	2 D89768	hypothetical prote
55	36	50.0	409	2 C82072	D-3-phosphoglycra
56	36	50.0	410	1 C64070	phosphoglycerate d
57	36	50.0	432	2 F81400	glutamy1-tRNA redu
58	36	50.0	455	2 G70089	hypothetical prote
59	36	50.0	486	2 D64474	hypothetical prote
60	36	50.0	506	1 FWEGA	H+-transporting tw
61	36	50.0	529	2 C82076	general secretion
62	36	50.0	529	2 AH1463	conserved membrane
63	36	50.0	551	2 H86260	protein T12C24.30
64	36	50.0	605	2 AC1139	internalin protein
65	36	50.0	611	2 AB1497	internalin protein
66	36	50.0	641	2 A54407	alpha-mannosidase
67	36	50.0	899	2 F88391	protein R06B10.4 [
68	36	50.0	900	1 S25322	beta-functional beta-
69	36	50.0	1086	2 T33893	hypothetical prote
70	36	50.0	1232	2 B39432	ATP-dependent deox
71	36	50.0	15281	2 S41309	cyclosporin synthe
72	35.5	49.3	239	2 H84886	probable VAMP-asso
73	35.5	49.3	382	2 S71669	finger protein MIG
74	35	48.6	255	2 H75346	hypothetical prote
75	35	48.6	298	2 F69502	hypothetical prote
76	35	48.6	304	2 AG1820	esterase imported
77	35	48.6	345	2 D97222	HD-GYP hydrolase d
78	35	48.6	358	2 T02383	hypothetical prote
79	35	48.6	379	2 S27383	elastase inhibitor
80	35	48.6	382	2 S09139	coii intron protei
81	35	48.6	382	2 G70946	probable dioxigena
82	35	48.6	388	2 E72354	probable hexosyltr
83	35	48.6	391	1 JQ1533	nucleocapsid prote
84	35	48.6	391	1 VHNZ1	nucleocapsid prote
85	35	48.6	391	1 VHNZ3	nucleocapsid prote
86	35	48.6	391	1 VHNZB4	nucleocapsid prote
87	35	48.6	393	1 VHNZPM	nucleocapsid prote
88	35	48.6	398	2 G90260	conserved hypotet
89	35	48.6	414	2 C82954	hypothetical prote
90	35	48.6	446	2 H83098	hypothetical prote
91	35	48.6	452	2 JC6561	UDP-N-acetylmuram
92	35	48.6	467	1 VHNZ	nucleocapsid prote
93	35	48.6	469	2 S48370	probable phosphogl
94	35	48.6	470	2 T52440	PRM1 homolog limpo
95	35	48.6	476	2 A83387	probable transport
96	35	48.6	489	2 H84106	teichuronopeptide
97	35	48.6	494	2 S57539	probable membrane
98	35	48.6	499	2 C71111	phenylalanine-tRNA
99	35	48.6	503	2 S78321	H+-transporting tw
100	35	48.6	529	2 AH1101	conserved membrane
101	35	48.6	547	2 I39593	exaA protein - Aer
102	35	48.6	563	2 D90531	excinuclease ABC s

103	35	48.6	573	1	S33212	INDAI protein - fu	176	34	47.2	763	2	AH1097	alpha-glucosidase
104	35	48.6	599	2	T17534	hypothetical prote	177	34	47.2	764	2	A47456	down-regulated in
105	35	48.6	605	2	S10197	NADH2 dehydrogenas	178	34	47.2	805	2	S64238	kinesin-related pr
106	35	48.6	663	2	T47802	hypothetical prote	179	34	47.2	1052	2	T37133	hypothetical prote
107	35	48.6	719	2	F96577	hypothetical prote	180	34	47.2	1325	2	S62497	probable nucleopor
108	35	48.6	735	2	A83006	hypothetical prote	181	34	47.2	2052	2	T37711	probable n-end-rec
109	35	48.6	759	1	C64345	replication licens	182	34	47.2	2764	2	T13945	neurofibromin - fr
110	35	48.6	776	2	S39865	late competence pr	183	34	47.2	2802	2	T13947	neurofibromin - fr
111	35	48.6	915	2	T21147	hypothetical prote	184	34	47.2	2802	2	T13947	reverse transcript
112	35	48.6	1008	2	C97726	acriflavin resista	185	33.5	46.5	120	2	S22049	hypothetical prote
113	35	48.6	1067	2	T18196	pol protein - silk	186	33.5	46.5	336	2	C64410	3-phosphoshikimate
114	35	48.6	1685	2	T43217	RNA polymerase (EC	187	33.5	46.5	427	2	C84966	DNA topoisomerase
115	35	48.6	5327	2	T13564	microtubule-associ	188	33	45.8	81	2	A41949	hypothetical prote
116	34.5	47.9	223	2	T51727	C-8, 7 sterol isome	189	33	45.8	85	2	H71248	hypothetical prote
117	34.5	47.9	314	2	T33862	hypothetical prote	190	33	45.8	111	2	H2561	hypothetical prote
118	34.5	47.9	330	2	T08667	hypothetical prote	191	33	45.8	122	2	S36276	Ig heavy chain V r
119	34.5	47.9	422	2	H96591	hypothetical prote	192	33	45.8	140	2	D72322	conserved hypothet
120	34.5	47.9	457	2	H84716	hypothetical prote	193	33	45.8	144	2	G75149	hypothetical prote
121	34.5	47.9	1955	2	T41170	probable 1,3-beta-	194	33	45.8	153	2	S23222	miGA protein - She
122	34.5	47.9	2163	2	T51397	hypothetical prote	195	33	45.8	153	2	H71248	hypothetical prote
123	34	47.2	75	2	S50353	hypothetical prote	196	33	45.8	179	2	S45551	hypothetical prote
124	34	47.2	76	2	S61601	hypothetical prote	197	33	45.8	193	2	T36285	probable hydrolase
125	34	47.2	101	2	S45387	hypothetical prote	198	33	45.8	222	2	F71309	probable phosphogl
126	34	47.2	110	2	S38067	hypothetical prote	199	33	45.8	224	2	D90235	hypothetical prote
127	34	47.2	110	2	S50345	hypothetical prote	200	33	45.8	230	2	C97104	hypothetical prote
128	34	47.2	136	2	PH1559	Ig heavy chain V r	201	33	45.8	232	1	R5BS1	ribosomal protein
129	34	47.2	184	2	F72247	hypothetical prote	202	33	45.8	234	2	E71905	hypothetical prote
130	34	47.2	190	2	D88957	protein ZK697.8 [i	203	33	45.8	236	2	E90153	conserved hypothet
131	34	47.2	251	2	H64212	hypothetical prote	204	33	45.8	240	2	R97782	ABC transporter At
132	34	47.2	251	2	AH3314	hypothetical membr	205	33	45.8	245	2	S21507	polyhedrin - lacke
133	34	47.2	258	2	H84941	hisp protein [limp	206	33	45.8	254	2	F71654	ABC transporter At
134	34	47.2	258	2	AC0188	histidine biosynth	207	33	45.8	257	2	E82238	imidazoleglycerol-
135	34	47.2	284	2	T18253	probable mitochond	208	33	45.8	263	2	A54543	beta-lactamase (EC
136	34	47.2	286	2	AG3220	hydrolase [impor	209	33	45.8	271	2	C89352	imidazoleglycerol-
137	34	47.2	291	2	JP0074	beta-lactamase (EC	210	33	45.8	275	2	D64953	NAD synthase (EC 6
138	34	47.2	294	2	S19006	beta-lactamase (EC	211	33	45.8	275	2	F90934	NAD synthetase [im
139	34	47.2	307	2	D69521	hypothetical prote	212	33	45.8	275	2	B85783	NAD synthetase, pr
140	34	47.2	313	2	E81782	adhesin MafA2 NMA2	213	33	45.8	279	2	T40445	phosphatidic acid
141	34	47.2	321	2	E84747	probable cinnamoyl	214	33	45.8	290	2	C96776	hypothetical prote
142	34	47.2	364	2	T34221	lir-1 protein - Ca	215	33	45.8	291	2	S42075	beta-lactamase (EC
143	34	47.2	370	2	E71306	probable polynucle	216	33	45.8	292	2	C70421	conserved hypothet
144	34	47.2	371	2	C95130	conserved hypothet	217	33	45.8	295	2	AG0547	probable carboxyvi
145	34	47.2	375	2	E98001	glycerate kinase [218	33	45.8	296	2	C64760	probable carboxyph
146	34	47.2	397	2	E95680	hypothetical prote	219	33	45.8	296	2	D85527	probable phosphono
147	34	47.2	410	1	DESCPG	phosphoglycerate d	220	33	45.8	296	2	A90677	probable phosphono
148	34	47.2	410	2	AD0874	D-3-phosphoglycera	221	33	45.8	297	1	WZECN	N-acetylneuraminat
149	34	47.2	410	2	D85947	D-3-phosphoglycera	222	33	45.8	297	2	AE0908	N-acetylneuraminat
150	34	47.2	410	2	H91101	D-3-phosphoglycera	223	33	45.8	297	2	E85986	N-acetylneuraminat
151	34	47.2	412	2	AD3611	phosphoglycerate d	224	33	45.8	297	2	B91141	N-acetylneuraminat
152	34	47.2	412	2	AG3637	cis,cis-muconate t	225	33	45.8	297	2	H64234	cytadherence acces
153	34	47.2	413	2	AC0112	phosphoglycerate d	226	33	45.8	298	2	A83545	carboxyphosphoen
154	34	47.2	421	2	JN0257	site-specific DNA-	227	33	45.8	303	2	F71680	hypothetical prote
155	34	47.2	427	2	B86266	hypothetical prote	228	33	45.8	305	2	E70410	hypothetical prote
156	34	47.2	445	2	A71699	UDP-N-acetylmuramo	229	33	45.8	311	2	JN0520	beta-lactamase (EC
157	34	47.2	447	2	C84306	hypothetical prote	230	33	45.8	311	2	H64157	sufi protein homol
158	34	47.2	450	2	H95079	UDP-N-acetylmuramo	231	33	45.8	313	2	G91262	probable carboxydr
159	34	47.2	450	2	C79947	UDP-N-acetylmuramo	232	33	45.8	313	2	B86103	probable carboxydr
160	34	47.2	451	2	D47691	UDP-N-acetylmuramo	233	33	45.8	321	2	G95920	probable epimerase
161	34	47.2	480	2	E75433	hypothetical prote	234	33	45.8	321	2	S10006	hypothetical prote
162	34	47.2	496	2	A31986	glucose transporte	235	33	45.8	339	1	S47643	alcohol dehydrogen
163	34	47.2	500	2	D75049	phenylalanine-tRNA	236	33	45.8	339	2	T34406	hypothetical prote
164	34	47.2	508	2	A89817	hypothetical prote	237	33	45.8	340	2	T46112	hypothetical prote
165	34	47.2	518	1	S40218	glycine hydroxymet	238	33	45.8	348	2	AG1041	Vi polysaccharide
166	34	47.2	543	2	G95118	RNA methyltransfer	239	33	45.8	348	2	C36892	Vi polysaccharide
167	34	47.2	543	2	D97988	conserved hypothet	240	33	45.8	350	2	D97298	uncharacterized co
168	34	47.2	561	2	C84721	hypothetical prote	241	33	45.8	351	2	T43493	hypothetical prote
169	34	47.2	575	2	C88346	protein F42G4.3a [242	33	45.8	354	1	RGHYO1	GTP-binding regula
170	34	47.2	579	2	AB1414	ABC transporter (A	243	33	45.8	354	1	RGHYO2	GTP-binding regula
171	34	47.2	579	2	A11789	ABC transporter (A	244	33	45.8	354	1	RGBOO1	GTP-binding regula
172	34	47.2	603	2	T21211	hypothetical prote	245	33	45.8	354	1	RGHUO1	GTP-binding regula
173	34	47.2	628	2	S44629	F22B7.10 protein -	246	33	45.8	354	1	RGHUO2	GTP-binding regula
174	34	47.2	632	2	B55225	stress-sensitive r	247	33	45.8	354	1	RGMSO1	GTP-binding regula
175	34	47.2	693	2	F82245	conserved hypothet	248	33	45.8	354	1	RGMSO2	GTP-binding regula

249	33	45.8	354	1	RGRT01	GTP-binding regula	322	32.5	45.1	494	2	S39607	transcription fact
250	33	45.8	354	1	RGRT02	G-protein - regula	323	32.5	45.1	542	2	S39608	transcription fact
251	33	45.8	354	2	S40509	G-protein - chicke	324	32.5	45.1	628	1	A33333	transcription fact
252	33	45.8	355	2	T34405	hypothetical prote	325	32.5	45.1	628	1	A39262	transcription fact
253	33	45.8	359	2	A46046	serine proteinase	326	32.5	45.1	630	1	A46149	transcription fact
254	33	45.8	374	2	T24162	hypothetical prote	327	32.5	45.1	631	1	A36749	transcription fact
255	33	45.8	379	2	S17979	pectin lyase (EC 4	328	32.5	45.1	634	1	S35574	transcription fact
256	33	45.8	380	2	E84748	probable protein p	329	32.5	45.1	702	2	A34434	arylphorin alpha c
257	33	45.8	382	2	T37836	hypothetical prote	330	32.5	45.1	841	2	D84513	probable retroelem
258	33	45.8	382	2	S62499	hypothetical prote	331	32	44.4	86	2	S54593	ribosomal protein
259	33	45.8	397	2	T33510	formaldehyde dehyd	332	32	44.4	102	2	PH1262	Ig heavy chain V r
260	33	45.8	399	2	A55577	hypothetical prote	333	32	44.4	108	2	G72717	hypothetical prote
261	33	45.8	403	2	C75405	streptomycin biosy	334	32	44.4	121	2	T24096	hypothetical prote
262	33	45.8	417	2	AF3448	hypothetical membr	335	32	44.4	126	2	PH1424	Ig heavy chain V r
263	33	45.8	418	2	A47281	pigment epithelial	336	32	44.4	130	2	G72609	hypothetical prote
264	33	45.8	426	2	F70723	probable transferra	337	32	44.4	133	2	A75039	hypothetical prote
265	33	45.8	434	2	F90184	cobyrinic acid A,C	338	32	44.4	134	2	PH1422	Ig heavy chain V r
266	33	45.8	448	2	AC2373	L-sorbose dehydr	339	32	44.4	137	2	S02155	NADH2 dehydrogenas
267	33	45.8	462	2	A40362	anthranilate synth	340	32	44.4	149	2	B72735	hypothetical prote
268	33	45.8	464	2	C82046	sensor protein Cpx	341	32	44.4	155	2	D75147	Iso ribosomal prot
269	33	45.8	475	2	C86863	N-acetylmuramoyl-L	342	32	44.4	155	2	B71187	probable ribosomal
270	33	45.8	479	2	G96605	hypothetical prote	343	32	44.4	157	2	F90219	Iso ribosomal prot
271	33	45.8	483	2	F71619	hypothetical prote	344	32	44.4	180	2	AD0134	probable prophage
272	33	45.8	510	2	B71017	hypothetical prote	345	32	44.4	184	2	C83911	hypothetical prote
273	33	45.8	527	2	S49827	probable membrane	346	32	44.4	188	2	F82569	dihydrofolate redu
274	33	45.8	534	2	B97352	polylacturonase	347	32	44.4	190	2	G70239	conserved hypotet
275	33	45.8	537	2	AH1277	probable transport	348	32	44.4	218	2	S74867	hypothetical prote
276	33	45.8	537	2	AH1640	probable transport	349	32	44.4	246	1	JQ1868	polyhedrin - Spodo
277	33	45.8	563	1	C64420	N-methylhydantoina	350	32	44.4	246	1	PVNVSF	polyhedrin - Spodo
278	33	45.8	583	2	T12574	phosphoglucosylase	351	32	44.4	254	2	T48732	2,5-diketo-D-gluco
279	33	45.8	590	2	T20537	hypothetical prote	352	32	44.4	254	2	C86277	F14L17.7 protein -
280	33	45.8	613	2	T33266	hypothetical prote	353	32	44.4	256	2	D69952	conserved hypotet
281	33	45.8	638	2	S36546	E1 protein - human	354	32	44.4	258	1	OYEBHF	cyclase hisf - Sal
282	33	45.8	668	2	H86729	excinuclease ABC s	355	32	44.4	258	1	AI0764	cyclase hisf [impo
283	33	45.8	690	2	C83958	DNA topoisomerase	356	32	44.4	258	2	I64070	cyclase hisf HI047
284	33	45.8	699	2	E97594	elongation factor	357	32	44.4	259	2	C43260	triose-phosphate i
285	33	45.8	699	2	AC2816	translation elonga	358	32	44.4	259	2	T24131	hypothetical prote
286	33	45.8	747	2	T22916	hypothetical prote	359	32	44.4	261	2	AH2031	hypothetical prote
287	33	45.8	819	2	D85440	Cu2+-transporting	360	32	44.4	266	2	D84953	pseudouridyate sy
288	33	45.8	822	2	T41941	glycoprotein B - h	361	32	44.4	266	2	G82386	amino acid ABC tra
289	33	45.8	830	2	B44439	protein kinase (EC	362	32	44.4	274	2	A80468	diaminopimelate ep
290	33	45.8	842	2	H68220	hypothetical prote	363	32	44.4	278	2	AB3114	hypothetical prote
291	33	45.8	856	2	A44439	protein kinase (EC	364	32	44.4	278	2	C98173	hypothetical prote
292	33	45.8	857	2	A42861	protein kinase RTK	365	32	44.4	281	2	G24723	tryptophan synthas
293	33	45.8	925	2	A72096	ct234 hypothetical	366	32	44.4	287	2	D87465	D-alanine aminotra
294	33	45.8	925	2	H81573	conserved hypotet	367	32	44.4	289	2	H96588	hypothetical prote
295	33	45.8	925	2	E86527	CT234 hypothetical	368	32	44.4	290	2	A70208	conserved hypotet
296	33	45.8	977	2	T38412	hypothetical prote	369	32	44.4	291	2	S62730	cyclin D1 - zebra
297	33	45.8	1003	2	T28654	transposase - pseu	370	32	44.4	293	2	H82634	site-specific DNA-
298	33	45.8	1019	2	F70342	cation efflux syst	371	32	44.4	294	2	AD1910	ABC transporter pe
299	33	45.8	1038	2	A71437	probable resistanc	372	32	44.4	300	2	D87497	MtTB family protei
300	33	45.8	1074	2	G96504	probable En/Spn-li	373	32	44.4	300	2	B99709	probable transcrip
301	33	45.8	1088	2	E86102	FlilA6.9 protein -	374	32	44.4	300	2	F85559	probable transcrip
302	33	45.8	1100	2	G83376	probable trehalose	375	32	44.4	300	2	A64794	YbdO protein - Esc
303	33	45.8	1258	2	D75453	5-methyltetrahydro	376	32	44.4	303	2	C97029	transcription regu
304	33	45.8	1278	2	A47462	probable DNA-direc	377	32	44.4	304	2	AF0730	probable membrane
305	33	45.8	1304	2	G85188	disease resistance	378	32	44.4	306	2	C64015	hypothetical prote
306	33	45.8	1317	2	H85189	disease resistance	379	32	44.4	307	2	B96745	unknown protein T9
307	33	45.8	1385	2	T13887	tIr protein - frui	380	32	44.4	309	2	H89832	hypothetical prote
308	33	45.8	1389	2	T13852	gene wheeler prote	381	32	44.4	316	1	PNBSLC	beta-lactamase (EC
309	33	45.8	1422	2	B71437	probable resistanc	382	32	44.4	321	1	RSUBP0	acidic ribosomal p
310	33	45.8	1737	2	A37491	hypothetical helic	383	32	44.4	323	2	H90282	hypothetical prote
311	33	45.8	1983	2	AC1922	two-component hylr	384	32	44.4	323	2	AB1659	hypothetical prote
312	33	45.8	2133	2	T42763	coagulation factor	385	32	44.4	329	2	T05728	probable cadmium-t
313	33	45.8	2413	2	S34670	splicing factor PR	386	32	44.4	332	2	T23503	hypothetical prote
314	33	45.8	2467	2	D71437	probable resistanc	387	32	44.4	335	2	T50393	probable mitochond
315	33	45.8	5147	1	IJFTMT	cadherin-related c	388	32	44.4	336	2	G90421	alcohol dehydrogen
316	32.5	45.1	218	2	B82226	thiopurine methylt	389	32	44.4	337	2	T52358	probable CELL Divi
317	32.5	45.1	365	2	E69220	conserved hypotet	390	32	44.4	338	2	C64551	oligopeptide ABC t
318	32.5	45.1	394	2	B70411	fimbrial assembly	391	32	44.4	339	2	A82441	ABC transporter, p
319	32.5	45.1	407	2	T00989	hypothetical prote	392	32	44.4	341	2	T33221	hypothetical prote
320	32.5	45.1	464	2	AB1480	PTS system, fructo	393	32	44.4	345	2	A97783	tRNA pseudouridine
321	32.5	45.1	464	2	AG1119	PTS system, fructo	394	32	44.4	353	2	I51572	maternal protein -

395	356	2	B89919	hypothetical prote	468	32	44.4	568	2	T03950	probable glucose-6
396	365	1	GNVSSC	genome polyprotein	469	32	44.4	581	2	T05550	hypothetical prote
397	366	2	A71880	probable outer mem	470	32	44.4	584	2	B82834	hypothetical prote
398	371	2	E71932	probable outer mem	471	32	44.4	586	1	JC4219	pyruvate kinase (E
399	372	2	A34261	alanine dehydrogen	472	32	44.4	592	2	D97171	uncharacterized co
400	378	2	S38962	serpin - pig	473	32	44.4	594	2	F82895	hypothetical prote
401	378	2	AG2833	hypothetical prote	474	32	44.4	596	2	D87710	TPR domain protein
402	378	2	C97611	hypothetical prote	475	32	44.4	606	2	H71065	hypothetical prote
403	378	2	H69505	conserved hypotet	476	32	44.4	610	2	T32917	hypothetical prote
404	380	1	GNVSM8	genome polyprotein	477	32	44.4	619	2	S40938	hypothetical prote
405	392	2	A95954	probable membrane	478	32	44.4	626	2	UQ2322	starch synthase (E
406	392	2	E95133	hypothetical prote	479	32	44.4	654	2	T14202	NAUH2 dehydrogenas
407	392	2	A99002	hypothetical prote	480	32	44.4	664	2	F70483	glycine-tRNA ligas
408	392	2	G83909	hypothetical prote	481	32	44.4	665	2	D90092	hypothetical prote
409	394	1	VXRP8R	inner capsid prote	482	32	44.4	714	2	T31819	hypothetical prote
410	395	1	A43386	inner capsid prote	483	32	44.4	767	2	E85079	hypothetical prote
411	395	1	VXRCR	inner capsid prote	484	32	44.4	777	2	T41075	hypothetical WD-re
412	400	2	A90999	penicillin-binding	485	32	44.4	783	2	T45899	receptor protein k
413	403	2	E83366	hypothetical prote	486	32	44.4	792	2	S63141	hypothetical prote
414	403	2	G71236	hypothetical prote	487	32	44.4	796	2	A97731	bifunctional penic
415	406	2	H71308	hypothetical prote	488	32	44.4	813	2	D71378	probable DNA gyras
416	407	2	H75515	tetracycline-efflu	489	32	44.4	814	2	D82101	oxidoreductase, ac
417	408	2	B82507	sodium/glutamate s	490	32	44.4	822	2	E97839	ATP-dependent heli
418	410	2	E70475	folypolyglutamate	491	32	44.4	833	2	T10695	transcription fact
419	415	2	A32853	plasmidogen activa	492	32	44.4	859	2	B64430	DNA-directed RNA p
420	416	2	T03243	FLO/LFY protein ho	493	32	44.4	862	2	B53689	homeotic protein C
421	418	2	A41044	chromosomal protei	494	32	44.4	862	2	S64821	probable membrane
422	423	2	AG1973	hypothetical prote	495	32	44.4	863	2	S37088	phycobilisome anch
423	425	2	E84631	probable serine ca	496	32	44.4	878	2	T21621	hypothetical prote
424	427	2	T39113	probable flavohemo	497	32	44.4	880	2	B45956	beta-glucosidase (
425	427	2	T36167	hypothetical prote	498	32	44.4	882	2	F86164	hypothetical prote
426	441	2	A55542	sensor kinase regB	499	32	44.4	940	2	AD1374	internalin protein
427	442	2	E57041	transcription regu	500	32	44.4	975	2	S33121	homeotic protein C
428	444	2	G65905	glucuronate permease	501	32	44.4	1008	2	T33672	hypothetical prote
429	449	2	C71959	glutamyl tRNA redu	502	32	44.4	1011	2	C84524	probable disease r
430	449	2	G64549	glutamyl-tRNA redu	503	32	44.4	1032	2	H64100	acriflavine resist
431	451	2	F97230	probable maltodext	504	32	44.4	1105	2	F71079	hypothetical prote
432	453	2	D84018	two-component resp	505	32	44.4	1126	1	WMFM12	125K protein - alf
433	454	2	F75571	chromosomal replic	506	32	44.4	1131	2	T38744	hypothetical prote
434	463	2	T04996	male sterility pro	507	32	44.4	1142	2	A45031	cysteine-rich fibr
435	464	2	C84428	probable ribophori	508	32	44.4	1175	2	S52417	E-selectin ligand-
436	465	2	B85358	SERINE CARBOXYPEPT	509	32	44.4	1253	2	T45787	disease resistance
437	468	2	A72619	probable NADH dehy	510	32	44.4	1289	2	AE2217	hypothetical prote
438	472	2	H90563	hypothetical prote	511	32	44.4	1332	1	I48314	homeotic protein C
439	474	2	D84631	probable serine ca	512	32	44.4	1374	2	T30809	plasmidogen relate
440	480	2	G85397	male sterility 2-l	513	32	44.4	1404	2	F86470	probable retroelem
441	480	2	T46047	hypothetical prote	514	32	44.4	1445	2	T15212	hypothetical prote
442	481	2	F86208	protein F22G5.30 [515	32	44.4	1450	2	S78060	probable DNA-direc
443	485	1	ANHU	angiotensin precur	516	32	44.4	1451	2	S42167	190K protein - hum
444	489	2	D87551	glutamyl-tRNA(Gln)	517	32	44.4	1713	2	A55347	adhesive ligand ep
445	492	2	T30066	hypothetical prote	518	32	44.4	1732	2	T43026	probable DNA-direc
446	498	2	T51430	dolichyl-phosphate	519	32	44.4	1787	2	AG1360	probable tape-meas
447	500	1	ITHUC1	complement C1 inhi	520	32	44.4	1788	2	AH1447	probable tape-meas
448	500	2	AD1625	transporter homolo	521	32	44.4	1794	2	T38459	hypothetical diver
449	501	2	AB1263	transporter homolo	522	32	44.4	1824	2	T07589	disease resistance
450	506	2	B63181	hypothetical prote	523	32	44.4	1895	2	T06609	disease resistance
451	507	1	PMLVA	H+-transporting tw	524	32	44.4	2150	1	GNVYH2	genome polyprotein
452	508	2	T45867	hypothetical prote	525	32	44.4	2195	2	S61103	SEC16 protein - ye
453	508	2	G83977	L-2,4-diaminobuty	526	32	44.4	3511	2	A59295	unconventional myo
454	516	2	A53772	transcription fact	527	32	44.4	4273	2	C96679	polyketide synthas
455	520	2	T16593	hypothetical prote	528	31.5	43.8	153	2	D71556	hypothetical prote
456	536	2	AB1983	hypothetical prote	529	31.5	43.8	249	2	T32566	hypothetical prote
457	541	2	A48717	glutamate formimid	530	31.5	43.8	254	2	E97358	inner membrane pro
458	544	2	E97051	site-specific DNA	531	31.5	43.8	269	2	F70377	shikimate 5-dehydr
459	549	2	D71969	L-lactate permease	532	31.5	43.8	305	2	S44159	hypothetical prote
460	549	2	D64537	L-lactate permease	533	31.5	43.8	306	2	G97457	hypothetical prote
461	552	2	S36786	carboxylesterase (534	31.5	43.8	306	2	AH2675	conserved hypotet
462	556	1	E69589	arginine-tRNA liga	535	31.5	43.8	342	2	S71398	farnesyl-pyrophosp
463	561	2	T09976	H+-transporting tw	536	31.5	43.8	385	2	C82478	probable integrase
464	564	1	S36787	carboxylesterase (537	31.5	43.8	594	2	JT0766	transcription fact
465	566	2	T45626	hypothetical prote	538	31.5	43.8	760	2	S62792	probable lipoprote
466	567	2	T03948	probable glucose-6	539	31.5	43.8	978	2	A70387	conserved hypotet
467	567	2	T02094	glucose-6-phosphat	540	31.5	43.8	1173	2	T08610	major core capsid

541	31.5	43.8	1556	2	F96587	hypothetical prote	614	31	43.1	261	2	T11081	cytochrome-c oxida
542	31.5	43.8	1816	2	E84845	probable ABC trans	615	31	43.1	270	2	G85078	probable transposo
543	31	43.1	39	2	E81540	hypothetical prote	616	31	43.1	273	2	D64201	methylenetetrahydr
544	31	43.1	50	2	G71716	hypothetical prote	617	31	43.1	273	2	AD2409	GDP-D-mannose dehy
545	31	43.1	70	2	AH0428	conserved hypotet	618	31	43.1	273	2	D70428	hypothetical prote
546	31	43.1	76	2	G63584	reverse transcript	619	31	43.1	278	2	T29994	hypothetical prote
547	31	43.1	81	2	T03712	reverse transcript	620	31	43.1	286	2	AE1200	3-hydroxyisobutyra
548	31	43.1	94	2	S13265	heme oxygenase (de	621	31	43.1	286	2	AC1558	3-hydroxyisobutyra
549	31	43.1	99	2	T43600	probable transposo	622	31	43.1	287	2	A64225	thymidylate synth
550	31	43.1	102	2	PH1267	ig heavy chain v r	623	31	43.1	290	2	F89605	protein F18G5.5 (i
551	31	43.1	103	2	G90223	ig heavy chain v r	624	31	43.1	291	2	B71097	hypothetical prote
552	31	43.1	113	2	G90223	DNA-directed RNA p	625	31	43.1	299	2	E83161	hypothetical prote
553	31	43.1	117	2	S19669	ig heavy chain v r	626	31	43.1	302	2	G72553	hypothetical prote
554	31	43.1	119	2	F71011	ig heavy chain v r	627	31	43.1	306	2	T43597	yop targeting nega
555	31	43.1	123	2	A88065	hypothetical prote	628	31	43.1	308	2	D83629	probable permease
556	31	43.1	126	2	AE1894	protein T16A1.5 (i	629	31	43.1	310	2	D87704	integral membra
557	31	43.1	126	2	PH1417	ig heavy chain v r	630	31	43.1	313	2	G81173	adhesin mafa - Nei
558	31	43.1	126	2	PH1418	ig heavy chain v r	631	31	43.1	313	2	S73033	probable metalloth
559	31	43.1	131	2	F70920	probable moaB prot	632	31	43.1	317	2	E84434	probable phloem-sp
560	31	43.1	136	2	G90557	hypothetical prote	633	31	43.1	318	2	T41838	BRO-c - Bombyx mor
561	31	43.1	137	2	E81355	hypothetical prote	634	31	43.1	320	2	T28992	hypothetical prote
562	31	43.1	138	2	AG1695	PTS mannose-specif	635	31	43.1	322	2	B65024	probable hydrogena
563	31	43.1	142	1	S5BY25	ribosomal protein	636	31	43.1	322	2	E85891	hydrogenase 4 memb
564	31	43.1	142	2	R30000	ribosomal protein	637	31	43.1	322	2	A91047	hydrogenase 4 memb
565	31	43.1	142	2	S29999	ribosomal protein	638	31	43.1	323	2	AD2753	lipoic Acid Synth
566	31	43.1	152	2	B71035	hypothetical prote	639	31	43.1	323	2	B97534	lipoic acid synth
567	31	43.1	153	2	T36799	hypothetical prote	640	31	43.1	325	2	T26260	hypothetical prote
568	31	43.1	156	2	I40704	gene eae ORFU homo	641	31	43.1	326	2	B71681	pyruvate dehydroge
569	31	43.1	156	2	D86045	hypothetical prote	642	31	43.1	327	1	D69751	glutaminase homolo
570	31	43.1	156	2	F91198	Cest protein (limpo	643	31	43.1	330	2	G81165	phenylalanyl-tRNA
571	31	43.1	156	2	I41196	Tir chaperone - Es	644	31	43.1	330	2	F81939	probable phenylala
572	31	43.1	157	2	H96993	transcription regu	645	31	43.1	330	2	C69649	transcription repr
573	31	43.1	161	2	A70207	conserved hypotet	646	31	43.1	330	2	B71015	hypothetical prote
574	31	43.1	169	2	T04207	phospholipid-hydro	647	31	43.1	333	2	F90225	alcohol dehydrogen
575	31	43.1	172	2	H72731	hypothetical prote	648	31	43.1	333	2	T40923	pyridoxal reductas
576	31	43.1	172	2	C82129	conserved hypotet	649	31	43.1	338	2	S38030	suppressor protein
577	31	43.1	175	2	G96532	hypothetical prote	650	31	43.1	338	2	F71957	ABC transporter, p
578	31	43.1	176	2	T35459	hypothetical prote	651	31	43.1	341	2	T29598	hypothetical prote
579	31	43.1	177	2	AF3129	hypothetical prote	652	31	43.1	342	2	AD2032	hypothetical prote
580	31	43.1	178	2	S67379	hypothetical prote	653	31	43.1	344	2	T25951	hypothetical prote
581	31	43.1	179	2	B72612	hypothetical prote	654	31	43.1	344	2	A84750	probable mitochond
582	31	43.1	181	2	F70105	ribonuclease H (rn	655	31	43.1	345	2	T44521	polyaacccharide bio
583	31	43.1	184	2	F90026	hypothetical prote	656	31	43.1	345	2	T44510	Vi polysaccharide
584	31	43.1	184	2	H84162	hypothetical prote	657	31	43.1	349	2	T41892	BRO-d orf2 - Bomby
585	31	43.1	186	2	C98158	hypothetical prote	658	31	43.1	351	2	T43791	cystathionine beta
586	31	43.1	190	2	A84029	septum formation m	659	31	43.1	360	2	T00882	hypothetical prote
587	31	43.1	193	2	AB3421	hypothetical prote	660	31	43.1	360	2	T29004	hypothetical prote
588	31	43.1	195	2	T32819	hypothetical prote	661	31	43.1	362	1	B70382	chorismate mutase/
589	31	43.1	203	2	D95152	v-type sodium ATP	662	31	43.1	362	2	S74433	GDP-D-mannose dehy
590	31	43.1	214	2	S17807	hypothetical prote	663	31	43.1	370	2	H89971	hypothetical prote
591	31	43.1	219	2	E82825	hypothetical prote	664	31	43.1	371	2	T30762	hypothetical prote
592	31	43.1	220	2	A81959	probable pseudourid	665	31	43.1	374	2	T15940	hypothetical prote
593	31	43.1	223	1	MFVNSV	matrix protein - s	666	31	43.1	377	2	AD3363	queine tRNA-ribos
594	31	43.1	225	2	T28319	ORF MSV158 probabl	667	31	43.1	378	2	G90770	probable third cyt
595	31	43.1	228	2	F89941	hypothetical prote	668	31	43.1	378	2	C85633	probable third cyt
596	31	43.1	228	2	S57697	hypothetical prote	669	31	43.1	378	2	A64839	cytochrome oxidase
597	31	43.1	228	2	G83700	hypothetical prote	670	31	43.1	378	2	B39790	hypothetical prote
598	31	43.1	230	2	S34645	fibrillar-like p	671	31	43.1	379	1	B28940	cytochrome d ubiqu
599	31	43.1	232	2	A99245	fibrillar-like p	672	31	43.1	379	2	A99725	cytochrome d ubiqu
600	31	43.1	233	2	E85888	hypothetical prote	673	31	43.1	379	2	B85576	cytochrome d ubiqu
601	31	43.1	233	2	B91044	hypothetical prote	674	31	43.1	381	2	F72756	probable multiple
602	31	43.1	233	2	C65021	Ethanolamine utili	675	31	43.1	382	2	S08595	TrfA transcription
603	31	43.1	234	2	T10217	hypothetical prote	676	31	43.1	384	2	C86831	hypothetical prote
604	31	43.1	241	2	S77548	lumQ protein - syn	677	31	43.1	388	2	T10765	patatin-like latex
605	31	43.1	243	2	D84474	hypothetical prote	678	31	43.1	388	2	T10770	patatin-like latex
606	31	43.1	243	2	T46461	hypothetical prote	679	31	43.1	388	2	T10763	patatin-like latex
607	31	43.1	248	2	F84277	uridine kinase (im	680	31	43.1	392	2	D70475	conserved hypotet
608	31	43.1	250	2	F75054	hypothetical prote	681	31	43.1	393	2	S03576	DNA-directed RNA p
609	31	43.1	252	2	F83443	hypothetical prote	682	31	43.1	393	2	AC1472	aminotransferase h
610	31	43.1	259	2	S58988	cytochrome-c oxida	683	31	43.1	394	2	G85829	O antigen polymera
611	31	43.1	259	2	G96673	hypothetical prote	684	31	43.1	394	2	D90984	O antigen polymera
612	31	43.1	261	2	T11028	cytochrome-c oxida	685	31	43.1	395	2	T23402	hypothetical prote
613	31	43.1	261	2	T11186	cytochrome-c oxida	686	31	43.1	397	2	H81744	conserved hypotet

687	31	43.1	398	2	A70520	probable aceAb pro	760	31	43.1	591	2	H86267	probable protein p
688	31	43.1	400	2	B36190	penicillin-binding	761	31	43.1	599	2	Ti2994	riboflavin biosynt
689	31	43.1	401	2	C83309	conserved hypotet	762	31	43.1	601	2	T38736	hypothetical prote
690	31	43.1	403	2	AF2151	aminotransferase [763	31	43.1	615	2	F64572	arginine decarboxy
691	31	43.1	405	2	S19355	hypothetical prote	764	31	43.1	615	2	C71867	arginine decarboxy
692	31	43.1	406	2	G70410	glutamyl tRNA redu	765	31	43.1	628	2	A84087	hypothetical prote
693	31	43.1	407	2	F64666	glucose/galactose	766	31	43.1	632	1	JC4919	2-oxoacid-ferredox
694	31	43.1	407	2	A71850	glucose/galactose	767	31	43.1	633	2	S61435	metalloproteinase
695	31	43.1	410	2	C84176	oxalate/formate an	768	31	43.1	635	2	T23874	hypothetical prote
696	31	43.1	417	2	S07286	hypothetical prote	769	31	43.1	642	2	H69466	conserved hypotet
697	31	43.1	418	2	F64473	D-alanine transami	770	31	43.1	649	2	S42894	metalloproteinase
698	31	43.1	418	2	T47818	hypothetical prote	771	31	43.1	650	2	Ti5972	hypothetical prote
699	31	43.1	425	2	F85360	SERINE CARBOXYPEPT	772	31	43.1	651	2	G69177	methionine-tRNA li
700	31	43.1	425	2	C97013	probable non-proce	773	31	43.1	651	2	D72042	conserved hypotet
701	31	43.1	428	2	JH0634	site-specific DNA-	774	31	43.1	651	2	B6581	CHLPN 76 kDa homol
702	31	43.1	429	2	AB2456	glycosyltransferas	775	31	43.1	658	2	T20042	hypothetical prote
703	31	43.1	429	2	S45459	TOM34 protein - ye	776	31	43.1	660	2	G82672	ATP sulfurylase, l
704	31	43.1	439	2	T49739	related to cyclohe	777	31	43.1	672	2	C69120	conserved hypotet
705	31	43.1	442	2	T03172	helicase homolog 0	778	31	43.1	677	2	T39713	zinc finger protei
706	31	43.1	445	2	H96560	hypothetical prote	779	31	43.1	696	2	T50391	probable anaphase-
707	31	43.1	449	2	S55092	hypothetical prote	780	31	43.1	703	2	T39997	Thalp - fission ye
708	31	43.1	453	2	S58318	Slx41 protein - ye	781	31	43.1	703	2	B34434	arylphorin beta ch
709	31	43.1	454	2	D75446	oxidoreductase - D	782	31	43.1	704	2	H95890	probable hydantoin
710	31	43.1	454	2	AC0862	conserved hypotet	783	31	43.1	715	2	Ti5124	hypothetical prote
711	31	43.1	454	2	A85931	hypothetical prote	784	31	43.1	724	2	C49423	senaphorin II prec
712	31	43.1	454	2	G65061	hypothetical prote	785	31	43.1	725	2	AG2547	hypothetical prote
713	31	43.1	454	2	G91085	hypothetical prote	786	31	43.1	730	2	T05345	hypothetical prote
714	31	43.1	456	2	A60090	peripherin - Afric	787	31	43.1	770	2	T04792	hypothetical prote
715	31	43.1	462	2	T47808	allyl alcohol dehy	788	31	43.1	777	2	T00208	transposase-like p
716	31	43.1	463	2	T45756	hypothetical prote	789	31	43.1	783	2	S51968	probable membrane
717	31	43.1	464	2	AE2650	glutamine syntheta	790	31	43.1	787	2	Ti6901	hypothetical prote
718	31	43.1	466	2	EB4132	aminopeptidase BH3	791	31	43.1	801	2	B83195	hypothetical prote
719	31	43.1	467	1	MNVUML	nonstructural prot	792	31	43.1	801	2	G82302	probable cellobios
720	31	43.1	468	2	A37176	glutamate-ammonia	793	31	43.1	802	2	S49252	penicillin amidase
721	31	43.1	469	2	A64411	hypothetical prote	794	31	43.1	802	2	I39665	penicillin amidase
722	31	43.1	476	2	T05269	adenylyl cyclase-a	795	31	43.1	825	1	BLHQ	UDP-N-acetylurama
723	31	43.1	477	2	H75026	oligopeptide abc t	796	31	43.1	833	2	B81737	probable endopepti
724	31	43.1	479	2	D97432	probable glutamine	797	31	43.1	848	2	C70834	disease resistanc
725	31	43.1	481	2	T14300	hypothetical prote	798	31	43.1	853	2	Ti7461	large helicase-rel
726	31	43.1	489	2	AP2970	conserved hypotet	799	31	43.1	857	2	E87546	hypothetical prote
727	31	43.1	489	2	D98312	hypothetical prote	800	31	43.1	881	2	T31739	hypothetical prote
728	31	43.1	491	2	B81558	conserved hypotet	801	31	43.1	885	1	T04321	endopeptidase la h
729	31	43.1	496	2	AE0305	probable sugar tra	802	31	43.1	892	2	D69393	large helicase-rel
730	31	43.1	502	2	T26256	hypothetical prote	803	31	43.1	900	2	T33482	hypothetical prote
731	31	43.1	506	1	ACRYG1	nicotinic acetylch	804	31	43.1	920	2	T40771	hypothetical prote
732	31	43.1	506	2	T07209	H+-transporting tw	805	31	43.1	926	2	T04679	hypothetical prote
733	31	43.1	506	2	G86509	monooxygenase [imp	806	31	43.1	940	2	AB1744	internalin protein
734	31	43.1	506	2	A72113	monooxygenase - Ch	807	31	43.1	958	2	S73012	polyketide synthas
735	31	43.1	508	2	S51809	phosphoprotein pho	808	31	43.1	968	2	C82452	hypothetical prote
736	31	43.1	510	2	C84718	probable kinesin 1	809	31	43.1	992	2	S04781	excinuclease ABC c
737	31	43.1	512	2	AD0416	probable type II s	810	31	43.1	1018	2	B83099	probable RND efflu
738	31	43.1	514	2	S12394	probable transport	811	31	43.1	1019	1	A45341	major structural c
739	31	43.1	514	2	A71362	probable nitrogen	812	31	43.1	1056	2	S55151	probable membrane
740	31	43.1	519	2	S58155	RNA binding protei	813	31	43.1	1076	2	I39580	ncca protein - Alc
741	31	43.1	530	2	F82271	transglycosylase,	814	31	43.1	1077	2	D90387	peptidase related
742	31	43.1	538	1	BWB5D5	BUD5 protein - yea	815	31	43.1	1079	2	C96772	probable receptor
743	31	43.1	543	2	T37570	WD repeat protein	816	31	43.1	1085	2	S55352	IFH1 protein - yea
744	31	43.1	544	2	F97170	uncharacterized co	817	31	43.1	1088	1	YGBSTB	phenylalanine race
745	31	43.1	549	2	F70774	probable atpA prot	818	31	43.1	1091	2	T48444	hypothetical prote
746	31	43.1	550	2	E72481	hypothetical prote	819	31	43.1	1104	2	A60999	alpha-amylase (EC
747	31	43.1	550	2	T22557	hypothetical prote	820	31	43.1	1104	2	S36773	GPrase-activation f
748	31	43.1	550	2	T32543	hypothetical prote	821	31	43.1	1147	2	T42627	ADP-ribosylation f
749	31	43.1	557	2	AF3091	hypothetical prote	822	31	43.1	1165	2	A48667	peroxisomal assemb
750	31	43.1	557	2	D98195	hypothetical prote	823	31	43.1	1215	2	H84513	probable disease r
751	31	43.1	558	2	T32028	hypothetical prote	824	31	43.1	1235	2	AC1358	ATP-dependent deox
752	31	43.1	559	2	S54358	transcription fact	825	31	43.1	1270	2	AC1358	related to verruco
753	31	43.1	563	2	T40705	conserved hypotet	826	31	43.1	1279	2	T41389	rna binding protei
754	31	43.1	566	2	A84562	probable integral	827	31	43.1	1335	2	JQ1258	RNA-directed RNA p
755	31	43.1	568	2	F86224	hypothetical prote	828	31	43.1	1429	2	T13720	gene expanded prot
756	31	43.1	581	2	S49096	penicillin-binding	829	31	43.1	1454	2	S48264	protein kinase vps
757	31	43.1	582	2	S49097	penicillin-binding	830	31	43.1	1474	2	F69009	probable membrane
758	31	43.1	582	2	S49091	penicillin-binding	831	31	43.1	1531	2	T42218	slit-1 protein hom
759	31	43.1	582	2	A36190	penicillin-binding	832	31	43.1	1613	2	D90129	hypothetical prote

833	31	43.1	1871	2	A87204	polyketide synthas	906	30	41.7	206	1	E70197	conserved hypothet
834	31	43.1	2021	2	AD2267	serine/threonine k	907	30	41.7	208	2	F97570	GTP cyclohydrolase
835	31	43.1	2114	2	E96505	hypothetical prote	908	30	41.7	208	2	AF2791	GTP cyclohydrolase
836	31	43.1	2345	1	A35578	acetyl-CoA carboxy	909	30	41.7	210	2	H82747	ubiquinol cytochro
837	31	43.1	3165	2	S15010	hypothetical prote	910	30	41.7	210	2	T17910	hypothetical prote
838	31	43.1	4092	1	S38128	dynein heavy chain	911	30	41.7	210	2	C97260	probable membrane
839	31	43.1	4196	2	T43274	dynein heavy chain	912	30	41.7	211	2	H65539	SSU ribosomal prot
840	31	43.1	4344	1	A53489	dynein heavy chain	913	30	41.7	213	2	S29924	cyclin 1 - alfalfa
841	31	43.1	4845	2	T31067	BIR repeat contain	914	30	41.7	215	2	F71456	hypothetical prote
842	30.5	42.4	69	2	A05061	hypothetical prote	915	30	41.7	216	2	T45901	GTPase AtRAB8 - Ar
843	30.5	42.4	70	2	T07575	ribosomal protein	916	30	41.7	217	1	WJWSX2	homeotic protein H
844	30.5	42.4	131	2	E64219	ribosomal protein	917	30	41.7	218	1	QE5C24	probable transcrip
845	30.5	42.4	286	2	S75740	hypothetical prote	918	30	41.7	218	2	AE0749	invasion response-
846	30.5	42.4	368	2	F48864	hypothetical prote	919	30	41.7	218	2	E85808	probable 2-compone
847	30.5	42.4	420	2	I51088	L-SF precursor - J	920	30	41.7	218	2	D90960	probable 2-compone
848	30.5	42.4	447	2	G70030	amino acid permeas	921	30	41.7	220	2	C40818	hypothetical prote
849	30.5	42.4	495	2	T25066	probable farnesyl	922	30	41.7	221	2	T25027	hypothetical prote
850	30.5	42.4	498	2	G70964	probable arsc prot	923	30	41.7	224	2	E81329	probable two-compo
851	30.5	42.4	553	2	E95160	hypothetical prote	924	30	41.7	224	2	F90606	conserved hypothet
852	30.5	42.4	553	2	D98026	hypothetical prote	925	30	41.7	224	2	T32185	hypothetical prote
853	30.5	42.4	611	2	E72114	oligoendopeptidase	926	30	41.7	224	2	S64867	probable membrane
854	30.5	42.4	611	2	H86507	oligoendopeptidase [im	927	30	41.7	231	2	D81283	hypothetical prote
855	30.5	42.4	768	2	G82251	cation transport A	928	30	41.7	235	2	T40009	hypothetical prote
856	30.5	42.4	3712	1	YGCEVC	alpha-aminoacyl-	929	30	41.7	235	2	B72369	ABC transporter, A
857	30	41.7	52	2	AF2556	hypothetical prote	930	30	41.7	237	2	T47499	hypothetical prote
858	30	41.7	61	2	S66329	protein kinase AK1	931	30	41.7	242	2	G90104	putative tetramer
859	30	41.7	64	2	F48858	hypothetical prote	932	30	41.7	242	2	E81337	ABC-transporter Ar
860	30	41.7	69	2	AE3620	hypothetical prote	933	30	41.7	244	2	F96733	hypothetical prote
861	30	41.7	71	2	F82606	hypothetical prote	934	30	41.7	244	2	H97139	phage related anti
862	30	41.7	76	2	I59567	histone H2A - rat	935	30	41.7	246	2	AH0393	probable exported
863	30	41.7	86	2	S20649	Ig heavy chain V r	936	30	41.7	251	2	C83053	triosephosphate is
864	30	41.7	96	2	H86681	prophage pil prote	937	30	41.7	251	2	G84957	di-trans,poly-cis-
865	30	41.7	101	2	T17689	hypothetical prote	938	30	41.7	252	2	B84097	cyclase hiaF (impo
866	30	41.7	111	2	B72476	hypothetical prote	939	30	41.7	252	2	A12523	site-specific DNA-
867	30	41.7	116	2	S56693	glutathione peroxi	940	30	41.7	253	2	G70317	cyclase hiaF [imi
868	30	41.7	121	2	C86783	hypothetical prote	941	30	41.7	254	1	G64346	hypothetical prote
869	30	41.7	123	2	T17538	hypothetical prote	942	30	41.7	254	2	E97242	signal peptidase t
870	30	41.7	127	2	PH1421	Ig heavy chain V r	943	30	41.7	256	2	AH3562	triose-phosphate i
871	30	41.7	128	2	S06986	probable nitrogen	944	30	41.7	256	2	I49846	spaz2 protein - Sh
872	30	41.7	129	2	C97182	biotin carboxyl ca	945	30	41.7	256	2	B75079	hypothetical prote
873	30	41.7	132	2	PH1427	Ig heavy chain V r	946	30	41.7	257	2	H95163	hydrolase, haloaci
874	30	41.7	133	2	AF1077	PTS system, fracto	947	30	41.7	257	2	G98029	N-acetyl-glucosami
875	30	41.7	135	2	S34192	cysB protein - Thi	948	30	41.7	259	2	AD3141	hypothetical prote
876	30	41.7	136	2	T22797	hypothetical prote	949	30	41.7	259	2	H98146	probable amino-aci
877	30	41.7	138	2	AE1324	PTS mannose-specif	950	30	41.7	261	2	B97028	probable xylanase/
878	30	41.7	141	2	T40501	60s ribosomal prot	951	30	41.7	262	2	T01562	hypothetical prote
879	30	41.7	142	2	T03074	dual specificity p	952	30	41.7	262	2	B97310	probable amidohdr
880	30	41.7	143	2	T45259	hypothetical prote	953	30	41.7	262	2	F97009	uncharacterized co
881	30	41.7	146	2	G69020	conserved hypothet	954	30	41.7	263	2	S30400	hypothetical prote
882	30	41.7	147	2	B69040	hypothetical prote	955	30	41.7	265	2	H84005	hypothetical prote
883	30	41.7	147	2	AH2948	hypothetical prote	956	30	41.7	265	2	E89891	conserved hypothet
884	30	41.7	147	2	B98334	hypothetical prote	957	30	41.7	266	2	B70132	bacitracin resista
885	30	41.7	150	2	I70163	integrin beta 3 su	958	30	41.7	266	2	AH2467	transcription regu
886	30	41.7	150	2	C86876	hypothetical prote	959	30	41.7	267	2	B71828	phosphatidylserine
887	30	41.7	151	2	E43584	15K cysteine-rich	960	30	41.7	270	2	G90595	conserved hypothet
888	30	41.7	154	2	S17149	rusticyanin - Thio	961	30	41.7	271	2	JN0850	hypothetical 28.3k
889	30	41.7	155	2	S29825	rusticyanin - Thio	962	30	41.7	272	2	F75412	spermidine/putresc
890	30	41.7	158	2	B71190	hypothetical prote	963	30	41.7	275	2	F84088	N-acetylmuramoyl-L
891	30	41.7	161	2	AD2214	hypothetical prote	964	30	41.7	275	2	T24608	hypothetical prote
892	30	41.7	164	2	T20143	hypothetical prote	965	30	41.7	275	2	E90501	hypothetical prote
893	30	41.7	167	1	S33618	glutathione peroxi	966	30	41.7	276	2	S27641	hypothetical prote
894	30	41.7	167	2	H86784	VPS29-like phospho	967	30	41.7	278	2	AC3479	ATP-dependent heli
895	30	41.7	169	2	G83992	cell-cycle regulat	968	30	41.7	279	2	T47942	hypothetical prote
896	30	41.7	169	2	E97775	hypothetical prote	969	30	41.7	279	2	AC3114	hypothetical prote
897	30	41.7	172	2	B95361	protein [imported	970	30	41.7	280	2	T04769	hypothetical prote
898	30	41.7	173	2	T31343	hypothetical prote	971	30	41.7	280	2	E85225	hypothetical prote
899	30	41.7	175	2	S14023	hypothetical prote	972	30	41.7	281	1	S26018	NADH2 dehydrogenas
900	30	41.7	180	2	T12633	glutathione peroxi	973	30	41.7	284	1	S74516	(adenine-N6,N6-)-d
901	30	41.7	184	2	S73532	ribosome releasing	974	30	41.7	284	1	F64338	agmatinase (EC 3.5
902	30	41.7	186	2	T17497	ankyrin repeat pro	975	30	41.7	288	2	H90216	hypothetical prote
903	30	41.7	182	2	S42941	viral infectivity	976	30	41.7	289	2	S04648	ampr protein - Rho
904	30	41.7	201	2	F72390	hypothetical prote	977	30	41.7	290	2	B69772	conserved hypothet
905	30	41.7	203	2	T23282	hypothetical prote	978	30	41.7	293	2	D90153	cobalamin biosynth

979 30 41.7 294 2 S44080
980 30 41.7 294 2 AD2387
981 30 41.7 298 1 C42902
982 30 41.7 298 2 C55223
983 30 41.7 299 1 RP8CGP
984 30 41.7 300 2 A69351
985 30 41.7 301 2 D90224
986 30 41.7 301 2 T24993
987 30 41.7 302 2 S61836
988 30 41.7 304 2 B98173
989 30 41.7 305 2 A25010
990 30 41.7 308 2 C84072
991 30 41.7 309 2 F72368
992 30 41.7 309 2 AH3122
993 30 41.7 309 2 G98164
994 30 41.7 310 2 AC2035
995 30 41.7 311 2 A72487
996 30 41.7 312 2 F86044
997 30 41.7 312 2 B91198
998 30 41.7 313 2 AC1101
999 30 41.7 313 2 AC1463
1000 30 41.7 313 2 T30139

beta-lactamase (BC
hypothetical prote
3-hydroxyisobutyra
minor tail protein
glycerol-3-phospha
heterodisulfide re
spermidine synthas
hypothetical prote
cher protein - Rhi
hypothetical prote
pectinesterase (BC
UDP-glucose 4-epim
hypothetical prote
IS3 family transpo
IS3 family orfB pr
phytoene synthase
hypothetical prote
secreted protein E
EspB protein (impo
L-lactate dehydrog
L-lactate dehydrog
hypothetical prote

ALIGNMENTS

RESULT 1
B48089
growth arrest-specific protein gas6 - human
C:Species: Homo sapiens (man)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: B48089
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>
A:Cross-references: UNIPROT:Q14393; GB:U13720; NID:G401766; PIDN:AAAS8494.1; PID:G401767
F:41-92/Domain: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:120-153/Domain: EGF homology <EG1>
F:160-195/Domain: EGF homology <EG2>
F:201-236/Domain: EGF homology <EG3>
F:242-277/Domain: EGF homology <EG4>
F:311-671/Domain: sex hormone-binding globulin homology <SHB>
F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 100.0%; Score 72; DB 2; Length 678;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 284 VPFSVAKSVKSLYL 298
|||||

RESULT 2
A48089
growth arrest-specific protein gas6 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
R:Manfioletti, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of
A:Reference number: A48089; MUID:93330291; PMID:8336730
A:Accession: A48089

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-673 <MAN>
A:Cross-references: UNIPROT:Q61592; GB:X59846; NID:G407060; PIDN:CAA42507.1; PID:G407061
A>Note: authors translated the codon CCC for residue 424 as Ile
C:Genetics:
A:Gene: gas6
C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
F:38-89/Domain: Gla domain homology #status atypical <GLA>
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-666/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 95.8%; Score 69; DB 2; Length 673;
Best Local Similarity 93.3%; Pred. No. 8.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSVAKSVKSLYL 295
|||||

RESULT 3
I55476
growth potentiating factor - rat
C:Species: Rattus sp. (rat)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.;
J. Biol. Chem. 270, 5702-5705, 1995
A:Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating factor f
A:Reference number: I55476; MUID:95197586; PMID:7890695
A:Accession: I55476
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-674 <RES>
A:Cross-references: UNIPROT:Q63772; GB:D42148; NID:G1526567; PIDN:BAA07719.1; PID:G89340;
F:29-89/Domain: plasma protein S; EGF homology; Gla domain homology
F:117-150/Domain: EGF homology <EG1>
F:157-192/Domain: EGF homology <EG2>
F:198-233/Domain: EGF homology <EG3>
F:239-274/Domain: EGF homology <EG4>
F:308-667/Domain: sex hormone-binding globulin homology <SHB>
F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 95.8%; Score 69; DB 2; Length 674;
Best Local Similarity 93.3%; Pred. No. 8.7e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSVAKSVKSLYL 295
|||||

RESULT 4
S28285
hypothetical protein C38C10.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28285
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28285
A:Molecule type: DNA
A:Residues: 1-374 <THO>
A:Cross-references: UNIPROT:Q03566; EMBL:Z19153; NID:G6644; PID:G6645
C:Genetics:
A:Introns: 8/2; 108/2; 149/3; 176/2; 225/3; 289/2; 349/1

C:Accession: S48877; S64008
R:Cunningham, K.W.; Fink, G.R.
J. Cell Biol. 124, 351-363, 1994
A:Title: Calceinurin-dependent growth control in *Saccharomyces cerevisiae* mutants lacking
A:Reference number: S48877; MUID:94124630; PMID:7507493
A:Accession: S48877
A:Molecule type: DNA
A:Residues: 1-1173 <CUN>
A:Cross-references: UNIPROT:P38929; EMBL:U03060; NID:G454002; PIDN:AAC48919.1; PID:G4540
R:Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64003
A:Accession: S64008
A:Molecule type: DNA
A:Residues: 1-1173 <HEB>
A:Cross-references: EMBL:Z72528; NID:G1322456; PIDN:CAA96706.1; PID:G1322457; MIPS:YGL00
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PMC1
A:Cross-references: SGD:S0002974; MIPS:YGL006w
A:Map position: 7L
C:Function:
A:Description: pumps Ca2+ into the vacuole; participates in the control of the cytosolic
C:Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
C:Keywords: calcium transport; hydrolase; transmembrane protein; yeast vacuole
F:119-135/Domain: transmembrane #status predicted <TM1>
F:157-173/Domain: transmembrane #status predicted <TM2>
F:344-360/Domain: transmembrane #status predicted <TM3>
F:386-402/Domain: transmembrane #status predicted <TM4>
F:732-907/Domain: ATPase nucleotide-binding domain homology <ATN>
F:904-920/Domain: transmembrane #status predicted <TM5>
F:933-949/Domain: transmembrane #status predicted <TM6>
F:978-994/Domain: transmembrane #status predicted <TM7>
F:1068-1084/Domain: transmembrane #status predicted <TM8>
F:1101-1117/Domain: transmembrane #status predicted <TM9>

Query Match 56.9%; Score 41; DB 2; Length 1173;
Best Local Similarity 46.2%; Pred. No. 34;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
DB 1089 PFSIARQTKSMWI 1101
|||:|: |||:
|||:|: |||:

RESULT 10
VGURF
M polyprotein - Rift Valley fever virus (strain ZH-548M12)
N:Contains: glycoprotein G1; glycoprotein G2; nonstructural protein NS-M
C:Species: Rift Valley fever virus
A:Note: host (mosquito); Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
A:Accession: A30183
R:Takehara, K.; Min, M.K.; Battles, J.K.; Sugiyama, K.; Emery, V.C.; Dalrymple, J.M.; B
Virology 169, 452-457, 1999
A:Title: Identification of mutations in the M RNA of a candidate vaccine strain of Rift
A:Reference number: A30183; MUID:89204917; PMID:2705307
A:Accession: A30183
A:Molecule type: Genomic RNA
A:Residues: 1-1197 <TAK>
A:Cross-references: UNIPROT:P21401; GB:M25276; NID:G538444; PIDN:AAA47449.1; PID:G538445
C:Genetics:
A:Map position: segment M
C:Superfamily: phlebovirus M polyprotein
C:Keywords: glycoprotein; nonstructural protein; polyprotein
F:1-153/Product: nonstructural protein NS-M #status predicted <NSM>
F:154-690/Product: glycoprotein G1 #status predicted <GG1>
F:691-1197/Product: glycoprotein G2 #status predicted <GG2>
F:88,438,794,829,1035,1077/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 41; DB 1; Length 1197;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKNSKKVYL 356
|||:|: |||:
|||:|: |||:

RESULT 11

VGURV

M polyprotein - Rift Valley fever virus (strain ZH-501)
N:Contains: glycoprotein G1; glycoprotein G2; nonstructural protein NS-M
C:Species: Rift Valley fever virus

A:Note: host (mosquito); Homo sapiens (man)

C:Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C:Accession: A04110

R:Collett, M.S.; Purchio, A.F.; Kegan, K.; Frazier, S.; Hays, W.; Anderson, D.K.; Parker;

Virology 144, 228-245, 1985

A:Title: Complete nucleotide sequence of the M RNA segment of Rift valley fever virus.

A:Reference number: A04110; MUID:86045943; PMID:2998042

C:Accession: A04110

A:Molecule type: genomic RNA

A:Residues: 1-1206 <COL>

A:Cross-references: UNIPROT:P03518

C:Genetics:

A:Map position: segment M

C:Superfamily: phlebovirus M polyprotein

C:Keywords: glycoprotein; nonstructural protein; polyprotein

F:1-153/Product: nonstructural protein NS-M #status predicted <NSM>

F:154-690/Product: glycoprotein G1 #status predicted <GG1>

F:691-1206/Product: glycoprotein G2 #status predicted <GG2>

F:88,794,1035,1077/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 56.9%; Score 41; DB 1; Length 1206;
Best Local Similarity 57.1%; Pred. No. 35;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKNSKKVYL 356
|||:|: |||:
|||:|: |||:

RESULT 12

D70335

hypothetical protein aq_391 - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C:Accession: D70335

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: D70335

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-250 <AQF>

A:Cross-references: UNIPROT:O66712; GB:AE000688; NID:G2983063; PIDN:AAC06677.1; PID:G2983

A:Experimental source: strain VFS

C:Genetics:

A:Gene: aq_391

C:Superfamily: Aquifex aeolicus hypothetical protein aq_391

Query Match 55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 13

A48359

glutamyl-tRNA reductase (EC 1.2.1.1-) Hema - Chlorobium vibrioforme

C;Species: Chlorobium vibrioforme
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48359; S27546
R;Majumdar, D.; Avisar, Y.J.; Wyche, J.H.; Beale, S.I.
Arch. Microbiol. 156, 281-289, 1991
A;Title: Structure and expression of the Chlorobium vibrioforme hema gene.
A;Reference number: A48359; MUID:92171712; PMID:1793335
A;Accession: A48359
A;Molecule type: DNA
A;Residues: 1-415 <NAJ>
A;Cross-references: UNIPROT:P28462; EMBL:M59194; NID:g144474; PID:g144475
A;Note: submitted to the EMBL Data Library, July 1991
A;Note: sequence extracted from NCBI backbone (NCIN:86184, NCBI:P:86186)
C;Function:
A;Description: catalyzes the reduction of glutamyl-tRNA (GLU) by NADPH to glutamic acid
A;Pathway: aminolevulinate biosynthesis; porphyrin biosynthesis
C;Superfamily: glutamyl-tRNA reductase
C;Keywords: aminolevulinate biosynthesis; NADP; oxidoreductase; porphyrin biosynthesis

Query Match 55.8%; Score 40; DB 1; Length 415;
Best Local Similarity 80.0%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRSVAKSVKS 11
Db 145 PFSVAKVKVT 154
|||||

RESULT 14
T08268
conserved hypothetical protein H0581 - Halobacterium sp. (strain NRC-1) plasmid pNRC100
N;Alternate names: hypothetical protein H1776
C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08375
R;Ng, W.V.; Clufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, D.; Faust, J.; Hall, B.;
Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic Archaeon: megaplasmid or
A;Reference number: Z16408; MUID:99063795; PMID:9847077
A;Accession: T08268
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-421 <NGW>
A;Cross-references: UNIPROT:O54630; EMBL:AF016485; NID:g2822278; PID:g2822329; HALOSP:H0
A;Experimental source: strain NRC-1
A;Genetics: COP1
A;Accession: T08375
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-421 <DAS>
A;Cross-references: EMBL:AF016485; NID:g2822278; PID:g2822436; HALOSP:H1776
A;Experimental source: strain NRC-1
A;Genetics: COP2
C;Genetics: <COP1>
A;Gene: HALOSP:H0581
A;Genome: plasmid pNRC100
C;Genetics: <COP2>
A;Gene: HALOSP:H1776
A;Genome: plasmid pNRC100
C;Superfamily: hypothetical protein b2322

Query Match 54.2%; Score 39; DB 2; Length 421;
Best Local Similarity 46.7%; Pred. No. 27;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
Db 60 VSFGIVKSIILNLYAG 74
| | | | |

RESULT 15
T48015

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48015
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer, T.
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T48015
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-461 <RIE>
A;Cross-references: UNIPROT:Q9MI01; EMBL:AL138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
A;Map position: 3
A;Note: T17J13.190

Query Match 54.2%; Score 39; DB 2; Length 461;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 111 IEFVSKNVKHLFL 124
| | | | |

RESULT 16
T25168
hypothetical protein T23F1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25168
R;Wilkinson, J.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19990
A;Accession: T25168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1362 <WIL>
A;Cross-references: UNIPROT:O18117; EMBL:Z81129; PIDN:CAB03404.1; GSPDB:GN00023; CESP:T2;
A;Experimental source: clone T23F1
C;Genetics:
A;Gene: CESP:T23F1.5
A;Map position: 5
A;Introns: 49/3; 201/1; 505/3; 609/3; 909/1; 944/2; 1025/2; 1079/1; 1168/3; 1225/1

Query Match 54.2%; Score 39; DB 2; Length 1262;
Best Local Similarity 42.9%; Pred. No. 87;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
Db 363 PFNDLKTIRPIYL 376
| | | | |

RESULT 17
S60949
probable phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O5064; protein YOR222w; protein YOR50-12
C;Species: Saccharomyces cerevisiae
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S60949; S67115; B37984; S71724
R;Gallison, F.; Dujon, B.
submitted to the EMBL Data Library, October 1995
A;Description: Sequence and analysis of a 33 kb fragment from the right arm of chromosome
A;Reference number: S60938
A;Accession: S60949
A;Molecule type: DNA
A;Residues: 1-307 <GAL>
A;Cross-references: UNIPROT:Q99297; EMBL:X92441; NID:g1050762; PID:g1050774
R;Boyer, J.; Fairhead, C.; Gallion, L.; Gallison, F.; Michaux, G.; Thierry, A.; Dujon, B.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67104

A;Accession: S67115
A;Molecule type: DNA
A;Residues: 1-307 <BOY>
A;Cross-references: EMBL:275130; NID:g1420513; PID:g1420514; MIPS:YOR222w
A;Experimental source: strain S288C
R;Guerin, B.; Bukusoglu, C.; Rakotonanana, F.; Wohlrab, H.
J. Biol. Chem. 265, 19736-19741, 1990
A;Title: Mitochondrial phosphate transport. N-ethylmaleimide insensitivity correlates with
A;Reference number: A37984; MUID:91060585; PMID:2246257
A;Accession: B37984
A;Molecule type: protein
A;Residues: 30,'X',32,'I',34-39 <GUE>
R;Galisson, F.; Dujon, B.
Yeast 12, 877-885, 1996
A;Title: Sequence and analysis of a 33 kb fragment from the right arm of chromosome XV of
A;Reference number: S71713; MUID:96437977; PMID:8840505
A;Accession: S71724
A;Molecule type: DNA
A;Residues: 1-307 <GAW>
A;Cross-references: EMBL:X92441; NID:g1050762; PIDN:CAA63185.1; PID:g1050774
C;Genetics:
A;Gene: SGD:ODC2
A;Cross-references: SGD:S0005748
A;Map position: 15R
A;Note: YOR222w
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C;Keywords: duplication; mitochondrion; transmembrane protein
F;9-107/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F;115-201/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F;208-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>
Query Match 52.8%; Score 38; DB 2; Length 307;
Best Local Similarity 52.6%; Pred. No. 30;
Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;
QY 1 VPFSVAK-----SVKSLYL 15
|||:| ||| |||
DB 137 VPFEIKIRMQDVKSYLG 155
|||:| ||| |||
RESULT 18
C75012
hypothetical protein PAB1275 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75012
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A;Reference number: A75001
A;Accession: C75012
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 <KAW>
A;Cross-references: UNIPROT:Q9UY75; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB5053
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1275
Query Match 52.8%; Score 38; DB 2; Length 317;
Best Local Similarity 50.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
|||:| ||| |||
DB 27 VPFGLENSIKSLVI 40
|||:| ||| |||
RESULT 19
B83902
transcription repressor (beta-galactosidase gene) lacR [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: B83902
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83902
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-330 <STO>
A;Cross-references: UNIPROT:Q9KBB0; GB:AP001514; GB:BA000004; NID:g10174613; PIDN:BAB0573
A;Experimental source: strain C-125
C;Genetics:
A;Gene: lacR
C;Superfamily: lac repressor
Query Match 52.8%; Score 38; DB 2; Length 330;
Best Local Similarity 77.8%; Pred. No. 32;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 7 KSVKSLYL 15
|||:| ||| |||
DB 312 KSVKTLYL 320
|||:| ||| |||
RESULT 20
S59308
probable membrane protein YMR315w - Yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YMR924.07
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S59308
R;Churcher, C.M.
submitted to the EMBL Data Library, September 1995
A;Reference number: S59302
A;Accession: S59308
A;Molecule type: DNA
A;Residues: 1-349 <CHU>
A;Cross-references: UNIPROT:Q04869; EMBL:Z54141; NID:g1072408; PID:g984688; GSPDB:GN00013
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR315w
A;Cross-references: SGD:S0004932
A;Map position: 13R
C;Superfamily: Streptomyces griseus strI protein
C;Keywords: transmembrane protein
F;189-205/Domain: transmembrane #status predicted <TMM>
Query Match 52.8%; Score 38; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 SVAKSVKSLYL 15
|||:| ||| |||
DB 307 AVSKKDKSLYL 318
|||:| ||| |||
RESULT 21
T03841
patatin homolog - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T03841
R;Draws, G.N.; Beals, T.P.; Bui, A.Q.; Goldberg, R.B.
Plant Cell 4, 1383-1404, 1992
A;Title: Regional and cell-specific gene expression patterns during petal development.
A;Reference number: Z15112; MUID:93120883; PMID:1477554
A;Accession: T03841
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-390 <DRE>
A;Cross-references: UNIPROT:O24152; EMBL:U68484; NID:g1546816; PIDN:AAB08428.1; PID:g1546
C;Superfamily: patatin

QY 1 VPFSVAKSVKSLYL 15
:| |::| | | | |
Db 143 IPLNQKLTESLYL 157

RESULT 26
G70446
hypothetical protein aq_1695 - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: G70446
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: G70446
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-296 <AQF>
A:Cross-references: UNIPROT:O67600; GB:AE000751; NID:g2984013; PIDN:AAC07562.1; PID:g298
A:Experimental source: strain VFS
C:Genetics:
A:Gene: aq_1695

Query Match 52.1%; Score 37.5; DB 2; Length 296;
Best Local Similarity 60.0%; Pred. No. 36;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 1 VPFSVAKS-VKSLYL 14
:| | | | | | | | | |
Db 234 IFFERAKSLVKMYL 248

RESULT 27
OYECHF
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [validated] - Esche
N:Alternate names: cyclase
C:Species: Escherichia coli
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 09-Jul-2004
C:Accession: JS0134; I76779; H64967
R:Carlomagno, M.S.; Chiarotini, L.; Alifano, P.; Nappo, A.G.; Bruni, C.B.
J. Mol. Biol. 203, 585-606, 1998
A:Title: Structure and function of the Salmonella typhimurium and Escherichia coli K-12
A:Reference number: JS0131; MUID:89094829; PMID:3062174
A:Accession: JS0134
A:Molecule type: DNA
A:Residues: 1-258 <CAR>
A:Cross-references: UNIPROT:P60664; GB:X13462; NID:g41706; PIDN:CAA31817.1; PID:g41714
A:Experimental source: strain K12
R:Sugiyama, T.; Kido, N.; Komatsu, T.; Ohta, M.; Jann, K.; Jann, B.; Saeki, A.; Kato, N.
Microbiology 140, 59-71, 1994
A:Title: Genetic analysis of Escherichia coli O9 rfb: identification and DNA sequence of
A:Reference number: I57096; MUID:94214678; PMID:8162191
A:Accession: I76779
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 109-258 <RES>
A:Cross-references: GB:D43637; NID:g598464; PIDN:BAA07754.1; PID:g598474
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:197426617; PMID:9278503
A:Accession: H64967
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-258 <BLAT>
A:Cross-references: GB:AE000293; NID:u00096; NID:g2367127; PIDN:AAC75086.1; PID:g1788336;
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: hisF

A:Map position: 44 min
C:Function:
A:Description: catalyzes the cyclization reaction that produces D-erythro-imidazole glyce
A:Pathway: histidine biosynthesis
A:Note: hisH and hisF gene products form a dimer that constitutes imidazole glycerol pho
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase; histidine biosynthesis

Query Match 51.4%; Score 37; DB 1; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
:| | | | | | | | | |
Db 75 IFFCVAGGIKSL 86

RESULT 28
B90982
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [similarity] - Esche
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: B90982
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: B90982
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <HAY>
A:Cross-references: UNIPROT:P60665; GB:BA000007; PIDN:BA0362294.1; PID:g13362294; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIND 0509952
C:Genetics:
A:Gene: ECS2826
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
:| | | | | | | | | |
Db 75 IFFCVAGGIKSL 86

RESULT 29
H85827
imidazoleglycerol-phosphate synthase (EC 4.3.2.-) cyclase chain hisF [similarity] - Esche
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85827
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85827
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <STO>
A:Cross-references: UNIPROT:P60665; GB:AE005174; NID:g12516206; PIDN:AAG57084.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: hisF
C:Superfamily: cyclase hisF
C:Keywords: amidine-lyase; carbon-nitrogen lyase

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : |||
Db 75 IPFCVAGGIKSL 86

RESULT 30
B54052
cyclase hisF - Klebsiella pneumoniae
C:Species: Klebsiella pneumoniae
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B54052
R:Bieder, G.; Merrick, M.J.; Castorpha, H.; Kleiner, D.
J. Biol. Chem. 269, 14386-14390, 1994
A:Title: Function of hisF and hisH gene products in histidine biosynthesis.
A:Reference number: A54052; MUID:94237842; PMID:8182043
A:Accession: B54052
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <RIE>
A:Cross-references: UNIPROT:P45603; GB:X56607; NID:G530021; PIDN:CAA39944.1; PID:G530022
A:Experimental source: M5a1
C:Note: sequence extracted from NCBI backbone (NCBIN:148607, NCBIP:148609)
C:Genetics:
A:Gene: hisF
C:Superfamily: cyclase hisF
C:Keywords: histidine biosynthesis

Query Match 51.4%; Score 37; DB 2; Length 258;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : |||
Db 75 IPFCVAGGIKSL 86

RESULT 31
T37185
probable gntR-family transcription regulator - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37185
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T37185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-259 <SEE>
A:Cross-references: UNIPROT:Q9X9T6; EMBL:AL096823; PIDN:CAB46970.1; GSPDB:GN000070; SCOE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE:SCQ11.15C
C:Superfamily: korA protein

Query Match 51.4%; Score 37; DB 2; Length 259;
Best Local Similarity 58.3%; Pred. No. 39;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSL 12
: || || : |||
Db 154 IPFEVAESVPAL 165

RESULT 32
S47620
beta-lactamase - Proteus vulgaris
C:Species: Proteus vulgaris
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S47620
R:Peduzzi, J.; Reynaud, A.; Baron, P.; Barthelemy, M.; Labia, R.
Biochim. Biophys. Acta 1207, 31-39, 1994

Query Match 51.4%; Score 37; DB 2; Length 271;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYIG 15
| : ||| : |||
Db 159 PIAMAKSLQALTIG 172

RESULT 33
S51044
beta-lactamase - Proteus vulgaris
C:Species: Proteus vulgaris
C>Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51044
R:Datz, M.; Joris, B.; Azab, E.A.M.; Galleni, M.; van Beeumen, J.; Frere, J.M.; Martin, F.
Eur. J. Biochem. 226, 149-157, 1994
A:Title: A common system controls the induction of very different genes. The class-A beta
A:Reference number: S51044; MUID:95045583; PMID:7957242
A:Accession: S51044
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <DAT>
A:Cross-references: UNIPROT:P52664; EMBL:X80128; NID:G511055; PIDN:CAA56427.1; PID:G5110:
C:Superfamily: beta-lactamase I

Query Match 51.4%; Score 37; DB 2; Length 300;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYIG 15
| : ||| : |||
Db 188 PIAMAKSLQALTIG 201

RESULT 34
A55792
beta-lactamase (EC 3.5.2.6) precursor - Proteus vulgaris
C:Species: Proteus vulgaris
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-2004
C:Accession: A55792
R:Tamaki, M.; Nukaga, M.; Sawai, T.
Biochemistry 33, 10200-10206, 1994
A:Title: Replacement of serine 237 in class A beta-lactamase of Proteus vulgaris modifies
A:Reference number: A55792; MUID:94339110; PMID:8060386
A:Accession: A55792
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <TAM>
A:Cross-references: UNIPROT:O52615; GB:D29982; NID:G484056; PIDN:BAA06252.1; PID:G599572:
C:Superfamily: Beta-lactamase I
C:Keywords: Hydrolase
F:46/Active site: Ser #status predicted

Query Match 51.4%; Score 37; DB 2; Length 300;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYIG 15
| : ||| : |||
Db 188 PIAMAKSLQALTIG 201

RESULT 35

A:Title: Chromosomally encoded cephalosporin-hydrolyzing beta-lactamase of Proteus vulgaris
A:Reference number: S47620; MUID:94318667; PMID:8043607
A:Accession: S47620
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-271 <PED>
A:Cross-references: UNIPROT:P80298
C:Superfamily: beta-lactamase I

S53908
hypothetical protein YNL072w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein N2369
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S53908; S63004; S63937
R:Poehlmann, R.; Philippsen, P.
submitted to the EMBL Data Library, April 1995
A:Reference number: S53896
A:Accession: S53908
A:Molecule type: DNA
A:Residues: 1-307 <POE>
A:Cross-references: UNIPROT:P53942; EMBL:X86470; NID:G791101; PID:G791114
R:Poehlmann, R.; Philippsen, P.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S62997
A:Accession: S63004
A:Molecule type: DNA
A:Residues: 1-307 <POW>
A:Cross-references: EMBL:Z71348; NID:G1301956; PID:E239686; PID:G1301957; MIPS:YNL072w
A:Experimental source: strain S288C
R:Poehlmann, R.; Philippsen, P.
Yeast 12, 391-402, 1996
A:Title: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV reveals 12
A:Reference number: S63925; MUID:96267764; PMID:8701611
A:Accession: S63937
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-307 <POF>
A:Cross-references: EMBL:X86470; NID:G791101; PIDN:CA60188.1; PID:G791114
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C:Genetics:
A:Gene: SGD:RNH35
A:Cross-references: SGD:S0005016; MIPS:YNL072w
A:Map position: 14L

```

Query Match      51.4%; Score 37; DB 2; Length 307;
Best Local Similarity 61.5%; Pred. No. 46;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLY 13
   | : |||
Db 174 VKFTVAKKADSLY 186

```

RESULT 36

A53120 intracellular coagulation inhibitor LICI precursor - horseshoe crab *Tachypileus tridentatus*

C/Species: *Tachypileus tridentatus*

C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004

C/Accession: A53120

R/Miura, Y.; Kawabata, S.; Iwanaga, S.

J. Biol. Chem. 269, 542-547, 1994

A/Title: A Limulus intracellular coagulation inhibitor with characteristics of the serpin

A/Reference number: A53120; MUID:94103268; PMID:8276848

A/Accession: A53120

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-418 <MTU>

A/Cross-references: UNIPROT:Q27085; GB:D14483; NID:G441213; PIDN:BAA03374.1; PID:G441214

C/Superfamily: intracellular coagulation inhibitor LICI

C/Keywords: serine proteinase inhibitor

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-418/Product: intracellular coagulation inhibitor LICI #status experimental <MAT>

```

RESULT 37
AGI028
prepin [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AGI028
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
  T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
  S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
  A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AGI028
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-435 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD09328.1; PID:gi60505328; GSPDB:GN00176
C:Genetics:
A:Gene: pilV
C:Superfamily: shufflon

Query Match          51.4%; Score 37; DB 2; Length 435;
Best Local Similarity 46.2%; Pred. No. 67;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

```

RESULT 38
G31090
H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - Anabaena sp.
C:Species: Anabaena sp.
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: G31090
R:McCaern, D.F.; Whitaker, R.A.; Alam, J.; Vrba, J.M.; Curtis, S.E.
J. Bacteriol. 170, 3448-3458, 1988
A:Title: Genes encoding the alpha, gamma, delta, and four F-0 subunits of ATP synthase cc
A:Reference number: A91875; MUID:88298650; PMID:2900236
A:Accession: G31090
A:Molecule type: mRNA
A:Residues: 1-506 <MCC>
A:Cross-references: UNIPROT:P12405; GB:M21659; NID:g141996; PIDN:AAA21991.1; PID:g142003
A:Experimental source: PCC 7120
C:Genetics:
A:Gene: atpA
C:Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase al
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding;
P:171-178/Region: nucleotide-binding motif A (P-loop)
P:196-368/Domain: H+-transporting ATP synthase alpha chain homology <ATP>

RESULT 39

ARP synthase chain alpha [imported] - Nostoc sp. (strain PCC 7120)

AE1807

C:Species: Nostoc sp. PCC 7120

C:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AE1807

R:Kaneko, T.; Nakamura, Y.; Sugi, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

QY 2 PFSVAKSVKSLYL 15
|| : : : :
Db 458 PFPVEEQIVSIYVG 471

RESULT 42
S42459
N:Contains: DNA polymerase (EC 2.7.7.7) Vent, intein containing precursor - Thermococcus
C:Species: Thermococcus litoralis
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: S42459; S42451; S42458
R:Perler, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Benner, J.
submitted to the EMBL Data Library, September 1992
A:Reference number: S42450; MUID:92302285; PMID:1608969
A:Accession: S42458
A:Accession: S42459
A:Molecule type: DNA
A:Residues: 1-1702 <P>1
A:CROSS-references: UNIPROT:P30317; EMBL:M74198; NID:G154685; PIDN:AAA72100.1; PID:G154685
R:Perler, F.B.; Comb, D.G.; Jack, W.E.; Moran, L.S.; Qiang, B.; Kucera, R.B.; Benner, J.,
Proc. Natl. Acad. Sci. U.S.A. 89, 5577-5581, 1992
A:Title: Intervening sequences in an Archaea DNA polymerase gene.
A:Reference number: S42450; MUID:92302285; PMID:1608969
A:Accession: S42451
A:Molecule type: DNA
A:Residues: 181-222;387-425;452-476;483-524;1021-1062;1076-1099;1466-1489;1533-1547 <P>1
R:Hodges, R.A.; Perler, F.B.; Noren, C.J.; Jack, W.E.
Nucleic Acids Res. 20, 6153-6157, 1992
A:Title: Protein splicing removes intervening sequences in an archaea DNA polymerase.
A:Reference number: S40788; MUID:93117083; PMID:1475179
A:Contents: annotation
C:Function: <VENT>
A:Description: nucleotidyltransferase
A:Note: DNA-directed DNA polymerase Vent
C:Function: <END1>
A:Description: endonuclease
A:Note: DNA endonuclease PI-T11
C:Function: <END2>
A:Description: endonuclease, hydrolase
A:Note: DNA endonuclease PI-T111
C:Superfamily: Thermococcus litoralis DNA-directed DNA polymerase Vent
F:1-494,1033-1081,1472-1702/Product: DNA-directed DNA polymerase Vent #status predicted <XT1>
F:1-494/DNA: DNA-directed DNA polymerase Vent extein 1 #status predicted <XT1>
F:495-1032/Product: DNA endonuclease PI-II (pol Vent intein 1) #status predicted <MAT2>
F:1033-1081/DNA: DNA-directed DNA polymerase Vent extein 2 #status predicted <XT2>
F:1082-1471/Product: DNA endonuclease PI-I (pol Vent intein 2) #status predicted <XT2>
F:1472-1702/DNA: DNA-directed DNA polymerase Vent extein 3 #status predicted <XT3>
F:494-1033/Cross-link: peptide (Asn-Ser) #status predicted
F:1081-1472/Cross-link: peptide (Asp-Thr) #status predicted

Query Match 51.4%; Score 37; DB 2; Length 1702;
Best Local Similarity 63.6%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSL 12
|| : : : :
Db 1195 PFBGLGKAVKSL 1205

RESULT 43
T00127
Hypothetical protein 5 - Leptosira interrogans
C:Species: Leptosira interrogans
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00127
R:Takahashi, Y.; Akase, K.; Hirano, H.; Fukunaga, M.
Gene 215, 37-45, 1998
A:Title: Physical and genetic maps of the Leptosira interrogans serovar icterohaemorrhagiae

A:Reference number: Z14115; MUID:98332717; PMID:9666070

A:Accession: T00127
A:Status: preliminary; translated from GB/EMBL/DBDJB
A:Molecule type: DNA
A:Residues: 1-437 <FA>

A:Cross-references: UNIPROT:P97044; EMBL:AB010203; NID:g2780763; PIDN:BAA24374.1; PID:g2780763; strain Ictero No.1; substrain icterohaemorrhagiae
A:Experimental source: strain Ictero No.1; substrain icterohaemorrhagiae
C:Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 50.7%; Score 36.5; DB 2; Length 437;
Best Local Similarity 50.0%; Pred. No. 84; Mismatches 2; Indels 1; Gaps 1;
Matches 8; Conservative 5;

QY 1 VPFSVAKSVKS-LYLIG 15
: : ||| : : : :
DB 304 IPYVAKVRSDLIMG 319

RESULT 44

C91278
hypothetical protein ECs5195 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli

C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C91278

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference number: A99623; MUID:21156231; PMID:11258796

A:Accession: C91278
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-81 <HAY>
A:Cross-references: UNIPROT:Q8XCG4; GB:BA000007; PIDN:BAE38618.1; PID:gl3364672; GSPDB:G

A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs5195

Query Match 50.0%; Score 36; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
: : ||| : : : :
DB 22 PLQVAKYVKILFRG 35

RESULT 45

C86119
hypothetical protein ytfK [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C86119

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: C86119
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-81 <STO>
A:Cross-references: UNIPROT:Q8XCG4; GB:AE005174; NID:gl2519216; PIDN:AAG59415.1; GSPDB:G

A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ytfK

Query Match 50.0%; Score 36; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
: : ||| : : : :
DB 22 PLQVAKYVKILFRG 35

RESULT 46

DS5233

hypothetical 9.6 kD protein in cysg-mara intergenic region - Escherichia coli (strain K-12)
N:Alternate names: hypothetical protein o81
C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: DS5233; S56442

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: DS5233
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-81 <BLAT>

A:Cross-references: UNIPROT:Q8XCG4; GB:AE000493; GB:U00096; NID:g2367360; PIDN:AAC77174.1
A:Experimental source: strain K-12, substrain MG1655

R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995

A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.8
A:Reference number: S56314; MUID:95334362; PMID:7610040

A:Accession: S56442
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 'V', 2-81 <BUR>

A:Cross-references: EMBL:U14003
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

C:Genetics:
A:Gene: ytfK

A:Start codon: GTG

Query Match 50.0%; Score 36; DB 2; Length 81;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
: : ||| : : : :
DB 22 PLQVAKYVKILFRG 35

RESULT 47

AH1054

conserved hypothetical protein ytfK [imported] - Salmonella enterica subsp. enterica sero
C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AH1054
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH1054
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-90 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD06885.1; PID:gl6505533; GSPDB:GN00176

C:Genetics:
A:Gene: ytfK

Query Match 50.0%; Score 36; DB 2; Length 90;
Best Local Similarity 57.1%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYLIG 15
: : ||| : : : :
DB 31 PLQVAKYVKILFRG 44

A64209
 ribosomal protein L1 - Mycoplasma genitalium
 C:Species: Mycoplasma genitalium
 C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C:Accession: A64209
 R:Praser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A:Title: The minimal gene complement of Mycoplasma genitalium.
 A:Reference number: A64200; MUID:96026346; PMID:7569993
 A:Accession: A64209

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 09:31:46 ; Search time 26.044 Seconds
(without alignments)
222.507 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72

Sequence: 1 VPFSVAKSVKSLYL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1726216 seqs, 386330316 residues

Total number of hits satisfying chosen parameters: 1726216

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/1/pubaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/1/pubaa/US10F_PUBCOMB.pep.*

19: /cgn2_6/ptodata/1/pubaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	510	16	US-10-367-094-34
2	72	100.0	678	16	US-10-671-054-3
3	72	100.0	678	17	US-10-696-909A-41
4	72	100.0	686	16	US-10-671-054-1
5	69	95.8	673	14	US-10-223-085-48
6	69	95.8	673	14	US-10-223-084-48
7	69	95.8	673	14	US-10-223-088-48
8	69	95.8	673	14	US-10-223-090-48
9	69	95.8	673	14	US-10-223-087-48
10	69	95.8	673	14	US-10-223-083-48
11	69	95.8	673	14	US-10-223-089-48
12	69	95.8	673	14	US-10-223-082-48
13	69	95.8	673	14	US-10-223-081-48
14	69	95.8	673	15	US-10-305-654-48
15	69	95.8	673	15	US-10-081-056-48
16	69	95.8	673	16	US-10-367-094-31
17	69	95.8	673	16	US-10-369-493-5833
18	69	95.8	673	16	US-10-437-963-128669
19	42.5	59.0	72	16	US-10-425-115-203276
20	42	58.3	291	15	US-10-062-188-1
21	42	58.3	1220	9	US-09-801-368-332
22	42	58.3	1220	15	US-10-369-493-22082
23	41	56.9	1283	16	US-10-425-115-268339
24	41	56.9	323	16	US-10-425-115-256726
25	41	56.9	366	16	US-10-733-930-9784
26	41	56.9	1173	15	US-10-369-493-21954
27	41	56.9	1235	17	US-10-741-849-7057
28	40	55.6	132	15	US-10-424-599-201272
29	40	55.6	969	14	US-10-032-585-7469
30	39	54.2	70	16	US-10-425-115-190887
31	39	54.2	369	14	US-10-328-675A-74
32	39	54.2	484	16	US-10-437-963-171845
33	39	54.2	829	16	US-10-437-963-126646
34	39	54.2	1256	16	US-10-437-963-171836
35	39	54.2	38	16	US-10-425-115-302429
36	38	52.8	78	16	US-10-437-963-188870
37	38	52.8	133	15	US-10-363-616-335
38	38	52.8	260	16	US-10-425-115-331872
39	38	52.8	307	15	US-10-369-493-22398
40	38	52.8	399	16	US-10-425-115-318065
41	38	52.8	418	14	US-10-092-771-10
42	38	52.8	441	16	US-10-437-963-120006
43	38	52.8	632	15	US-10-424-599-183414
44	38	52.8	637	15	US-10-425-114-37208
45	38	52.8	645	16	US-10-437-963-132886
46	38	52.8	661	15	US-10-038-854-135
47	38	52.8	661	15	US-10-037-417-107
48	38	52.8	1870	16	US-10-437-963-133517
49	37	51.4	54	16	US-10-425-115-254685
50	37	51.4	62	9	US-09-864-761-36016
51	37	51.4	126	15	US-10-424-599-205095
52	37	51.4	120	15	US-10-424-599-204741
53	37	51.4	134	16	US-10-425-115-261777
54	37	51.4	258	15	US-10-369-493-883
55	37	51.4	266	15	US-10-424-599-232408
56	37	51.4	307	9	US-09-799-848-4
57	37	51.4	307	15	US-10-369-493-1382
58	37	51.4	307	16	US-10-679-761-9
59	37	51.4	364	16	US-10-437-963-177728
60	37	51.4	506	15	US-10-369-493-18942
61	37	51.4	531	15	US-10-432-422-54
62	37	51.4	601	14	US-10-156-761-14851
63	37	51.4	812	15	US-10-432-422-47
64	37	51.4	1146	16	US-10-437-963-118157
65	36.5	50.7	966	14	US-10-153-244-105
66	36.5	50.7	966	14	US-10-210-152-22
67	36.5	50.7	966	15	US-10-405-793-22
68	36	50.0	56	15	US-10-424-599-235642
69	36	50.0	58	15	US-10-424-599-143502
70	36	50.0	70	15	US-10-424-599-285491
71	36	50.0	95	15	US-10-424-599-274743
72	36	50.0	106	16	US-10-425-115-367968
73	36	50.0	161	16	US-10-767-701-40439
74	36	50.0	203	15	US-10-424-599-164629
75	36	50.0	226	15	US-10-282-122A-63436
76	36	50.0	297	9	US-09-991-211-4
77	36	50.0	394	10	US-09-879-389B-2
78	36	50.0	410	9	US-09-815-242-11028
79	36	50.0	432	15	US-10-282-122A-54356
80	36	50.0	498	16	US-10-425-115-32263
81	36	50.0	529	15	US-10-282-122A-77475
82	36	50.0	641	15	US-10-231-913-57
83	36	50.0	876	14	US-10-198-070-119
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Sequence 77475, A
Sequence 57, Appl
Sequence 119, App
Sequence 124, App


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961 35 48.6 775 14 US-10-124-823-120 Sequence 120, App
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998 35 48.6 775 15 US-10-147-535-120 Sequence 120, App
999 35 48.6 775 15 US-10-147-537-120 Sequence 120, App
1000 35 48.6 775 15 US-10-152-376-120 Sequence 120, App
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ALIGNMENTS

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RESULT 1
US-10-367-094-34
; Sequence 34, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-094-34
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Query Match 100.0%; Score 72; DB 16; Length 510;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYLG 15
Db 122 VPFSVAKSVKSLYLG 136
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RESULT 2
US-10-671-054-3
; Sequence 3, Application US/10671054
; Publication No. US20040157774A1
; GENERAL INFORMATION:
; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPITOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/413157
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-3
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Query Match 100.0%; Score 72; DB 16; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298
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RESULT 3
US-10-696-909A-41
; Sequence 41, Application US/10696909A
; Publication No. US20050118604A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Atchison, Robert E.
; APPLICANT: Friera, Anabella
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-005820US
; CURRENT APPLICATION NUMBER: US/10/696,909A
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: US 60/512,251
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 60/421,989
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 678
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: growth arrest-specific 6 (GAS6), AXL stimulatory
; OTHER INFORMATION: factor
US-10-696-909A-41
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Query Match 100.0%; Score 72; DB 17; Length 678;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 VPFSVAKSVKSLYLG 15
Db 284 VPFSVAKSVKSLYLG 298
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RESULT 4
US-10-671-054-1
; Sequence 1, Application US/10671054
; Publication No. US20040157774A1
; GENERAL INFORMATION:
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; APPLICANT: Johnson & Johnson
; TITLE OF INVENTION: EPTOPE TAGGED RECOMBINANT GROWTH ARREST SPECIFIC GENE 6
; FILE REFERENCE: CEN-5015USNP
; CURRENT APPLICATION NUMBER: US/10/671,054
; PRIOR FILING DATE: 2003-09-24
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-671-054-1

Query Match 100.0%; Score 72; DB 16; Length 686;
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 284 VPFSVAKSVKSLYLIG 298

RESULT 5
US-10-223-085-48
; Sequence 48, Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PC10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-084-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-085-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLIG 15
Db 281 VPFSVAKSVKSLYLIG 295

RESULT 6
US-10-223-084-48
; Sequence 48, Application US/10223084
; Publication No. US20030105011A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PC15
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-084-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      281 VPFSMAKSVKSLYLG 295

RESULT 7
US-10-223-088-48
; Sequence 48, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P3235PIC6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-223-088-48

Query Match      95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VPFSMAKSVKSLYLG 15
Db      281 VPFSMAKSVKSLYLG 295

RESULT 9
US-10-223-087-48
; Sequence 48, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
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APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C4
CURRENT APPLICATION NUMBER: US/10/223,087
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/232,887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092

PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-223-087-48
Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 15
DB 281 VPFSVAKSVKSLYL 295
RESULT 10
US-10-223-083-48
Sequence 48, Application US/10223083
Publication No. US20030119112A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C8
CURRENT APPLICATION NUMBER: US/10/223,083
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C3
CURRENT APPLICATION NUMBER: US/10/223,082
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-02-20
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-25
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-223-082-48

Query Match 95.8%; Score 69; DB 14; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 14
US-10-305-654-48
Sequence 48, Application US/10305654
Publication No. US20030224984A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hans-Peter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, J.

APPLICANT: Paoni, N. P.
APPLICANT: Stephan, J-P F.
APPLICANT: Watanabe, C.K.
APPLICANT: Wood, W.I.
APPLICANT: Williams, P.M.
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235R1C1
CURRENT APPLICATION NUMBER: US/10/305,654
CURRENT FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 383
SEQ ID NO 48
LENGTH: 673
TYPE: PRT
ORGANISM: Murine
US-10-305-654-48

Query Match 95.8%; Score 69; DB 15; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYLG 15
Db 281 VPFSMAKSVKSLYLG 295

RESULT 15
US-10-081-056-48
Sequence 48, Application US/10081056
Publication No. US20040043927A1
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Ferrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Marsters, Scot A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Williams, P.Mickey
APPLICANT: Ye, Weilan
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
FILE REFERENCE: P3235P1C1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07

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; PRIOR APPLICATION NUMBER: US 60/000,000
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/664,610
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/242,922
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 09/709,238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30952
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/767,609
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 09/796,498
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 48
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Murine
US-10-081-056-48

```

```

Query Match          95.8%; Score 69; DB 15; Length 673;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLYLG 15
Db      281 VPFSMAKSVKSLYLG 295
      ||||:|||||

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RESULT 16

```

US-10-367-094-31
; Sequence 31, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(697)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-367-094-31

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Query Match          95.8%; Score 69; DB 16; Length 697;
Best Local Similarity 93.3%; Pred. No. 0.001;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 VPFSVAKSVKSLYLG 15
Db      314 VPFSMAKSVKSLYLG 328
      ||||:|||||

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RESULT 17

```

US-10-369-493-5833
; Sequence 5833, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5833
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5833

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Query Match          61.1%; Score 44; DB 15; Length 374;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```

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QY      1 VPFSVAKSVKSLY 13
Db      142 LPFAIAASVNSLY 154
      :|||:|||||

```

RESULT 18

```

US-10-437-963-128669
; Sequence 128669, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

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; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128669
; LENGTH: 606
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_31000C.1.pep
US-10-437-963-128669

Query Match          59.7%; Score 43; DB 16; Length 606;
Best Local Similarity 61.5%; Pred. No. 55;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKSLY 13
DB      323 LPFSVVGVKVMY 335

RESULT 19
US-10-425-115-203276
; Sequence 203276, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 203276
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_116975C.1.pep
US-10-425-115-203276

Query Match          59.0%; Score 42.5; DB 16; Length 72;
Best Local Similarity 73.3%; Pred. No. 5.8;
Matches 11; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY      2 PRSV---AKSVKSLY 13
DB      40 PPSVLFVSVKSVKSLY 54

RESULT 20
US-10-062-188-1
; Sequence 1, Application US/10062188
; Publication No. US20040096826A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Glen A.
; TITLE OF INVENTION: Methods For Creating Recombination
; TITLE OF INVENTION: Products Between Nucleotide Sequences
; FILE REFERENCE: P-EA 5008
; CURRENT APPLICATION NUMBER: US/10/062,188
```

```
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-062-188-1

Query Match          58.3%; Score 42; DB 15; Length 291;
Best Local Similarity 64.3%; Pred. No. 36;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 PFSVAKSVKSLYLG 15
DB      184 PAAVAKSLKTLALG 197

RESULT 21
US-09-801-368-332
; Sequence 332, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: Royer, John
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-332

Query Match          58.3%; Score 42; DB 9; Length 1220;
Best Local Similarity 81.8%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 VPFSVAKSVKS 11
DB      955 VKFSVAKSVKS 965

RESULT 22
US-10-369-493-22082
; Sequence 22082, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
```

```
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22082
; LENGTH: 1220
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22082

Query Match          58.3%; Score 42; DB 15; Length 1220;
Best Local Similarity 81.8%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11
   |||||:|
Db 955 VKFSVAKSIKS 965

RESULT 23
US-10-425-115-268339
; Sequence 268339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 268339
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(283)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_176326C.1.ppep
US-10-425-115-268339

Query Match          56.9%; Score 41; DB 16; Length 283;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
   ||:||||:|
Db 146 PFNGAKSVRDLY 157

RESULT 24
US-10-425-115-256726
; Sequence 256726, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

```
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256726
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165723C.1.ppep
US-10-425-115-256726

Query Match          56.9%; Score 41; DB 16; Length 323;
Best Local Similarity 53.8%; Pred. No. 62;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
   |||||:|
Db 292 LPFSVVKVQTIY 304

RESULT 25
US-10-739-930-9784
; Sequence 9784, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9784
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-C176_291.p
US-10-739-930-9784

Query Match          56.9%; Score 41; DB 16; Length 366;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
   ||:||||:|
Db 146 PFNGAKSVRDLY 157

RESULT 26
US-10-369-493-21954
; Sequence 21954, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 21954
; LENGTH: 1173
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-21954

Query Match          56.9%; Score 41; DB 15; Length 1173;
Best Local Similarity 46.2%; Pred. No. 2.7e+02;
```


Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|: |||:|:
Db 1089 PFSIARQTKSMWI 1101

RESULT 27
US-10-741-849-7057
; Sequence 7057, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; PRIOR FILING DATE: 2003-12-19
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7057
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-741-849-7057

Query Match 56.8%; Score 41; DB 17; Length 1235;
Best Local Similarity 53.8%; Pred. No. 2.9e+02;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
|||:|: |||:|:
Db 52 PFNVKSLQTIYL 64

RESULT 28
US-10-424-599-201272
; Sequence 201272, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201272
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(132)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23774C.1.pap
US-10-424-599-201272

Query Match 55.6%; Score 40; DB 15; Length 132;
Best Local Similarity 61.5%; Pred. No. 34;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
|||:|: |||:|:
Db 9 YSIMRTTSLYL 21

Db 115 FSVCRSFGSLYL 127

RESULT 29
US-10-032-585-7469
; Sequence 7469, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7469
; LENGTH: 969
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7469

Query Match 55.6%; Score 40; DB 14; Length 969;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
|||:|: |||:|:
Db 792 LPFGVAKSKSKELG 806

RESULT 30
US-10-425-115-190887
; Sequence 190887, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 190887
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_105668C.1.pap
US-10-425-115-190887

Query Match 54.2%; Score 39; DB 16; Length 70;
Best Local Similarity 46.2%; Pred. No. 25;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
|||:|: |||:|:
Db 9 YSIMRTTSLYL 21

RESULT 31
US-10-328-675A-74
; Sequence 74, Application US/10328675A
; Publication No. US20030159171A1
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael

RESULT 35
US-10-425-115-302429`
; Sequence 302429, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 302429
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_38890C.1.pep
US-10-425-115-302429

Query Match 52.8%; Score 38; DB 16; Length 38;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
Db 22 PFSISKSVTILLI 34
|||:||||:|:
|||:||||:|:

RESULT 36
US-10-437-963-188870
; Sequence 188870, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 188870
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85433C.1.pep
US-10-437-963-188870

Query Match 52.8%; Score 38; DB 16; Length 78;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 PFSVAKSVKS 11
Db 8 PFSIAQSIKN 17
|||:||||:|:
|||:||||:|:

RESULT 37
US-10-363-616-335
; Sequence 335, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03

; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 335
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-335

Query Match 52.8%; Score 38; DB 15; Length 133;
Best Local Similarity 34.8%; Pred. No. 79;
Matches 8; Conservative 5; Mismatches 2; Indels 8; Gaps 1;

QY 1 VPFSVAKS-----VKSLYL 15
Db 73 IPFEVSKGEPQPKDNLIRSLFLG 95
:||||:|:
:||||:|:

RESULT 38
US-10-425-115-331872
; Sequence 331872, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 331872
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_65774C.1.pep
US-10-425-115-331872

Query Match 52.8%; Score 38; DB 16; Length 260;
Best Local Similarity 56.2%; Pred. No. 17e+02;
Matches 9; Conservative 4; Mismatches 1; Indels 2; Gaps 1;

QY 1 VPFSVAK--SVKSLYL 14
Db 177 IPFSVGEMTSLKSLWL 192
:||||:|:
:||||:|:

RESULT 39
US-10-369-493-22398
; Sequence 22398, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22398
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22398

Query Match 52.8%; Score 38; DB 15; Length 307;
 Best Local Similarity 52.6%; Pred. No. 2.1e+02;
 Matches 10; Conservative 1; Mismatches 4; Indels 4; Gaps 1;

QY 1 VPFSVAK-----SVKSLYL 15
 ||| : | ||| |||
 Db 137 VPFEKIRMQDVKSSYL 155

RESULT 40
 US-10-425-115-318065
 ; Sequence 318065, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 318065
 ; LENGTH: 399
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(399)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_53150C.1.pep
 US-10-425-115-318065

Query Match 52.8%; Score 38; DB 16; Length 399;
 Best Local Similarity 66.7%; Pred. No. 2.8e+02;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLY 13
 | ||| |||
 Db 338 PXCVAKKVVDLY 349

RESULT 41
 US-10-092-771-10
 ; Sequence 10, Application US/10092771
 ; Publication No. US20030064381A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
 ; FILE REFERENCE: D0128NP
 ; CURRENT APPLICATION NUMBER: US/10/092,771
 ; CURRENT FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: US 60/273,963
 ; PRIOR FILING DATE: 2001-03-07
 ; PRIOR APPLICATION NUMBER: US 60/278,927
 ; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 76
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 10
 ; LENGTH: 418
 ; TYPE: PRT
 ; ORGANISM: SUS SCROFA
 US-10-092-771-10

Query Match 52.8%; Score 38; DB 14; Length 418;
 Best Local Similarity 46.2%; Pred. No. 2.9e+02;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
 | : : | | : | |
 Db 198 PYATASSIVSFYL 210

RESULT 42
 US-10-437-963-120006
 ; Sequence 120006, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 120006
 ; LENGTH: 441
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_23167C.1.pep
 US-10-437-963-120006

Query Match 52.8%; Score 38; DB 16; Length 441;
 Best Local Similarity 53.8%; Pred. No. 3.1e+02;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
 : ||| : : | : |
 Db 161 LPFVSQMVKFVY 173

RESULT 43
 US-10-599-183414
 ; Sequence 183414, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 183414
 ; LENGTH: 632
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_136636C.1.pep
 US-10-424-599-183414

Query Match 52.8%; Score 38; DB 15; Length 632;
 Best Local Similarity 60.0%; Pred. No. 4.8e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 ||| : | ||| |||
 Db 3 VPFSVAAAPASLYVG 17

RESULT 44

US-10-425-114-37208
; Sequence 37208, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37208
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3051-110-D8_FLI.pbp
US-10-425-114-37208

Query Match 52.8%; Score 38; DB 15; Length 637;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLK 15

Db 8 VPFSVAAAPASLYG 22

RESULT 45

US-10-437-963-132886
; Sequence 132886, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132886
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34810C.1.pbp
US-10-437-963-132886

Query Match 52.8%; Score 38; DB 16; Length 645;
Best Local Similarity 53.3%; Pred. No. 4.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLK 15

Db 240 VFSPFKQLKLLFLG 254

RESULT 46

US-10-038-854-135
; Sequence 135, Application US/10038854

Publication No. US20040022781A1

; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glennnda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 135
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-038-854-135

Query Match 52.8%; Score 38; DB 15; Length 661;
Best Local Similarity 46.7%; Pred. No. 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYLK 15

Db 143 IPLHNQKTLESYLK 157

RESULT 47

US-10-037-417-107

; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 107
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-107

Query Match 52.8%; Score 38; DB 15; Length 661;
Best Local Similarity 46.7%; Pred. NO. 56+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
; :| |::|
Db 143 IPLHOKTLESYL 157

RESULT 48
US-10-437-963-193517
; Sequence 193517, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 193517
; LENGTH: 1870
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_89649C.1.pap
US-10-437-963-193517

Query Match 52.8%; Score 38; DB 16; Length 1870;
Best Local Similarity 69.2%; Pred. NO. 1.7e+03;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 FSVAKSVKSLYL 15
; :| |::|
Db 1482 FSPGTSNKSLL 1494

RESULT 49
US-10-425-115-254685
; Sequence 254685, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 254685
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_163853C.1.pap
US-10-425-115-254685

Query Match 51.4%; Score 37; DB 16; Length 54;
Best Local Similarity 61.5%; Pred. NO. 42;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 14
; :| |::|
Db 13 PVSFAKSTKQLHL 25

RESULT 50
US-09-864-761-36016
; Sequence 36016, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36016
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008053.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.97
; OTHER INFORMATION: EST HUMAN HIT: BE176836.1, EVALUE 1.00e-30
; OTHER INFORMATION: SWISSPROT HIT: P79400, EVALUE 3.40e+00
US-09-864-761-36016

Query Match 51.4%; Score 37; DB 9; Length 62;
Best Local Similarity 46.2%; Pred. No. 50;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKVKSLY 13
Db 30 IPYSITFSMSLY 42

Search completed: July 7, 2005, 10:29:31
Job time : 41.044 secs

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GenCore version 5.1.1.6
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OM protein.- protein search, using sw model

Run on: July 7, 2005, 08:51:19 ; Search time 20.0687 Seconds
(without alignments)
382.745 Million cell updates/sec

Title: US-10-671-019-2

Perfect score: 72
Sequence: 1 VPFSVAKSVKSLYLIG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_treml.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72	100.0	721	1 GAS66 HUMAN	Q14393 homo sapien
2	69	95.8	674	1 GAS66 MOUSE	Q61592 mus musculus
3	69	95.8	674	1 GAS66 RAT	Q63772 rattus norv
4	69	95.8	674	1 GAS66 RAT	Q61711 rattus norv
5	46	63.9	668	2 Q6PAE0	Q6PAE0 xenopus lae
6	44	61.1	374	1 YLD1 CAEEL	Q03566 caenorhabdi
7	44	61.1	571	1 UVRC_MYCAA	Q84899 mycoplasma
8	43	59.7	417	2 Q624E5	Q624E5 oryza sativ
9	43	59.7	606	2 Q624E7	Q624E7 oryza sativ
10	43	59.7	669	2 Q6DPA5	Q6DPA5 xenopus lae
11	42	58.3	252	2 Q9Y984	Q9Y984 aeropyrum p
12	42	58.3	292	1 BLAN_ENTCL	P52663 enterobacte
13	42	58.3	292	2 Q46991	Q46991 enterobacte
14	42	58.3	344	2 Q6AMY9	Q6AMY9 desulfotale
15	42	58.3	1220	1 SLN1 YEAST	P39928 saccharomyc
16	42	58.3	4345	2 Q9VLA0	Q9VLA0 drosophila
17	42	58.3	4374	2 Q7KTG2	Q7KTG2 drosophila
18	41	56.9	218	2 Q9QXB0	Q9QXB0 rift valley
19	41	56.9	242	2 Q9QXB1	Q9QXB1 rift valley
20	41	56.9	242	2 Q9QXB2	Q9QXB2 rift valley
21	41	56.9	242	2 Q9QXB3	Q9QXB3 rift valley
22	41	56.9	242	2 Q9QXB4	Q9QXB4 rift valley
23	41	56.9	243	2 Q8JUF8	Q8JUF8 rift valley
24	41	56.9	243	2 Q9QKC6	Q9QKC6 rift valley
25	41	56.9	244	2 Q9QXB5	Q9QXB5 rift valley
26	41	56.9	244	2 Q9QXB6	Q9QXB6 rift valley
27	41	56.9	244	2 Q9QXB9	Q9QXB9 rift valley
28	41	56.9	245	2 Q9QKC1	Q9QKC1 rift valley
29	41	56.9	245	2 Q9QKC4	Q9QKC4 rift valley
30	41	56.9	246	2 Q9QXB6	Q9QXB6 rift valley
31	41	56.9	246	2 Q9QXB7	Q9QXB7 rift valley

32	41	56.9	246	2 Q9QKC0	Q9QKC0 rift valley
33	41	56.9	246	2 Q9QKC2	Q9QKC2 rift valley
34	41	56.9	246	2 Q9QKC3	Q9QKC3 rift valley
35	41	56.9	246	2 Q9QKC5	Q9QKC5 rift valley
36	41	56.9	354	1 Y419 METUA	Q57862 methanococ
37	41	56.9	355	2 Q7N4C9	Q7N4C9 photorhabdu
38	41	56.9	377	2 Q8JU22	Q8JU22 lumpy skin
39	41	56.9	381	1 VQ3L_CAPVK	Q86917 capripoxvir
40	41	56.9	381	2 Q8JTY0	Q8JTY0 lumpy skin
41	41	56.9	381	2 Q91M23	Q91M23 lumpy skin
42	41	56.9	381	2 Q91T39	Q91T39 lumpy skin
43	41	56.9	1173	1 ATC2_YEAST	P38929 saccharomyc
44	41	56.9	1197	1 VGLM_RVFPVZ	P21401 rift valley
45	41	56.9	1206	1 VGLM_RVFPVZ	P03518 rift valley
46	41	56.9	3457	2 Q6EEL1	Q6EEL1 maize chlor
47	40	55.6	250	2 Q66712	Q66712 aquifex aeo
48	40	55.6	405	2 Q93CR3	Q93CR3 shigella bo
49	40	55.6	413	2 Q9U7C8	Q9U7C8 dictyosteli
50	40	55.6	424	1 HEM1_CHLVI	P28462 chlorobium
51	40	55.6	471	2 Q70LJ0	Q70LJ0 legioneella
52	40	55.6	587	2 Q7WBV0	Q7WBV0 bordetella
53	40	55.6	587	2 Q7WPU6	Q7WPU6 bordetella
54	40	55.6	630	2 Q6BK57	Q6BK57 debaryomyce
55	40	55.6	722	2 Q86J22	Q86J22 dictyosteli
56	40	55.6	945	2 Q6L465	Q6L465 solanum dem
57	40	55.6	1721	2 Q6L450	Q6L450 solanum dem
58	40	55.6	2573	2 Q6L432	Q6L432 solanum dem
59	39	54.2	256	2 Q6MBS9	Q6MBS9 parachlamyd
60	39	54.2	310	2 Q9L106	Q9L106 streptomyce
61	39	54.2	341	2 Q94AA9	Q94AA9 arabidopsis
62	39	54.2	406	2 Q6LYS6	Q6LYS6 methanococ
63	39	54.2	407	2 Q6LYS7	Q6LYS7 methanococ
64	39	54.2	421	2 Q54630	Q54630 halobacteri
65	39	54.2	440	2 Q94HN0	Q94HN0 oryza sativ
66	39	54.2	440	2 Q7XGJ4	Q7XGJ4 oryza sativ
67	39	54.2	461	2 Q9M1Q1	Q9M1Q1 arabidopsis
68	39	54.2	465	2 Q7SA07	Q7SA07 neurospora
69	39	54.2	507	2 Q7UFB7	Q7UFB7 rhodospirell
70	39	54.2	522	2 Q86J22	Q86J22 dictyosteli
71	39	54.2	588	2 Q6GUE9	Q6GUE9 nicotiana t
72	39	54.2	1256	2 Q8L4N8	Q8L4N8 oryza sativ
73	39	54.2	1262	2 Q18117	Q18117 caenorhabdi
74	39	54.2	1826	1 BGS3_SCHPO	Q9P377 schizosacch
75	38	52.8	91	2 Q91FX1	Q91FX1 chilo iride
76	38	52.8	95	2 Q9DKL6	Q9DKL6 spodoptera
77	38	52.8	180	2 Q9U7D2	Q9U7D2 caenorhabdi
78	38	52.8	199	2 Q8EWV4	Q8EWV4 mycoplasma
79	38	52.8	263	2 Q7DMC7	Q7DMC7 nicotiana t
80	38	52.8	275	2 Q9BFX0	Q9BFX0 okapia john
81	38	52.8	275	2 Q9BFX1	Q9BFX1 sus scrofa
82	38	52.8	275	2 Q9BFX2	Q9BFX2 tragelaphus
83	38	52.8	275	2 Q9BFX4	Q9BFX4 hippopotamu
84	38	52.8	275	2 Q9BP04	Q9BP04 muscardinus
85	38	52.8	277	2 Q71BQ3	Q71BQ3 cynocephalu
86	38	52.8	277	2 Q9BFX7	Q9BFX7 cynocephalu
87	38	52.8	291	2 Q7W8M4	Q7W8M4 bordetella
88	38	52.8	305	1 NAA2_ECOL6	Q6KDU7 escherichia
89	38	52.8	305	2 Q6KD26	Q6KD26 escherichia
90	38	52.8	306	1 MTSA_STRMU	Q9K1J3 streptococc
91	38	52.8	307	1 QDC2_YEAST	Q99297 saccharomyc
92	38	52.8	317	2 Q9U775	Q9U775 pyrococcus
93	38	52.8	330	2 Q9KBB0	Q9KBB0 bacillus ha
94	38	52.8	333	1 Y282_BUCAP	Q8K9N9 buchnera ap
95	38	52.8	349	1 YM94_YEAST	Q04869 saccharomyc
96	38	52.8	369	2 Q6FPH7	Q6FPH7 candida gla
97	38	52.8	382	2 Q8VHP7	Q8VHP7 mus musculu
98	38	52.8	390	2 Q4L52	Q24152 nicotiana t
99	38	52.8	401	2 Q9LFU8	Q9LFU8 arabidopsis
100	38	52.8	408	2 Q9FFN2	Q9FFN2 arabidopsis
101	38	52.8	409	2 Q6GN71	Q6GN71 xenopus lae
102	38	52.8	409	2 Q6P614	Q6P614 xenopus tro
103	38	52.8	418	1 B2AR_BOVIN	Q28044 bos taurus
104	38	52.8	418	1 B2AR_FIG	Q28997 sus scrofa

981 Q8U0A6 pyrococcus
 982 Q29439 archaeoglob
 983 Q9NHY4 habesiae equ
 984 Q8XDZ9 escherichia
 985 Q8FN06 escherichia
 986 P18843 escherichia
 987 Q8CNP1 staphylococ
 988 Q9UUA6 schizosacch
 989 Q64BW2 bcdulvibri
 990 Q6MKK1 bcdulvibri
 991 Q8KGU7 arabidopsis
 992 Q88AC9 pseudomonas
 993 Q88R39 pseudomonas
 994 Q88T09 mus musculus
 995 Q62347 caenorhabdi
 996 Q8RSU3 klebsiella
 997 Q8FSU4 klebsiella
 998 P23954 klebsiella
 999 Q8RLU6 klebsiella
 1000 Q8RSU5 klebsiella

ALIGNMENTS

RESULT 1

GA56 HUMAN
 ID GAS6_HUMAN STANDARD; PRT; 721 AA.
 AC Q14393; Q9Z7N3;
 DC 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Growth-arrest-specific protein 6 precursor (GAS-6).
 GN Name=GA56;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2), AND TISSUE SPECIFICITY.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=9330291; PubMed=8336730;
 RA Manfioletti G., Brancolini C., Avanzi G., Schneider C.;
 RT "The protein encoded by a growth arrest-specific gene (gas6) is a new
 RT member of the vitamin K-dependent proteins related to protein S, a
 RT negative coregulator in the blood coagulation cascade.";
 RL Mol. Cell. Biol. 13:4976-4985(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Munoz X., Sumoy L., de Frutos P., Sala N.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Uterus;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
 RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
 RA Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
 RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
 RA Omura Y., Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M.,
 RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
 RA Fujimori K., Tanai H., Kimata S., Watanabe M., Hirooka S., Chiba Y.,
 RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yoshida M., Hottu T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiani S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohara N., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Fetal lung, and Fetal spleen;
 RX MEDLINE=22388252; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-85 FROM N.A.
 RA Maree A.O., Hillmann A., McRedmond J.P., Fitzgerald D.J.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP RECEPTOR INTERACTION.
 RX PubMed=7854420; DOI=10.1038/373623a0;
 RA Varnum B.C., Young C., Elliott G., Garcia A., Bartley T.D.,
 RA Fridell Y.W., Hunt R.W., Trail G., Clogston C., Toso R.J.,
 RA Yanagihara D., Bennett L., Sylber M., Merewether L.A., Tseng A.,
 RA Escobar E., Liu E.T., Yamane H.K.;
 RT "Axl receptor tyrosine kinase stimulated by the vitamin K-dependent
 RT protein encoded by growth-arrest-specific gene 6.";
 RL Nature 373:623-626(1995).
 RN [7]
 RP RECEPTOR INTERACTION.
 RX PubMed=7867073; DOI=10.1016/0092-8674(95)90520-0;
 RA Stitt T.N., Conn G., Gore M., Lai C., Bruno J., Radziejewski C.,
 RA Mattsson K., Fisher J., Gies D.R., Jones P.F., Maslakowski P.,
 RA Ryan T.E., Tobkes N.J., Chen D.H., Distefano P.S., Long G.L.,
 RA Basilico C., Goldfarb M.P., Lemke G., Glass D.J., Yancopoulos G.D.;
 RT "The anticoagulation factor protein S and its relative, Gas6, are
 RT ligands for the Tyro 3/Axl family of receptor tyrosine kinases.";
 RL Cell 80:661-670(1995).
 RN [8]
 RP ALTERNATIVE SPLICING (ISOFORM 1), AND TISSUE SPECIFICITY.
 RX PubMed=9326368; DOI=10.1016/S0014-5793(97)01094-6;
 RA Marcandalli P., Gostissa M., Varnum B., Goruppi S., Schneider C.;
 RT "Identification and tissue expression of a splice variant for the
 RT growth arrest-specific gene gas6.";
 RL FEBS Lett. 415:56-58(1997).
 RN [9]
 RP RECEPTOR INTERACTION.
 RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;
 RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H.,
 RA Mizuno K.;

cell adhesion and cell migration (By similarity). plays a role in thrombosis by amplifying platelet aggregation and secretion in response to known agonists.

-!- SUBUNIT: Monomer (By similarity).

-!- SUBCELLULAR LOCATION: Secreted (By similarity).

-!- PTM: Gamma-carboxyglutamate residues are formed by vitamin K dependent carboxylation. These residues are essential for the binding of calcium (By similarity). show protection against thrombosis, but no spontaneous bleeding.

-!- SIMILARITY: Contains 4 EGF-like domains.

-!- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

-!- SIMILARITY: Contains 2 laminin G-like domains.

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EMBL; X59846; CAA42507.1; -.

DR EMBL; BC005444; AAH05444.1; -.

DR PIR; A48089; A48089.

DR HSP; P00740; ICFH.

DR MGD; MGI:95660; Gas6.

DR InterPro; IPR00152; Asx hydroxyl S.

DR InterPro; IPR008985; ConA like lec_gl.

DR InterPro; IPR000742; EGF 2.

DR InterPro; IPR001881; EGF Ca.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR002383; GLA blood.

DR InterPro; IPR001791; Laminin G.

DR InterPro; IPR003129; TSP N.

DR InterPro; IPR000294; VitK_dep_GLA.

DR Pfam; PF00008; EGF; 4.

DR Pfam; PF00594; Gla; 1.

DR Pfam; PF00054; Laminin G; 2.

DR PRINTS; PR00001; GLABLOOD.

DR SMART; SM00179; EGF CA; 3.

DR SMART; SM00069; GLA; 1.

DR SMART; SM00282; LamG; 2.

DR PROSITE; PS00010; ASX_HYDROXYL; 4.

DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01186; EGF 2; 3.

DR PROSITE; PS00026; EGF 3; 4.

DR PROSITE; PS01187; EGF CA; 3.

DR PROSITE; PS00011; GLA 1; 1.

DR PROSITE; PS00998; GLA 2; 1.

DR PROSITE; PS50025; LAM G_DOMAIN; 2.

KW Calcium-binding; EGF-like domain; Gamma-carboxyglutamic acid; Growth regulation; Repeat; Signal; Vitamin K.

FT SIGNAL 1 27 Potential.

FT CHAIN 28 674 Growth-arrest-specific protein 6.

FT DOMAIN 50 91 Gla.

FT DOMAIN 113 151 EGF-like 1, calcium-binding (Potential).

FT DOMAIN 153 193 EGF-like 2, calcium-binding (Potential).

FT DOMAIN 194 234 EGF-like 3, calcium-binding (Potential).

FT DOMAIN 235 275 EGF-like 4, calcium-binding (Potential).

FT DOMAIN 295 467 Laminin G-like 1.

FT DOMAIN 474 666 Laminin G-like 2.

FT METAL 326 326 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 328 328 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 437 437 Calcium (via carbonyl oxygen) (By similarity).

FT METAL 652 652 Calcium (By similarity).

FT DISULFID 117 130 By similarity.

FT DISULFID 122 139 By similarity.

FT DISULFID 141 150 By similarity.

FT DISULFID 157 168 By similarity.

FT DISULFID 164 177 By similarity.

FT DISULFID 179 192 By similarity.

FT DISULFID 198 209 By similarity.

FT DISULFID 204 218 By similarity.

FT DISULFID 220 233 By similarity.

FT DISULFID 239 248 By similarity.

FT DISULFID 244 257 By similarity.

FT DISULFID 259 274 By similarity.

FT DISULFID 280 566 By similarity.

FT DISULFID 441 467 By similarity.

FT DISULFID 639 666 By similarity.

FT CARBOHYD 417 417 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 488 488 N-linked (GlcNAc...) (Potential).

FT CONFLICT 530 530 Missing (in Ref. 1).

SQ SEQUENCE 674 AA; 74609 MW; 7C41F7693903F401 CRC64;

Query Match 95.8%; Score 69; DB 1; Length 674;

Best Local Similarity 93.3%; Pred. No. 0.0014;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15

DB 281 VPFSMAKSVKSLYL 295

RESULT 3

GAS6_RAT STANDARD; PRT; 674 AA.

ID AC Q63772;

DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUL-2004 (Rel. 44, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Growth-arrest-specific protein 6 precursor (GAS-6) (Growth-

DE Potentiating factor) (GFP).

GN Name=Gas6;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1] NAME=10116;

RP SEQUENCE FROM N.A.

RX MEDLINE=95197586; PubMed=7890695; DOI=10.1074/jbc.270.11.5702;

RA Nakano T., Higashino K., Kikuchi N., Kishino J., Nomura H., Fujita H., Ohara O., Arita H.

RT "Vascular smooth muscle cell-derived, Gla-containing growth-

RT potentiating factor for Ca(2+)-mobilizing growth factors.";

RL J. Biol. Chem. 270:5702-5705(1995).

RN [2]

RP RECEPTOR INTERACTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.

RX PubMed=7559388; DOI=10.1074/jbc.270.39.22681;

RA Ohashi K., Nagata K., Toshima J., Nakano T., Arita H., Tenda H., Suzuki K., Mizuno K.

RT "Stimulation of sky receptor tyrosine kinase by the product of growth arrest-specific gene 6.";

RL J. Biol. Chem. 270:22681-22684(1995).

RN [3]

RP RECEPTOR INTERACTION

RX PubMed=8939948; DOI=10.1074/jbc.271.47.30022;

RA Nagata K., Ohashi K., Nakano T., Arita H., Zong C., Hanafusa H., Mizuno K.

RT "Identification of the product of growth arrest-specific gene 6 as a common ligand for Axl, Sky, and Mer receptor tyrosine kinases.";

RL J. Biol. Chem. 271:30022-30027(1996).

RN [4]

RP GAMMA-CARBOXYGLUTAMIC ACIDS.

RX PubMed=9163328;

RA Nakano T., Kawamoto K., Kishino J., Nomura K., Higashino K., Arita H.

RT "Requirement of gamma-carboxyglutamic acid residues for the biological activity of Gas6: contribution of endogenous Gas6 to the proliferation of vascular smooth muscle cells.";

RL Biochem. J. 323:387-392(1997).

CC -!- FUNCTION: Ligand for tyrosine-protein kinase receptors AXL, TYRO3 and MER whose signaling is implicated in cell growth and survival,

FT	DISULFID	198	209		By similarity.
FT	DISULFID	204	218		By similarity.
FT	DISULFID	220	233		By similarity.
FT	DISULFID	239	257		By similarity.
FT	DISULFID	244	248		By similarity.
FT	DISULFID	259	274		By similarity.
FT	DISULFID	280	566		By similarity.
FT	DISULFID	441	467		By similarity.
FT	CARBOHYD	639	666		N-linked (GlcNac. . .) (Potential).
FT	CARBOHYD	417	417		N-linked (GlcNac. . .) (Potential).
FT	CARBOHYD	488	488		N-linked (GlcNac. . .) (Potential).
SQ	SEQUENCE	674 AA;	74637 MW; FBF8FB8664D6F2E CRG64;		

Query Match 95.8%; Score 69; DB 1; Length 674;
Best Local Similarity 93.3%; Pred. No. 0.0014;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VFPSSAKSVKSLYLGL 15	
		:	
DB	281	VFPSSAKSVKSLYLGL 295	

RESULT 4

Q6IRL1	PRELIMINARY;	PRT;	674 AA.
ID	Q6IRL1		
AC	Q6IRL1;		
DT	05-JUL-2004 (TrEMBLrel. 27, Created)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)		
DE	Gas6 protein.		
GN	Name=Gas6;		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
NCBI_TaxId=10116;			
LN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.P., Jordan H., Moore T.I., Wang X.J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton L., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Vitalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton B., Kettaman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Skrawski J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Grimalko U., Smalish U., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RL	(2)		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	Strausberg R.;		
RA	Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.		
CC	-I- SIMILARITY: Contains 1 EGF-like domain.		
DR	EMBL; BC070881; RAH70881.1; -		
DR	HSPB; P00736; IAPQ.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005509; F:calcium ion binding; IEA.		
DR	GO; GO:0005198; F:structural molecule activity; IEA.		
DR	GO; GO:0007155; P:cell adhesion; IEA.		
DR	InterPro; IPRO00152; Asx hydroxyl S.		

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DR InterPro; IPR008985; ConA_like_1ec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006283; GLA blood.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 2.
DR Pfam; PF00594; Glaf; 1.
DR Pfam; PF02210; Laminin_G_2; 2.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 4.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 674 AA; 74671 MW; CC9A5EBD04480AE7 CRC64;

Query Match 95.8%; Score 69; DB 2; Length 674;
Best Local Similarity 93.3%; Pred. No. 0.0014;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
| | | | | | | | | | | | | | |
Db 281 VPFSMAKSVKSLYL 295

RESULT 5
Q6PAE0 PRELIMINARY; PRT; 668 AA.
AC Q6PAE0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC68463 protein.
GN Name=MGC68463;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettunen M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Klein S., Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC060355; AAH60355.1; -.
DR HSSP; P00743; LAPO.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_1ec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002383; GLA blood.
DR InterPro; IPR006210; IEFG.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSP_N.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00594; Glaf; 1.
DR Pfam; PF02210; Laminin_G_2; 1.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00179; EGF_CA; 4.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00282; LamG; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 3.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00011; GLA_1; 1.
DR PROSITE; PS50025; LAM_G_DOMAIN; 2.
KW EGF-like domain.
SQ SEQUENCE 668 AA; 74905 MW; 8BEE5232F4EF3916 CRC64;

Query Match 63.9%; Score 46; DB 2; Length 668;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
| | | | | | | | | | | | | | |
Db 278 IPFASAKSVKSLYL 292

RESULT 6
YLD1_CABEL STANDARD; PRT; 374 AA.
ID YLD1_CABEL
AC Q03566;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor C38C10.1.
GN ORFNames=C38C10.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.

```

OK NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398; DOI=10.1039/368032a0;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonnenhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
CC -!- FUNCTION: Not known. Putative receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; Z19153; CAA79546.1; --
DR PIR; S28285; S28285.
DR HSSP; P02699; 1P88.
DR WormBase; WBGene00008576; tkr-1.
DR WormPep; C38C10.1; CR00104.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR001681; Neurokin_receptor.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCRHOOPSN.
DR PRINTS; PR00244; NEUROKININR.
DR PROSITE; PS00237; G_PROTEIN_RECP FL1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECP FL2; 1.
KW G-protein coupled receptor; Glycoprotein; Hypothetical protein;
KW Transmembrane.
FT DOMAIN 1 12 Extracellular (Potential).
FT TRANSMEM 13 37 1 (Potential).
FT DOMAIN 38 45 Cytoplasmic (Potential).
FT TRANSMEM 46 66 2 (Potential).
FT DOMAIN 67 83 Extracellular (Potential).
FT TRANSMEM 84 104 3 (Potential).
FT DOMAIN 105 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 4 (Potential).
FT DOMAIN 148 172 Extracellular (Potential).
FT TRANSMEM 173 193 5 (Potential).
FT DOMAIN 194 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 285 Extracellular (Potential).
FT TRANSMEM 286 374 7 (Potential).
FT DOMAIN 287 374 Cytoplasmic (Potential).
SQ SEQUENCE 374 AA; 42940 MW; 1311AE2743014C01 CRC64;
Query Match 61.1%; Score 44; DB 1; Length 374;
Best Local Similarity 61.5%; Pred. No. 26;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 13
DB 142 LPFAIAASVNSLY 154
RESULT 7
UVR_C_MYCAA
ID UVR_C_MYCAA STANDARD; PRT; 571 AA.
AC O84899;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UvrABC system protein C (UvrC protein) (Excinuclease ABC subunit C).
GN Name=uvrC;
OS Mycoplasma agalactiae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2110;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PG2;
RC MEDLINE=98329280; PubMed=9664578; DOI=10.1006/mcpr.1998.0160;
RA Subramaniam S., Bergonier D., Poumarat F., Capaul S., Schlatter Y.,
RA Nicolet J., Frey J.;
RT "Species identification of Mycoplasma bovis and Mycoplasma agalactiae
RT based on the uvrC genes by PCR.";
RL Mol. Cell. Probes 12:161-169(1998).
CC -!- FUNCTION: The UvrABC repair system catalyzes the recognition and
CC processing of DNA lesions. UvrC both incises the 5' and 3' sides
CC of the lesion. The N-terminal half is responsible for the 3'
CC incision and the C-terminal half is responsible for the 5'
CC incision (By similarity).
CC -!- SUBUNIT: Interacts with uvrB in an incision complex (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the uvrC family.
CC -!- SIMILARITY: Contains 1 UVR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF003960; AAC32310.1; --
DR HAMAP; MF_00203; --; 1.
DR InterPro; IPR010994; Ruva 2 like.
DR InterPro; IPR001943; UvrB/C.
DR InterPro; IPR009055; UvrB C.
DR InterPro; IPR004791; UvrC_ABC.
DR InterPro; IPR001162; UvrC_C.
DR InterPro; IPR00305; UvrC_N.
DR Pfam; PF01541; GIY-YIG; 1.
DR Pfam; PF02151; UVR; 1.
DR ProDom; PD005870; UvrC C; 1.
DR SMART; SM00465; GIYC; 1.
DR TIGRPFAMs; TIGR00194; uvrC; 1.
DR PROSITE; PS50151; UVR; 1.
DR PROSITE; PS50164; UVR_C_1; 1.
DR PROSITE; PS50165; UVR_C_2; 1.
KW DNA excision; DNA recombination; DNA repair; Excision nuclease;
KW SOS response.
FT DOMAIN 184 219 UVR.
SQ SEQUENCE 571 AA; 66214 MW; 74403690A5FE203C CRC64;
Query Match 61.1%; Score 44; DB 1; Length 571;
Best Local Similarity 72.7%; Pred. No. 40;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLY 11
|||||

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Db          557 VPFNVAKSIKN 567

RESULT 8
Q624E5      PRELIMINARY;      PRT;      417 AA.
AC Q624E5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 25-OCT-2004 (TrEMBLrel. 27, Last sequence update)
DE Limonene cyclase like protein.
GN Name=OSJNB0084L07.20-3; Synonym=OSJNB0002L09.8-3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0084L07.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0002L09.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005179; BAC83915.1; -.
DR EMBL; AP005877; BAD31849.1; -.
DR InterPro; IPR004263; Exostosin.
DR Pfam; PF03016; Exostosin; 1.
SQ SEQUENCE 417 AA; 44610 MW; 676689A53B1DC6A CRC64;

Query Match          59.7%; Score 43; DB 2; Length 417;
Best Local Similarity 61.5%; Pred. No. 45;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy          1 VPFNVAKSVKSLY 13
Db          323 LPFSVVKVMKMIY 335

RESULT 9
Q624E7      PRELIMINARY;      PRT;      606 AA.
AC Q624E7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 25-OCT-2004 (TrEMBLrel. 27, Last sequence update)
DE Putative pectin-glucuronyltransferase.
GN Name=OSJNB0084L07.20-1; Synonym=OSJNB0002L09.8-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0084L07.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0002L09.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005179; BAC83913.1; -.
DR EMBL; AP005877; BAD31848.1; -.
DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008151; P:cell growth and/or maintenance; IEA.
DR InterPro; IPR004263; Exostosin.
DR Pfam; PF03016; Exostosin; 1.
KW Transferase.
SQ SEQUENCE 606 AA; 65830 MW; F90248E809A18266 CRC64;

Query Match          59.7%; Score 43; DB 2; Length 606;
Best Local Similarity 61.5%; Pred. No. 65;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy          1 VPFNVAKSVKSLY 13
Db          323 LPFSVVKVMKMIY 335

RESULT 10
Q6DFA5      PRELIMINARY;      PRT;      669 AA.
AC Q6DFA5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Gas6-prov protein.
GN Name=gas6-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
DR EMBL; BC076835; AAH76835.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
```

DR GO: GO:0007155; P-cell adhesion; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl S.
 DR InterPro; IPR000895; ConA_like_lec_gl.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002383; GLA_blood.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001791; Laminin G.
 DR InterPro; IPR003129; TSP N.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 3.
 DR Pfam; PF07645; EGF_CA; 2.
 DR Pfam; PF00594; Glf; 1.
 DR Pfam; PF00054; Laminin_G.1; 1.
 DR Pfam; PF02210; Laminin_G.2; 1.
 DR PRINTS; PR00001; GLABLOOD.
 DR SMART; SM00181; EGF; 4.
 DR SMART; SM00179; EGF_CA; 4.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00282; LamG; 2.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS00266; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00011; GLA_1; 1.
 DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
 KW EGF-like domain.
 SQ SEQUENCE 669 AA; 75232 MW; A8DE1E362540F643 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 669;
 Best Local Similarity 60.0%; Pred. No. 72;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 15
 DB 279 LPFASEKRSRLYL 293

RESULT 11
 QY984 PRELIMINARY; PRT; 252 AA.
 AC QY984
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein APE2401.
 GN OrderedLocustNames=APE2401;
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
 RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1";
 RL DNA Res. 6:83-101(1999).
 DR EMBL; AP000064; BA841416.1; -.
 DR FIR; H72469; H72469.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 252 AA; 25912 MW; 527C1D8A70FFDC14 CRC64;

Query Match 58.3%; Score 42; DB 2; Length 252;
 Best Local Similarity 61.5%; Pred. No. 41;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 13
 DB 34 VAFSILRSLSLYL 46

RESULT 12
 BLAN ENTCL
 ID BLAN ENTCL STANDARD; PRT; 292 AA.
 AC P52663;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Imipenem-hydrolyzing beta-lactamase precursor (EC 3.5.2.6)
 DE (Carbapenemase) (NMC-A).
 GN Name=nmcA;
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Enterobacter.
 OX NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-34.
 RC STRAIN=NOR-1;
 RX MEDLINE=94329582; PubMed=8052644;
 RA Naas T., Nordmann P.;
 RT "Analysis of a carbapenem-hydrolyzing class A beta-lactamase from
 RT Enterobacter cloacae and of its LysR-type regulatory protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7693-7697(1994).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.89 ANGSTROMS).
 RC STRAIN=NOR-1;
 RX MEDLINE=99395084; PubMed=10464248; DOI=10.1074/jbc.274.36.25260;
 RA Mourey L., Koura L.P., Bellettini J., Bulychiev A., O'Brien M.,
 RA Miller M.J., Mobashery S., Samama J.-P.;
 RT "Inhibition of the broad spectrum nonmetallo-carbapenemase of class A
 RT (NMC-A) beta-lactamase from Enterobacter cloacae by monocyclic beta-
 RT lactams.";
 RL J. Biol. Chem. 274:25260-25265(1999).
 CC -!- FUNCTION: Hydrolyzes carbapenems such as imipenem, which are
 CC extended-spectrum beta-lactam antibiotics.
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
 CC amino acid.
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.
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 DR EMBL; Z21956; CAA79967.1; -.
 DR FIR; S35915; S35915.
 DR PDB; 1BUE; X-ray; A=28-292.
 DR PDB; 1BUL; X-ray; @=28-292.
 DR InterPro; IPR001466; Beta_lactamase.
 DR InterPro; IPR000871; Beta_lactamase_A.
 DR Pfam; PF00144; Beta_lactamase; 1.
 DR PRINTS; PR00118; BLACTAMASEA.
 DR PROSITE; PS00146; BETA_LACTAMASE_A; FALSE_NEG.
 KW 3D-structure; Antibiotic resistance; Direct protein sequencing;
 KW Hydrolase; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 292 Imipenem-hydrolyzing beta-lactamase.
 FT ACT_SITE 71 71 Acyl-ester intermediate.
 FT SITE 236 238 Substrate binding (By similarity).
 FT DISULFID 70 240
 FT TURN 30 31
 FT HELIX 32 42
 FT TURN 43 43
 FT STRAND 45 52

RT "A yeast protein similar to bacterial two-component regulators."; Science 262:566-569(1993).

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN=9288C / AB972;

RX MEDLINE=97313266; PubMed=9169870;

RA Churche C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,

RA Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G., Moulis S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,

RA Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IX.;

RL Nature 387:84-87(1997).

RN [3]

RP MUTAGENESIS OF HIS-576 AND ASP-1144.

RX MEDLINE=94339498; PubMed=8183345; DOI=10.1038/369242a0;

RA Maeda T., Wurgler-Murphy S.M., Saito H.; "A two-component system that regulates an osmosensing MAP kinase

RT cascade in yeast.;"

RL Nature 369:242-245(1994).

CC -!- FUNCTION: Forms part of a two-component regulatory system

CC SLN1/SSK1 activated by changes in the osmolarity of the

CC extracellular environment. This system controls the SSK2/SSK22->

CC PBS2->HOG1 pathway. Inactive SLN1 allows the unphosphorylated SSK1

CC protein to activate SSK2 and SSK22, two MAPKKs that further

CC stimulate the PBS2-HOG1 MAPK cascade. In low osmolarity media, the

CC activated SLN1 histidine kinase represses the activation of the

CC PBS2-HOG1 kinase cascade through phosphorylation of SSK1.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- PTM: Activation probably requires a transfer of a phosphate group

CC between a His in the transmitter domain and an Asp of the receiver

CC domain.

CC -!- SIMILARITY: Contains 1 histidine kinase domain.

CC -!- SIMILARITY: Contains 1 response regulatory domain.

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CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL; Z38059; CAAB6131.1; -;

DR EMBL; U01835; AAC48912.1; -;

DR PIR; S48387; S48387.

DR PDB; 1OXB; X-ray; B=1087-1220.

DR PDB; 1OKX; X-ray; B/D/F/H/J/L=1087-1220.

DR Germline; 139682; -;

DR SGD; S000001409; SLN1.

DR GO; GO:0004673; F:protein-histidine kinase activity; IDA.

DR GO; GO:0007234; P:osmosensory signaling pathway via two-compo. .; IDA.

DR GO; GO:0042542; P:response to hydrogen peroxide; IMP.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR011006; CheY-like.

DR InterPro; IPR009082; His_kin_homodim.

DR InterPro; IPR003661; His_kin_N.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR001789; Response_reg.

DR Pfam; PF02518; HATPase_c; 1.

DR Pfam; PF00512; HisKA; 1.

DR Pfam; PF00072; Response_reg; 1.

DR PRINTS; PR00344; BCTRLSENSOR.

DR ProDom; PD000039; Response_reg; 1.

DR SMART; SM00387; HATPase_c; 1.

DR SMART; SM00388; HisKA; 1.

DR SMART; SM00448; REC; 1.

DR PROSITE; PS01109; HIS_KIN; 1.

DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.

DR 3D-structure; Kinase. Phosphorylation; Sensory transduction;

DR Transferase; Transmembrane; Two-component regulatory system.

DOMAIN 1 22 Cytoplasmic (Potential).

FT TRANSMEM 23 46 Potential.

FT DOMAIN 47 333 Extracellular (Potential).

FT TRANSMEM 334 354 Potential.

FT DOMAIN 355 1220 Cytoplasmic (Potential).

FT DOMAIN 573 928 Histidine kinase.

FT DOMAIN 1089 1210 Response regulatory.

FT MOD_RES 576 576 Phosphohistidine (by autocatalysis) (Probable).

FT MOD_RES 1144 1144 4-aspartylphosphate (Probable).

FT CARBOHYD 100 100 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 138 138 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 142 142 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 181 181 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 224 224 N-linked (GlcNAc . .) (Potential).

FT CARBOHYD 272 272 N-linked (GlcNAc . .) (Potential).

FT MUTAGEN 576 576 H->Q: Inactive.

FT MUTAGEN 891 891 G->D: In SLN1-1; slow growth.

FT MUTAGEN 1144 1144 D->N: Inactive.

SQ SEQUENCE 1220 AA; 134434 MW; 45FFE24A8165486B CRC64;

Query Match 58.3%; Score 42; DB 1; Length 1220;

Best Local Similarity 81.8%; Pred. No. 2e+02;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKS 11

DB 955 VKFSVAKSIKS 965

RESULT 16

ID Q9VLA0

AC Q9VLA0

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DE CG15828-PA.

ORFNames=CG15828;

GN Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

NI [1]

SEQUENCE FROM N.A.

RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glöcker A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Swirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whittied E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AS003625; AAS64667.1; -;
DR GO; GO:0003319; Flippid transporter activity; IEA.
DR GO; GO:0008669; Flippid transport; IEA.
DR InterPro; IPR009454; DUF1081.
DR InterPro; IPR001747; Lipid transprt N.
DR InterPro; IPR011030; LV superhelical.
DR InterPro; IPR001846; VWF D.
DR Pfam; PF06448; DUF1081; 1.
DR Pfam; PF01347; Vitellogenin_N; 1.
DR Pfam; PF00094; VWD; 1.
DR SMART; SM00638; LFD_N; 1.
DR SMART; SM00216; VWD; 1.
SQ SEQUENCE 4374 AA; 498710 MW; C13F0DB2453D0F95 CRC64;
Query Match 58.3%; Score 42; DB 2; Length 4374;
Best Local Similarity 63.6%; Pred. No. 7.3e+02;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 PFSVAKSVKSL 12
DB 2144 PFAVAKNRSI 2154
RESULT 18
QYQKB0 ID Q9QKB0 PRELIMINARY; PRT; 218 AA.
AC Q9QKB0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZH 548;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134508; AAD56355.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 242
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

FT NON_TER 1 1
FT NON_TER 218 218
SQ SEQUENCE 218 AA; 23982 MW; F23A1BDB31F30308 CRC64;
Query Match 56.9%; Score 41; DB 2; Length 218;
Best Local Similarity 57.1%; Pred. No. 54;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFKNSKKVYL 91
RESULT 19
QYQKB1 ID Q9QKB1 PRELIMINARY; PRT; 242 AA.
AC Q9QKB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MP12;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134507; AAD56354.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 242
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;
Query Match 56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 VPFSVAKSVKSLYL 14
DB 78 VPFAVFKNSKKVYL 91
RESULT 20
QYQKB2 ID Q9QKB2 PRELIMINARY; PRT; 242 AA.
AC Q9QKB2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H EGY93;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134506; AAD56353.1; -;
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 242
FT SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

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Query Match          56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 21
Q9QKB3 ID Q9QKB3 PRELIMINARY; PRT; 242 AA.
AC Q9QKB3;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B EGY93;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134505; AAD56352.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 26426 MW; 74AA95C8F05EA419 CRC64;

Query Match          56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 22
Q9QKB4 ID Q9QKB4 PRELIMINARY; PRT; 242 AA.
AC Q9QKB4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=384-97.1;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134504; AAD56351.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 242
SQ SEQUENCE 242 AA; 26410 MW; 74AA8D7353461FBA CRC64;

Query Match          56.9%; Score 41; DB 2; Length 242;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 23
Q8JUF8 ID Q8JUF8 PRELIMINARY; PRT; 243 AA.
AC Q8JUF8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 protein (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SA01-1322;
RA Miller B.R., Godsey M.S., Crabtree M.B., Al-Mazrao Y., Al-Jeffri M.H.,
RA Abdoon A.M., Al-Seghayer S.M., Ksiazek T.G.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF393745; AAM73695.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 243
SQ SEQUENCE 243 AA; 26497 MW; 8E44AA8D7353461F CRC64;

Query Match          56.9%; Score 41; DB 2; Length 243;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 24
Q9QKC6 ID Q9QKC6 PRELIMINARY; PRT; 243 AA.
AC Q9QKC6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lunyo;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134492; AAD56339.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 243
SQ SEQUENCE 243 AA; 26480 MW; 792801271AF69C60 CRC64;

Query Match          56.9%; Score 41; DB 2; Length 243;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91
```

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Q9QKB9
ID Q9QKB9 PRELIMINARY; PRT; 244 AA.
AC Q9QKB9;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D104769;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134499; AAD56346.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 244
SQ SEQUENCE 244 AA; 26711 MW; CAA54862A9BD1449 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 244;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 28
Q9QKC1
ID Q9QKC1 PRELIMINARY; PRT; 245 AA.
AC Q9QKC1;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D38457;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134497; AAD56344.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 245
SQ SEQUENCE 245 AA; 26660 MW; 2BD996075AA93B3F CRC64;

Query Match 56.9%; Score 41; DB 2; Length 245;
Best Local Similarity 57.1%; Pred. NO. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFNKSKVYL 91

RESULT 29
Q9QKC4
ID Q9QKC4 PRELIMINARY; PRT; 245 AA.
AC Q9QKC4;

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DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H 047502;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134494; AAD56341.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 245
FT NON_TER 245 245
SQ SEQUENCE 245 AA; 26651 MW; B224AD8BDCE89B4 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 245;
Best Local Similarity 57.1%; Pred. No. 60;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:
Db 78 VPFAVFKNSKKVYL 91

RESULT 30
Q9QKB6
ID Q9QKB6 PRELIMINARY; PRT; 246 AA.
AC Q9QKB6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=An K6087;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134502; AAD56349.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 246
FT NON_TER 246 246
SQ SEQUENCE 246 AA; 26794 MW; 766A4F9E1B312F5B CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:
Db 78 VPFAVFKNSKKVYL 91

RESULT 31
Q9QKB7
ID Q9QKB7 PRELIMINARY; PRT; 246 AA.
AC Q9QKB7;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)

DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Smithburn;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134501; AAD56348.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 246
FT NON_TER 246 246
SQ SEQUENCE 246 AA; 26759 MW; 7DBC4674FC4D0BAC CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:|:|:|:
Db 78 VPFAVFKNSKKVYL 91

RESULT 32
Q9QKC0
ID Q9QKC0 PRELIMINARY; PRT; 246 AA.
AC Q9QKC0;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar D38611;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RA Thiongane Y., Bouloy M.;
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134498; AAD56345.1; -.
DR InterPro; IPR010826; Phlebovirus G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1 246
FT NON_TER 246 246
SQ SEQUENCE 246 AA; 26773 MW; F7DD00B294AA95C8 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFSVAKSVKSLYL 14
|||:|:~|:|:|:
Db 78 VPFAVFKNSKKVYL 91

RESULT 33
Q9QKC2
ID Q9QKC2 PRELIMINARY; PRT; 246 AA.
AC Q9QKC2;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.

```

OX  NCBI_TaxID=11588;
RN  SEQUENCE FROM N.A.
RP  STRAIN=H D47408;
RX  MEDLINE=99412335; PubMed=10482570;
RA  Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT  "Genetic reassortment of Rift Valley fever virus in nature.";
RL  J. Virol. 73:8196-8200(1999).
DR  EMBL; AF134496; AAD56343.1; -.
DR  InterPro; IPR010826; Phlebovirus_G1.
FT  Pfam; PF07243; Phlebovirus_G1; 1.
FT  NON_TER 1
FT  NON_TER 246
SQ  SEQUENCE 246 AA; 26761 MW; 79BCDDE390EB809A CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFKSKVYL 91

RESULT 34
Q9QKC3 PRELIMINARY; PRT; 246 AA.
AC Q9QKC3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=H D47311;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134495; AAD56342.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
DR Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26759 MW; EF66A3B294B81758 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFKSKVYL 91

RESULT 35
Q9QKC5 PRELIMINARY; PRT; 246 AA.
AC Q9QKC5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE G2 (Fragment).
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OX NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=Ar B1976;
RX MEDLINE=99412335; PubMed=10482570;
RA Sall A.A., Zanotto P.M., Sene O.K., Zeller H.G., Digoutte J.P.,
RT "Genetic reassortment of Rift Valley fever virus in nature.";
RL J. Virol. 73:8196-8200(1999).
DR EMBL; AF134493; AAD56340.1; -.
DR InterPro; IPR010826; Phlebovirus_G1.
FT Pfam; PF07243; Phlebovirus_G1; 1.
FT NON_TER 1
FT NON_TER 246
SQ SEQUENCE 246 AA; 26804 MW; 446D2C1C6D282E58 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 246;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
Db 78 VPFAVFKSKVYL 91

RESULT 36
Y419_METJA STANDARD; PRT; 354 AA.
ID Y419_METJA
AC Q57862;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein MJ0419.
GN OrderedoccNames=MJ0419;
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=21190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC EMBL; U67494; AAB98417.1; -.
CC PIR; C64352; C64352.
CC TIGR; MJ0419; -.
CC InterPro; IPR002760; DUF70.
CC Pfam; PF01901; DUF70; 1.
CC Complete proteome; Hypothetical protein; Transmembrane.
FT TRANSMEM 29
FT TRANSMEM 31
FT TRANSMEM 51
FT TRANSMEM 76
FT TRANSMEM 96
FT TRANSMEM 109
FT TRANSMEM 129
FT TRANSMEM 144
FT TRANSMEM 164
FT TRANSMEM 185
FT TRANSMEM 205
FT TRANSMEM 278
FT TRANSMEM 298
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FT TRANSMEM 306 326 Potential.
FT TRANSMEM 327 347 Potential.
SQ SEQUENCE 354 AA; 40036 MW; D6C7180C6418A641 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 354;
Best Local Similarity 53.8%; Pred. No. 87;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 FSVAKSVKSLYL 15
: ||| ||| |||
Db 298 YKLAKDVRGIVLG 310

RESULT 37
Q7N4C9 PRELIMINARY; PRT; 355 AA.
AC Q7N4C9;
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Similarities with unknown protein.
GN OrderedLocusNames=plu2412;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Sude C., Chandler M., Charles J.-F.,
RA Dassa E., Derose R., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanos A., Powell K., Siguer P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313(2003).
DR EMBL; BX571867; CAE14776.1; -.
DR PhotoList; plu2412; -.
KW Complete proteome.
SQ SEQUENCE 355 AA; 41645 MW; 2A2D08E121C8578A CRC64;

Query Match 56.9%; Score 41; DB 2; Length 355;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VPFVSAKSVKSLYL 14
||| ||| ||| |||
Db 70 VPYRASAIAKIYIL 83

RESULT 38
Q8JU22 PRELIMINARY; PRT; 377 AA.
AC Q8JU22;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CC chemokine receptor-like protein.
GN Name=L0011.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22710395; PubMed=12827464;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Abolnik C., Lu Z.,
RA Vreede F.T., Taljaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Comparative sequence analysis of the South African vaccine strain and
RT two virulent field isolates of Lumpy skin disease virus."
RL Arch. Virol. 148:1335-1356(2003).

DR EMBL; AF409137; AAN02577.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000355; Chmkin receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00857; CCHEMOKINER.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 377 AA; 42992 MW; 57C476D32A897E36 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 377;
Best Local Similarity 64.3%; Pred. No. 93;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VPFVSAKSVKSLYL 14
: ||| ||| ||| |||
Db 303 LPFSVTVFVSLYL 316

RESULT 39
VQ3L CAPVK STANDARD; PRT; 381 AA.
ID VQ3L CAPVK
AC Q86917;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE G-protein coupled receptor homolog Q2/3L.
GN Name=Q2/3L;
OS Capripoxvirus (strain KS-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=10269;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266308; PubMed=7747471;
RA Cao J.X., Gershon P.D., Black D.N.;
RT "Sequence analysis of HindIII Q2 fragment of capripoxvirus reveals a
RT putative gene encoding a G-protein-coupled chemokine receptor
RT homologue."
RL Virology 209:207-212(1995).
CC -!- FUNCTION: Putative chemokine receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-----
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-----
DR EMBL; S78201; AAC32894.1; -.
DR InterPro; IPR000355; Chmkin receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 91 Extracellular (Potential).
FT TRANSMEM 92 112 1 (Potential).
FT DOMAIN 113 126 Cytoplasmic (Potential).
FT TRANSMEM 127 147 2 (Potential).
FT DOMAIN 148 165 Extracellular (Potential).
FT TRANSMEM 166 186 3 (Potential).
FT DOMAIN 187 206 Cytoplasmic (Potential).
FT TRANSMEM 207 227 4 (Potential).
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FT DOMAIN 228 251 Extracellular (Potential).
FT TRANSMEM 252 272 5 (Potential).
FT DOMAIN 273 294 Cytoplasmic (Potential).
FT TRANSMEM 295 315 6 (Potential).
FT DOMAIN 316 336 Extracellular (Potential).
FT TRANSMEM 337 357 7 (Potential).
FT DOMAIN 358 381 Cytoplasmic (Potential).
FT CARBOHYD 2 2 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 15 15 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 19 19 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 41 41 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 50 50 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 56 56 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 62 62 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 381 AA; 43421 MW; 287E8736E56C90C8 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 40
Q8JTYO PRELIMINARY; PRT; 381 AA.
AC Q8JTYO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE CC chemokine receptor-like protein.
GN Name=LW011;
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RX MEDLINE=22710395; PubMed=12827464;
RA Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Abolnik C., Lu Z.,
RA Vreede F.T., Rajjaard L.C.F., Zsak A., Viljoen G.J., Rock D.L.;
RT "Comparative sequence analysis of the South African vaccine strain and
RT two virulent field isolates of Lumpy skin disease virus.";
RL Arch. Virol. 148:1335-1356(2003).
DR EMBL; AF409138; AAN02735.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000355; Chkine receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PS00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43398 MW; AD97874F3B7COA13 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 41
Q91MZ3 PRELIMINARY; PRT; 381 AA.
ID Q91MZ3
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```
AC Q91MZ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE LSDV011 CC chemokine receptor-like protein S78201.
GN Name=LSDV011;
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RX MEDLINE=21329495; PubMed=11435593;
RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "Genome of lumpy skin disease virus.";
RL J. Virol. 75:7122-7130(2001).
DR EMBL; AF325528; AAK84972.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43407 MW; 287E81ED5E56C90C8 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
:|||||
Db 307 LPFSVTVFVSSLYL 320

RESULT 42
Q91T39 PRELIMINARY; PRT; 381 AA.
ID Q91T39
AC Q91T39;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE G-protein-coupled chemokine receptor-like protein.
OS Lumpy skin disease virus (LSDV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Capripoxvirus.
OX NCBI_TaxID=59509;
RN [1]
RX STRAIN=Neethling;
RA Stipinovich C., Vreede F.T., Kara P.D., Wallace D.B., Nel L.H.,
RA Viljoen G.J.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF336128; AAK43551.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PROSITE; PR00237; GPCRHHODOPSN.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 381 AA; 43349 MW; AD979B9EF67COA13 CRC64;

Query Match 56.9%; Score 41; DB 2; Length 381;
Best Local Similarity 64.3%; Pred. No. 94;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      1 VPFSVAKSVKSLYL 14
DB      307 LPFSVTVFVSSLYL 320

RESULT 43
ATC2 YEAST
ID ATC2 YEAST STANDARD; PRT; 1173 AA.
AC P38929;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Calcium-transporting ATPase 2 (EC 3.6.3.8) (Vacuolar Ca(2+)-ATPase).
GN Name=PMC1; OrderedLocNames=YGL006W;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
ON NCBI_TaxID=4932;
RX [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124630; PubMed=7507493; DOI=10.1083/jcb.124.3.351;
RA Cunningham K.W., Fink G.R.;
RT "Calcineurin-dependent growth control in Saccharomyces cerevisiae
RL mutants lacking PMC1, a homolog of plasma membrane Ca2+ ATPases.";
RL J. Cell Biol. 124:351-363(1994).
RX [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97313265; PubMed=9169869;
RA Tettelin H., Agostoni Carbone M.L., Albermann K., Albers K.,
RA Arroyo K., Backes U., Barrios T., Bertani I., Bjournson A.J.,
RA Brueckner M., Bruschi C.V., Carignani G., Castagnoli L., Cerdan E.,
RA Clemence M.L., Coblenz A., Coglievina M., Coissac E., Defoor E.,
RA Del Bibo S., Delius H., Delner D., de Wergifosse P., Dujon B.,
RA Durand P., Entian K.-D., Exaso P., Escribano V., Fabiani L.,
RA Farman B., Feroli F., Feuermann M., Frontali L., Garcia-Gonzalez M.,
RA Garcia-Saez M.I., Goffeau A., Guerreiro P., Hani J., Hansen M.,
RA Hebling U., Hernandez K., Heumann K., Hilger F., Hofmann B.,
RA Indge K.J., James C.M., Klima R., Koetter P., Kramer B., Kramer W.,
RA Lauquin G., Leuther H., Louis E.J., Maillier E., Marconi A.,
RA Martegani E., Mazon M.J., Mazzoni C., McReynolds A.D.K.,
RA Melchiorretto P., Mewes H.-W., Minenkova O., Mueller-Auer S.,
RA Nawrocki A., Netter P., Neu R., Nombela C., Oliver S.G., Panzeri L.,
RA Paoluzi S., Plevani P., Portetelle D., Portillo F., Potier S.,
RA Purnelle B., Rieger M., Riles L., Rinaldi T., Robben J.,
RA Rodrigues-Pousada C., Rodriguez-Beimonte E., Rodriguez-Torres A.M.,
RA Rose M., Ruzzi M., Saliola M., Sanchez-Perez M., Schaefer B.,
RA Schaefer M., Scharfe M., Schmidheini T., Schreier A., Skala J.,
RA Souciet J.-L., Steensma H.Y., Talla E., Thierry A., Vandebol M.,
RA van der Aart Q.J.M., Van Dyck L., Vanoni M., Verhasselt P., Voet M.,
RA Volckaert G., Wambutt R., Watson M.D., Weber N., Wedler E., Wedler H.,
RA Wipfli P., Wolf K., Wright L.F., Zaccaria P., Zimmermann M.,
RA Zollner A., Kleine K.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome VII.";
RL Nature 387:81-84(1997).
CC -!- FUNCTION: This magnesium-dependent enzyme catalyzes the hydrolysis
CC of ATP coupled with the transport of calcium. Transports the
CC calcium to the vacuole and participates in the control of the
CC cytosolic free calcium.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+) (Cis) = ADP + phosphate +
CC Ca(2+) (Trans).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Vacuolar.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases).
CC
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DR EMBL; U03060; AAC48919.1; -.
DR EMBL; Z72528; CAA96706.1; -.
DR PIR; S48877; S48877.
DR Geronline; 141054; -.
DR SGD; S000002974; PMC1.
DR GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
DR GO; GO:0005388; P:calcium-transporting ATPase activity; IMP.
DR GO; GO:0006874; P:calcium ion homeostasis; IMP.
DR GO; GO:0006816; P:calcium ion transport; IMP.
DR InterPro; IPR006408; ATPase-IIB_Ca.
DR InterPro; IPR001757; ATPase_EI-E2.
DR InterPro; IPR006068; Cation_ATPase_C.
DR InterPro; IPR004014; Cation_ATPase_N.
DR InterPro; IPR005834; Dehal_like_hydro.
DR InterPro; IPR008250; EI-E2_ATPase_reg.
DR Pfam; PF00689; Cation_ATPase_C; 1.
DR Pfam; PF00690; Cation_ATPase_N; 1.
DR Pfam; PF00122; EI-E2_ATPase; 1.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR00119; CATATPASE.
DR TIGRFAMs; TIGR01517; ATPase-IIB_Ca; 1.
DR TIGRFAMs; TIGR01494; ATPase_P-type; 7.
DR PROSITE; PS00154; ATPase_EI-E2; 1.
KW ATP-binding; Calcium transport; Hydrolase; Magnesium; Phosphorylation;
KW Transmembrane.
FT DOMAIN 1 114 Cytoplasmic (Potential).
FT TRANSMEM 115 139 Potential.
FT DOMAIN 140 152 Extracellular (Potential).
FT TRANSMEM 153 173 Potential.
FT DOMAIN 174 349 Cytoplasmic (Potential).
FT TRANSMEM 350 368 Potential.
FT DOMAIN 369 388 Extracellular (Potential).
FT TRANSMEM 389 409 Potential.
FT DOMAIN 410 899 Cytoplasmic (Potential).
FT TRANSMEM 900 922 Potential.
FT DOMAIN 923 929 Extracellular (Potential).
FT TRANSMEM 930 950 Potential.
FT DOMAIN 951 976 Cytoplasmic (Potential).
FT TRANSMEM 977 998 Potential.
FT DOMAIN 999 1010 Extracellular (Potential).
FT TRANSMEM 1011 1029 Potential.
FT DOMAIN 1030 1065 Cytoplasmic (Potential).
FT TRANSMEM 1066 1086 Potential.
FT DOMAIN 1087 1099 Extracellular (Potential).
FT TRANSMEM 1100 1120 Potential.
FT DOMAIN 1121 1173 Cytoplasmic (Potential).
FT ACT_SITE 445 445 4-aspartylphosphate intermediate (By
SQ SEQUENCE 1173 AA; 130860 MW; 5BD9ECFF8508F396 CRC64;
similarity).
Query Match 56.9%; Score 41; DB 1; Length 1173;
Best Local Similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 PFSVAKSVKSLYL 14
DB 1089 PFSIARQTKSMWI 1101
|||||:|:|:|:
RESULT 44
VGLM RVFVZ
ID VGLM RVFVZ STANDARD; PRT; 1197 AA.
AC P21401.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE M polypeptide precursor [Contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN Name=M;
OS Rift valley fever virus (strain ZH-548 M12) (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
ON NCBI_TaxID=11589;
RX [1]
```

RP SEQUENCE FROM N.A.
RX MEDLINE=89204917; PubMed=2705307;
RA Takehana K., Min M.K., Batties J.K., Sugiyama K., Emery V.C.,
RT Dalrymple J.M., Bishop D.H.L.;
RA "Identification of mutations in the M RNA of a candidate vaccine
strain of Rift Valley fever virus.";
RL Virology 169:452-457(1989)
CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins
CC including nonstructural protein NS-M, glycoprotein G1, and
CC glycoprotein G2.
CC
CC -1- SIMILARITY: Belongs to the phleboviruses M polyprotein family.
CC -----
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CC -----
CC EMBL; M25276; AAA47449.1; -;
CC PIR; A30183; VGVURF.
CC InterPro; IPR010826; Phlebovirus G1.
CC InterPro; IPR009878; Phlebovirus G2.
CC InterPro; IPR009879; Phlebovirus NSM.
CC Pfam; PF07243; Phlebovirus G1; 1.
CC Pfam; PF07245; Phlebovirus G2; 1.
CC Pfam; PF07246; Phlebovirus NSM; 1.
CC Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
CC Glycoprotein G1.
CC CHAIN 1 153 Nonstructural protein NS-M.
FT CHAIN 154 690 Glycoprotein G1.
FT CHAIN 691 1197 Glycoprotein G2.
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 794 794 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1077 1077 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1197 AA; 130804 MW; 860B822CD968767F CRC64;

Query Match 56.9%; Score 41; DB 1; Length 1197;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKSKKLYL 356
|||||:|:|:|:|:|:|

RESULT 45
VGLM RVFV STANDARD; PRT; 1206 AA.
AC P03518; Q86494; Q86495;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE M polyprotein precursor [Contains: Nonstructural protein NS-M;
DE Glycoprotein G1; Glycoprotein G2].
GN Name=M;
OS Rift valley fever virus (RVFV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Phlebovirus.
OC NCBI_TaxID=11588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86045943; PubMed=2998042;
RA Collett M.S., Purchio A.P., Keegan K., Frazier S., Hays W.,
RA Anderson D.K., Parker M.D., Schmaljohn C.S., Schmidt J.,
RA Dalrymple J.M.;
RA "Complete nucleotide sequence of the M RNA segment of Rift Valley
RT fever virus.";
RL Virology 144:228-245(1985).
CC -1- PTM: Specific enzymatic cleavages in vivo yield mature proteins
CC including nonstructural protein NS-M, glycoprotein G1, and
CC glycoprotein G2.

CC -1- SIMILARITY: Belongs to the phleboviruses M polyprotein family.
CC -----
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CC -----
CC EMBL; M11157; AAA47450.1; -;
CC PIR; A04110; VGVURV.
CC InterPro; IPR010826; Phlebovirus G1.
CC InterPro; IPR009878; Phlebovirus G2.
CC InterPro; IPR009879; Phlebovirus NSM.
CC Pfam; PF07243; Phlebovirus G1; 1.
CC Pfam; PF07245; Phlebovirus G2; 1.
CC Pfam; PF07246; Phlebovirus NSM; 1.
CC Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
CC Glycoprotein G1.
CC CHAIN 1 153 Nonstructural protein NS-M.
FT CHAIN 154 690 Glycoprotein G1.
FT CHAIN 691 1206 Glycoprotein G2.
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 794 794 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1035 1035 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1077 1077 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 1206 AA; 132053 MW; D2E801719285924 CRC64;

Query Match 56.9%; Score 41; DB 1; Length 1206;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSVAKSVKSLYL 14
DB 343 VPFAVFKSKKLYL 356
|||||:|:|:|:|:|:|

RESULT 46
Q6EEL1 PRELIMINARY; PRT; 3457 AA.
AC Q6EEL1;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Polyprotein.
OS Maize chlorotic dwarf virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Sequiviridae;
OC Waikavirus.
OX NCBI_TaxID=51354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Severe;
RX PubMed=15246276; DOI=10.1016/j.virol.2004.04.039;
RA Chaouch-Hamada R., Redinbaugh M.G., Gingery R.E., Willie K.,
RA Hogenhout S.A.;
RT "Accumulation of Maize chlorotic dwarf virus proteins in its plant
RT host and leafhopper vector.";
RL Virology 325:379-388(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Severe;
RA Chaouch Hamada R., Redinbaugh M.G., Gingery R.E., Willie K.,
RA Hogenhout S.A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY362551; AAR14150.1; -;
DR GO; GO:0003723; F:RNA binding; IEA.
DR GO; GO:0003724; F:RNA helicase activity; IEA.
DR GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR GO; GO:0006350; P:transcription; IEA.
DR GO; GO:0019079; P:viral genome replication; IEA.
DR InterPro; IPR001091; Met_trans_CN4.
DR InterPro; IPR009003; Pept_ser_Cys.

```
DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR001205; RNA_pol_PSD.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
DR PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
KW Polypoteine.
SQ SEQUENCE 3457 AA; 388956 MW; 3B388792325D9C5E CRC64;

Query Match          56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
Db 1386 VPFSAKTAQVL 1397

RESULT 47
O66712 PRELIMINARY; PRT; 250 AA.
AC O66712;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE Hypothetical protein aq391.
DE OrderedLocusNames=AQ_391;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RT Nature 392:353-358(1998).
DR EMBL; AE000688; AAC06677.1; -.
DR PIR; D70335; D70335.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR009051; Helical_ferredoxn.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 250 AA; 29458 MW; 46FBD1A3576A434B CRC64;

Query Match          55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSLY 13
Db 181 IPFDVGKSVKTAW 193

RESULT 48
Q93CR3 PRELIMINARY; PRT; 405 AA.
AC Q93CR3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE O-antigen polymerase.
DE Name=wzy;
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

DR InterPro; IPR000605; RNA helicase.
DR InterPro; IPR007095; RNA_pol_DS_Ps.
DR InterPro; IPR001205; RNA_pol_PSD.
DR InterPro; IPR007094; RNA_pol_PSVir.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
DR Pfam; PF00910; RNA_helicase; 1.
DR PROSITE; PS00093; N4_MTASE; UNKNOWN_1.
KW Polypoteine.
SQ SEQUENCE 3457 AA; 388956 MW; 3B388792325D9C5E CRC64;

Query Match          56.9%; Score 41; DB 2; Length 3457;
Best Local Similarity 66.7%; Pred. No. 8.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSL 12
Db 1386 VPFSAKTAQVL 1397

RESULT 47
O66712 PRELIMINARY; PRT; 250 AA.
AC O66712;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE Hypothetical protein aq391.
DE OrderedLocusNames=AQ_391;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RT Nature 392:353-358(1998).
DR EMBL; AE000688; AAC06677.1; -.
DR PIR; D70335; D70335.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR009051; Helical_ferredoxn.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW Complete proteome.
SQ SEQUENCE 250 AA; 29458 MW; 46FBD1A3576A434B CRC64;

Query Match          55.6%; Score 40; DB 2; Length 250;
Best Local Similarity 53.8%; Pred. No. 93;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 VPFSAKSVKSLY 13
Db 181 IPFDVGKSVKTAW 193

RESULT 48
Q93CR3 PRELIMINARY; PRT; 405 AA.
AC Q93CR3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE O-antigen polymerase.
DE Name=wzy;
OS Shigella boydii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21481970; PubMed=11598067;
RX DOI=10.1128/IAI.69.11.6923-6930.2001;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence analysis of four Shigella boydii O-antigen loci: implication
RT for Escherichia coli and Shigella relationships."
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF402315; AAL27351.1; -.
SQ SEQUENCE 405 AA; 46810 MW; 0F1002BF45B083FA CRC64;

Query Match          55.6%; Score 40; DB 2; Length 405;
Best Local Similarity 44.4%; Pred. No. 1.5e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 VPFSV---AKSVKSLYL 14
Db 335 IPFTIGLCGKSIKSYL 352

RESULT 49
Q9U7C8 PRELIMINARY; PRT; 413 AA.
AC Q9U7C8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Putative calmodulin-binding protein Cam-BP46.
DE Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Day D.H., Henley C., Myre M.A.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140043; AAD56609.1; -.
DR DictyBase; DB0201645; cmdb.
DR InterPro; IPR008615; FNIP.
DR Pfam; PF05725; FNIP; 6.
SQ SEQUENCE 413 AA; 46581 MW; FB1054612318FEDF CRC64;

Query Match          55.6%; Score 40; DB 2; Length 413;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PFSVAKSVKSLYL 15
Db 176 PLVIPKSLRSLFLG 189

RESULT 50
HEM1 CHLVI STANDARD; PRT; 424 AA.
AC P28462; O87494;
DT 01-DEC-1992 (Rel. 24, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glutaryl-tRNA reductase (EC 1.2.1.-) (GluTR).
GN Name=hema;
OS Chlorobium vibrioforme.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Prosthecochloris.
OX NCBI_TaxID=1098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=f. thiosulfatophilum / NCIB 8327;
RX MEDLINE=92171712; PubMed=1793335;
RA Majumdar D., Avissar Y.J., Wyche J.H., Beale S.I.;
RT "Structure and expression of the Chlorobium vibrioforme hema gene."
RL Arch. Microbiol. 156:281-289(1991).
RN [2]
```

RP REVISIONS TO C-TERMINUS.
RA Willows R.D., Beale S.I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Glutamyl-tRNA(Glu) + NADPH = glutamate-1-
CC semialdehyde + NADP(+) + tRNA(Glu).
CC -!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; first step.
CC -!- INVOLVED in chlorophyll biosynthesis.
CC -!- SIMILARITY: belongs to the glutamyl-tRNA reductase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M96364; AAC23112.1; -;
DR EMBL: AF080069; AAC61856.1; -;
DR PIR: A48359; A48359.
DR HSP: Q42843; 1B29.
DR HAMAP: MF 00087; -; 1.
DR InterPro: IPR00343; GlutR.
DR Pfam: PF00745; GlutR dimer; 1.
DR Pfam: PF05201; GlutR_N; 1.
DR Pfam: PF05200; GlutR_NAD bind; 1.
DR TIGRFAMs: TIGR01035; hemaA; 1.
DR PROSITE: PS00747; GLUTR; 1.
KW Chlorophyll biosynthesis; NADP; Oxidoreductase;
KW Porphyrin biosynthesis.
FT ACT_SITE 50 50 Nucleophile (By similarity).
FT ACT_SITE 99 99 Proton acceptor (By similarity).
SQ SEQUENCE 424 AA; 47968 MW; E65D0DBB8C1F9625 CRC64;

Query Match 55.6%; Score 40; DB 1; Length 424;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PFSVAKSVKS 11
Db |||||
145 PFSVAKVKVT 154

Search completed: July 7, 2005, 09:35:41
Job time : 60.0687 secs

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